

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 10, 2005, 17:30:38 ; Search time 218 Seconds  
(without alignments)  
8961.504 Million cell updates/sec

Title: US-10-029-020-14  
Perfect score: 14887  
Sequence: 1 MDVKERKPYRSLTRRRDAER.....ELSDSANNIHFMRQSEMGR 2769

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt\_05.80.\*  
1: uniprot\_sprot.\*  
2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	14529	97.6	2771	2 Q9WTS7_MOUSE	Q9wts7 mus musculu
2	14269	95.8	2825	2 O70465_MOUSE	O70465 mus musculu
3	12033.5	80.8	2824	2 Q9W7R3_BRARE	Q9w7r3 brachydanio
4	10227	68.7	2715	2 Q9WTS6_MOUSE	Q9wts6 mus musculu
5	10095.5	67.8	2500	2 Q4RFP1_TETNG	Q4rfp1 tetraodon n
6	9968	67.0	2192	2 Q804R1_BRARE	Q804r1 brachydanio
7	9642	64.8	2705	2 Q9W6V6_CHICK	Q9w6v6 gallus gall
8	9636	64.7	2765	2 Q5NBW7_MOUSE	Q5nbw7 mus musculu
9	9620.5	64.6	2764	2 Q5NBW8_MOUSE	Q5nbw8 mus musculu
10	9616.5	64.6	2802	2 Q9DER5_CHICK	Q9der5 gallus gall
11	9610.5	64.6	2764	2 Q9WTS5_MOUSE	Q9wts5 mus musculu
12	9607	64.5	2731	2 Q9WTS4_MOUSE	Q9wts4 mus musculu
13	9601	64.5	2765	2 Q9RIK2_RAT	Q9rik2 rattus norv
14	9584	64.4	2725	2 Q5JZ17_HUMAN	Q5jz17 homo sapien
15	9501	63.8	2725	2 Q9UKZ4_HUMAN	Q9ukz4 homo sapien
16	9303	62.5	2590	2 Q9W7R4_BRARE	Q9w7r4 brachydanio
17	9145	61.4	2346	2 Q9JLC1_MOUSE	Q9jlc1 mus musculu
18	8059.5	54.1	2144	2 Q9ULJ2_HUMAN	Q9ulu2 homo sapien
19	8025.5	53.9	2742	2 Q4SZV7_TETNG	Q4szv7 tetraodon n
20	7826.5	52.6	2319	2 Q4RT87_TETNG	Q4rt87 tetraodon n
21	7340	49.3	1399	2 Q6N022_HUMAN	Q6n022 homo sapien
22	7179	48.2	2086	2 Q4S403_TETNG	Q4s403 tetraodon n
23	7063	47.4	1828	2 Q80TD2_MOUSE	Q80td2 mus musculu
24	6774	45.5	1769	2 Q9P273_HUMAN	Q9p273 homo sapien
25	6189	41.6	1198	2 Q80TF5_MOUSE	Q80tf5 mus musculu
26	5638	37.9	1086	2 Q9P2P4_HUMAN	Q9p2p4 homo sapien
27	5614	37.7	1071	2 Q7Z3C7_HUMAN	Q7z3c7 homo sapien
28	4670.5	31.4	1405	2 Q4SZV6_TETNG	Q4szv6 tetraodon n
29	4528.5	30.4	1465	2 Q4RTA7_TETNG	Q4rta7 tetraodon n
30	3979.5	26.7	1045	2 Q9NVW1_HUMAN	Q9nvw1 homo sapien
31	3918.5	26.3	2594	2 Q7QK12_ANOGA	Q7qk12 anopheles g

32	3854	25.9	730	2 Q96MS6_HUMAN	Q96ms6 homo sapien
33	3822	25.7	2731	2 O61307_DROME	O61307 drosophila
34	3820.5	25.7	2731	2 Q9VNU6_DROME	Q9vnu6 drosophila
35	3813	25.6	2731	2 O18366_DROME	O18366 drosophila
36	3804.5	25.6	2515	2 Q24551_DROME	Q24551 drosophila
37	3753	25.2	991	2 Q8CAT1_MOUSE	Q8cat1 mus musculu
38	3730	25.1	964	2 Q9NV77_HUMAN	Q9nv77 homo sapien
39	3517	23.6	3004	2 Q24550_DROME	Q24550 drosophila
40	3515	23.6	3004	2 Q9VYN8_DROME	Q9vyn8 drosophila
41	3398.5	22.8	930	2 Q9JLC0_MOUSE	Q9jlc0 mus musculu
42	3175.5	21.3	1426	2 Q4RTA6_TETNG	Q4rta6 tetraodon n
43	3111.5	20.9	849	2 Q9NT68_HUMAN	Q9nt68 homo sapien
44	2378	16.0	831	2 Q9PU49_CHICK	Q9pu49 gallus gall
45	2351	15.8	625	2 Q96SY2_HUMAN	Q96sy2 homo sapien

ALIGNMENTS

RESULT 1  
Q9WTS7\_MOUSE PRELIMINARY; PRT; 2771 AA.  
AC Q9WTS7;  
DT 01-NOV-1999 (Tremblrel. 12, Created)  
DT 01-NOV-1999 (Tremblrel. 12, Last sequence update)  
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)  
DE Ten-m4.  
GN Name=Odz4; Synonyms=ten-m4;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=Balb/c; TISSUE=Brain;  
RA Oohashi.T., Zhou X., Feng K., Richter B., Moergelin M., Perez M.T.,  
RA Su W., Chiquet-Ehrismann R., Rauch U., Faessler R.;  
RT "Mouse Ten-m/Odz is a new family of dimeric type II transmembrane  
proteins expressed in many tissues."  
RL J\_Cell\_Biol. 0:0-0(1999).  
DR EMBL; AB025413; BAA77399.1; -; mRNA.  
DR HSSP; P16109; 1FSB.  
DR MGI; MGI:2447063; Odz4.  
DR InterPro; IPR000742; EGF\_2.  
DR InterPro; IPR006209; EGF\_like.  
DR InterPro; IPR006210; IEGF.  
DR InterPro; IPR001258; NHL.  
DR InterPro; IPR009471; Ten\_N.  
DR InterPro; IPR006530; YD.  
DR Pfam; PF01436; NHL; 6.  
DR Pfam; PF05593; RHS\_repeat; 5.  
DR Pfam; PF06484; Ten\_N; 1.  
DR SMART; SM00181; EGF; 7.  
DR TIGRFAMs; TIGR01643; YD\_repeat\_2x; 5.  
DR PROSITE; PS00022; EGF\_1; UNKNOWN\_8.  
DR PROSITE; PS01186; EGF\_2; 7.  
DR PROSITE; PS50026; EGF\_3; 5.  
SQ SEQUENCE 2771 AA; 308499 MW; 1492E1EE1A0DBF0C CRC64;

Query Match 97.6%; Score 14529; DB 2; Length 2771;  
Best Local Similarity 97.0%; Pred. No. 0;  
Matches 2688; Conservative 40; Mismatches 41; Indels 2; Gaps 1;

Qy	1	MDVKERKPYRSLTRRRDAERRYSSADSEEGKAPQKYSYSSSETLKAYDQDARLAYGSRV	60
Db	1	MDVKERKPYRSLTRRRDAERRYSSADSEEGKAPQKYSYSSSETLKAYDQDARLAYGSRV	60
Qy	61	KDIVPQEAEEFCRTGANFTLRELGLEEVTPPHGTLVYRTDIGLPQCGYSMGAGSDADMEAD	120
Db	61	KDMVPQEAEEFCRTGTNTFTLRELGLGEMTPPHGTLVYRTDIGLPQCGYSMGAGSDADLEAD	120
Qy	121	TVLSPEHPVRLWGRSTRSGRSSCLSSRANSNLTLTDTEHENTETDHPGGLQNHLRTPP	180

Db 121 TVLSPHPVRLWGRSTRGRSSCLSSRANSNLTLTDTEHENTETDHPSSLQNHPRLRTPP 180  
Qy 181 PPLSHAHTPNQHHAASINSLNRGNFTPRSNPSPAPTDHSLSGEPPAGGAQEPAHAQENWL 240  
Db 181 PPLPHAHTPNQHHAASINSLNRGNFTPRSNPSPAPTDHSLSGEPPAGSAQEPTHAQDNWL 240  
Qy 241 LNSNTPLETRNLGKOPFLGTLQDNLIEMDILGASRRHDGAYSDBGHFLFKPGGTSPLFCTTS 300  
Db 241 LNSNTPLETRNLGKOPFLGTLQDNLIEMDILSASRRHDGAYSDBGHFLFKPGGTSPLFCTTS 300  
Qy 301 PGYPLTSSTVSYSPPPRPLPRSTFARPAFNLKKPSKYCNWKCAALSAIVISATLVILLAYF 360  
Db 301 PGYPLTSSTVSYSPPPRPLPRSTFARPAFNLKKPSKYCNWKCAALSAILISATLVILLAYF 360  
Qy 361 VAMHLFGLNWHLQPMEG--QMYEITEDTASSWPVPTDVSLYPSGGTGLETPDRKGKGTTE 418  
Db 361 VAMHLFGLNWHLQPMEGQMOMEYITEDTASSWPVPTDVSLYPSGGTGLETPDRKGKGAAE 420  
Qy 419 GKPSFPPEDSFIDSGEIDVGRASQKIPPGTFWRSQVFDHPVHLKFNVSGLKAAALVGI 478  
Db 421 GKPSLFPPEDSFIDSGEIDVGRASQKIPPGTFWRSQVFDHPVHLKFNVSGLKAAALVGI 480  
Qy 479 YGRKGLPSSHTQDFVELLDGRRLLTQEARSLGTPRQSRGTVPSSSHETGFIQYLDSGI 538  
Db 481 YGRKGLPSSHTQDFVELLDGRRLLTQEARSLGTPRQSRGVPVPSSSHETGFIQYLDSGI 540  
Qy 539 WHLAFYNDGKESEVVSFLTTAIESVDNCPNSCYNGGDCISGTCHCFGLGFLGPDCCGRASCP 598  
Db 541 WHLAFYNDGKESEVVSFLTTAIESVDNCPNSCYNGGDCISGTCHCFGLGFLGPDCCGRASCP 600  
Qy 599 VLCSGNGQYMKGRCLCHSGWKGAECDVPTNQCIDVACSNHGTICITGTICINPGYKGESCE 658  
Db 601 VLCSGNGQYMKGRCLCHSGWKGAECDVPTNQCIDVACSSHGTICIMGTICINPGYKGESCE 660  
Qy 659 EVDCMDPTCSGRGVCVRGECHCFVWGWTNCETPRATCLDQCSGHTFLPDTGLCSCDPS 718  
Db 661 EVDCMDPTCSSRSGVCVRGECHCSVWGWTNCETPRATCLDQCSGHTFLPDTGLCNC DPS 720  
Qy 719 WTGHDCSIBICAADCGHGVCVGGTCRCEDGWMGAACDQACHPRCAEHGTCRDGKCECS 778  
Db 721 WTGHDCSIBICAADCGHGVCVGGTCRCEDGWMGAACDQACHPRCAEHGTCRDGKCECS 780  
Qy 779 PGWNGEHCTIAHYLDRVWKEGCPGLCNGNGRCTLDLNGWHCVCOLGWRGAGCDTSMETAC 838  
Db 781 PGWNGEHCTIAHYLDRVWKEGCPGLCNGNGRCTLDLNGWHCVCOLGWRGTGCDTSMETGC 840  
Qy 839 GDSKDNDDGLVDCMDPDCCLQPLCHINPLCLGSPNPLDIIQETQVPVSQQNLHSSFYDRI 898  
Db 841 GDGKDNDDGLVDCMDPDCCLQPLCHVNPLCLGSPDPLDIIQETQAPVSQQNLNPFYDRI 900  
Qy 899 KFLVGRDSTHIIIPGENPFDGGHACVIRGQVMTSDGTPLVGVNISFVNNPLFGYTTISRQDG 958  
Db 901 KFLVGRDSTHSIPGENPFDGGHACVIRGQVMTSDGTPLVGVNISFINNPLFGYTTISRQDG 960  
Qy 959 SFDLVTNGGISIIILRFERAPFITQEHTLWLPWDRFFVMETIIMRHEENEIPSCDLSNFAR 1018  
Db 961 SFDLVTNGGISIIILRFERAPFITQEHTLWLPWDRFFVMETIIMRHEENEIPSCDLSNFAR 1020  
Qy 1019 PNPVSPSPILTSFASSCAEKGPVPEIQALQEEIISGCKMRLSYLSRTPGYKSVLRIS 1078  
Db 1021 PNPVSPSPILTSFASSCAEKGPVPEIQALQEEIIVIA GCKMRLSYLSRTPGYKSVLRIS 1080  
Qy 1079 LTHPTIPFNLMKVHLMVAVEGRLFRKWFAAAPDLSYYFIWDKTDVYNQKVFGLSAEFVSU 1138  
Db 1081 LTHPTIPFNLMKVHLMVAVEGRLFRKWFAAAPDLSYYFIWDKTDVYNQKVFGSEAFVSU 1140  
Qy 1139 GYEYESCPDILILWEKRTTVLQGYEIDASKLGGWSLDKHHALNIQSGILHKGNGENQFVSQ 1198  
Db 1141 GYEYESCPDILILWEKRTAVLQGYEIDASKLGGWSLDKHHALNIQSGILHKGNGENQFVSQ 1200  
Qy 1199 QPPVIGSIMGNRRRSISCPSCNGLADGNKLLAPVALTCGSDGSLYVGDFNYIRRIFFPSG 1258

Db 1201 QPPVIGSIMGNRRRSISCPSCNGLADGNKLLAPVALTCGSDGSLYVGDFNYIRRIFFPSG 1260  
Qy 1259 NVTNILELRNKDFRHSHPAHKYYLATDPMGSAVFLSDSNRRRVFKIKSTVVVKDLVKNS 1318  
Db 1261 NVTNILEMRNKDFRHSHPAHKYYLATDPMGSAVFLSDTNSRRVFKVKSTTVVKDLVKNS 1320  
Qy 1319 EVVAGTGDOCLPFDDTRCGDGGKATEATLTNPRGITVDKFGLIYFVDGTMIRRIDQNGII 1378  
Db 1321 EVVAGTGDOCLPFDDTRCGDGGKATEATLTNPRGITVDKFGLIYFVDGTMIRRVQDNGII 1380  
Qy 1379 STLLGSNDLTSARPLSCDSVMDISQVRLEWPTDLAINPMDNSLYVLDNNVVLQISENHQV 1438  
Db 1381 STLLGSNDLTSARPLSCDSVMEISQVRLEWPTDLAINPMDNSLYVLDNNVVLQISENHQV 1440  
Qy 1439 RIVAGRPMHCQVPGIDHFLLSKVAIHATLESATALAVSHNGVLYIAETDEKKINRIRQVT 1498  
Db 1441 RIVAGRPMHCQVPGIDHFLLSKVAIHATLESATALAVSHNGVLYIAETDEKKINRIRQVT 1500  
Qy 1499 TSGEISLVAGAPSGCDCKNDANCDGSGDDGYAKDAKLNTPSSLAVCADGELYVADLJNI 1558  
Db 1501 TSGEISLVAGAPSGCDCKNDANCDGSGDDGYAKDAKLNTPSSLAVCADGELYVADLJNI 1560  
Qy 1559 RIRFIRKNKPFNTQNMVELSSPIDQELYLFDTTGKHYLQSLPTGDYLYNFYTGDDGI 1618  
Db 1561 RIRFIRKNKPFNTQNMVELSSPIDQELYLFDTSGKHYLQSLPTGDYLYNFYTGDDGI 1620  
Qy 1619 TLITDNGNMVNVRDSTGMPLWLVPDQGVYVWTMGTSNLSALKSVTTQGHELAMMTYHGN 1678  
Db 1621 THITDNGNMVNVRDSTGMPLWLVPDQGVYVWTMGTSNLSALRSVTTQGHELAMMTYHGN 1680  
Qy 1679 SGLLATKSNENGWTTFYEYDSFGRLTNVTFTPTGOVSSFRSDTSSVHVQVETSSKDDVTI 1738  
Db 1681 SGLLATKSNENGWTTFYEYDSFGRLTNVTFTPTGOVSSFRSDTSSVHVQVETSSKDDVTI 1740  
Qy 1739 TTNLSASGAFYTLQDQVRNSYYIGADGSLRLLLANGMEVALQTEPHLLAGTVNPTVGKR 1798  
Db 1741 TTNLSASGAFYTLQDQVRNSYYIGADGSLRLLLANGMEVALQTEPHLLAGTVNPTVGKR 1800  
Qy 1799 NVTLPIDNGLNLVEWRORKEQARGQVTVFGRRRLRVHNRNLLSLDFORVTRTEKIYDDHRK 1858  
Db 1801 NVTLPIDNGLNLVEWRORKEQARGQVTVFGRRRLRVHNRNLLSLDFRVRTREKIYDDHRK 1860  
Qy 1859 FTLRILYDQAGRPSLWSPSSRLGNVNTYSPGGYIAGIQGIMSERMEYDQAGRITSRIF 1918  
Db 1861 FTLRILYDQAGRPSLWSPSSRLGNVNTYSPGGHIAGIQGIMSERMEYDQAGRITSRIF 1920  
Qy 1919 ADGKTWSYTYLEKSMVLLHLSORQYIFEFDKNDRLSSVTMPNVARQTLETIRSVGYRNI 1978  
Db 1921 ADGKMWSYTYLEKSMVLLHLSORQYIFEFDKNDRLSSVTMPNVARQTLETIRSVGYRNI 1980  
Qy 1979 YQPPEGNASVIQDFTEDGHLLHTFYLGTGRRRVYKYGKLSKLAETLYDTTKVSFTYDETA 2038  
Db 1981 YQPPEGNASVIQDFTEDGHLLHTFYLGTGRRRVYKYGKLSKLAETLYDTTKVSFTYDETA 2040  
Qy 2039 GMLKTINLQNEGFTCTIRYRQIGPLIDRQIFRFTTEEGMVNARFDYNDNSFRVTSMQAVI 2098  
Db 2041 GMLKTVNLQNEGFTCTIRYRQIGPLIDRQIFRFTTEEGMVNARFDYNDNSFRVTSMQAVI 2100  
Qy 2099 NETPLPIDLYRYDDVSGKTEQFGKFGVIYDINQIIITTAVMTHTKHFDAYGRMKEVQYEI 2158  
Db 2101 NETPLPIDLYRYDDVSGKTEQFGKFGVIYDINQIIITTAVMTHTKHFDAYGRMKEVQYEI 2160  
Qy 2159 FRSLMYWMTVOYDNMGRVVKKELKVGPYANTTRYSYEYDADGQLQTVSINDKPLWRYSD 2218  
Db 2161 FRSLMYWMTVOYDNMGRVVKKELKVGPYANTTRYSYEYDADGQLQTVSINDKPLWRYSD 2220  
Qy 2219 LNGNLHLLSPGNSARLTPLRYDIRDRITRLGDVQYKMDDEDGFLRQRGGDIFEYNSAGLLI 2278  
Db 2221 LNGNLHLLSPGNSARLTPLRYDLDRDRIITRLGDVQYKMDDEDGFLRQRGGDVEYNSAGLLI 2280  
Qy 2279 KAYNRAGSWSVRYRYDGLGRRVSSKSSSHHLQFFYADLTNPTKVTHLYNHSSSEITSLY 2338  
Db 2281 KAYNRASGWSVRYRYDGLGRRVSSKSSSHHLQFFYADLTNPTKVTHLYNHSSSEITSLY 2340



QY 2339 YDLQGHLFAMELSSGDEFYIACDNIGTPTLAVFSGTGLMIKQILYATAYGEIYMDTNPNFQI 2398  
Db 2341 YDLQGHLFAMELSSGDEFYIACDNIGTPTLAVFSGTGLMIKQILYATAYGEIYMDTNPNFQI 2400  
QY 2399 IIGYHGGLYDPLTKLVHMGRRDYDVLGRWTSPPDHELVKHLSSSNVMPFNLYMFKNNPI 2458  
Db 2401 IIGYHGGLYDPLTKLVHMGRRDYDVLGRWTSPPDHELVKHLSSSNVMPFNLYMFKNNPI 2460  
QY 2459 SNSQDIKCFMTDVNSWLLTFGFLHNVIPGYPKPMDMAMEPSYELIHTQMKTQEWDSKS 2518  
Db 2461 SNSQDIKCFMTDVNSWLLTFGFLHNVIPGYPKPMDTAMEPSYELVHTQMKTQEWDSKS 2520  
QY 2519 ILGVQCEVQQLKAFVTLERFDQLYGSTITSCQQAQPKTKKFASSGSVFGKGVKFAKDG 2578  
Db 2521 ILGVQCEVQQLKAFVTLERFDQLYGSTITSCQQAQPKTKKFASSGSIFGKGVKFAKDG 2580  
QY 2579 VTIDIISVANEDGRRVAAILNHAHYLENLHFTIDGVDTYFVKPGPSEGDLAII LSGGR 2638  
Db 2581 VTIDIISVANEDGRRVAAILNHAHYLENLHFTIDGVDTYFVKPGPSEGDLAII LSGGR 2640  
QY 2639 RTLENGVNVTVSQINTVLNGRTRRYTDIQLQYGALCLNTRYGTTLDEEKARVLELARQ 2698  
Db 2641 RTLENGVNVTVSQINTVLNGRTRRYTDIQLQYRALCLNTRYGTTVDEEKVRVLELARQ 2700  
QY 2699 VRQAWAREQORLREGEEGLRAWTEGEKQVLSTGRVQYDGFVVISVEQYPELSDSANNI 2758  
Db 2701 VRQAWAREQORLREGEEGLRAWTDGEKQVLNTRGVQYDGFVTSVEQYPELSDSANNI 2760  
QY 2759 HPMRQSEMGR 2769  
Db 2761 HPMRQSEMGR 2771

RESULT 2  
O70465 MOUSE  
ID O70465 MOUSE PRELIMINARY; PRT; 2825 AA.  
AC O70465;  
DT 01-AUG-1998 (TrEMBLrel. 07, Created)  
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE DOC4.  
GN Name=Odz4; Synonyms=Doc4;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=NIH/Swiss;  
RX MEDLINE=98315054; PubMed=9649432; DOI=10.1093/emboj/17.13.3619;  
RA Wang X.-Z., Kuroda M., Sok J., Batchvarova N., Kimmel R., Chung P.,  
RA Zinszner H., Ron D.;  
RT "Identification of novel stress-induced genes downstream of chop.";  
RL EMBO J. 17:3619-3630(1998).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=NIH/Swiss;  
RA Wang X.-Z., Ron D.;  
RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF059485; AAC31807.1; -; mRNA.  
DR PIR; T14271; T14271.  
DR HSSP; P16109; 1FSB.  
DR Ensembl; ENSMUSG00000048078; Mus musculus.  
DR MGI; MGI:2447063; Odz4.  
DR InterPro; IPR000742; EGF 2.  
DR InterPro; IPR006209; EGF-like.  
DR InterPro; IPR006210; IEGF.  
DR InterPro; IPR01258; NHL.  
DR InterPro; IPR009471; Ten\_N.  
DR InterPro; IPR006530; YD.  
DR Pfam; PF01436; NHL; 6.

DR Pfam; PF05593; RHS\_repeat; 5.  
DR Pfam; PF06484; Ten\_N; 1.  
DR SMART; SM00181; EGF; 7.  
DR TIGRFAMs; TIGR01643; YD\_repeat\_2x; 5.  
DR PROSITE; PS00022; EGF\_1; UNKNOWN\_8.  
DR PROSITE; PS01186; EGF\_2; 7.  
DR PROSITE; PS00026; EGF\_3; 4.  
SQ SEQUENCE 2825 AA; 313485 MW; A120D98080886032 CRC64;  
  
Query Match 95.8%; Score 14269; DB 2; Length 2825;  
Best Local Similarity 93.4%; Pred. No. 0;  
Matches 2654; Conservative 47; Mismatches 52; Indels 88; Gaps 4;  
  
QY 1 MDVKERKPYRSLTRRDAERRYTSSSADSEEGKAPQKSYSSSETLKAYDQDARLAYGSRV 60  
Db 1 MDVKERKPYRSLTRRDAERRYTSSSADSEEGKAPQKSYSSSETLKAYDQDARLAYGSRV 60  
QY 61 KDIVPQEAEEFCRTGANFTLRELGLEEVTPPHGFLYRTDIGLPQCGYSMGAGSDADMEAD 120  
Db 61 KDMVPQEAEEFCRTGNFTLRELGLGEMTPPHGFLYRTDIGLPQCGYSMGAGSDADLEAD 120  
QY 121 TVLSPEHPVRLWGRSTRSGRSSCLSSRANSNLTLTDTEHENTET-----DHPGGL 170  
Db 121 TVLSPEHPVRLWGRSTRSGRSSCLSSRANSNLTLTDTEHENTETGAPLHCSSASSTPIEQ 180  
QY 165 -----DHPGGL 170  
Db 181 SPSPPPPPANESQRRLLGNQVAQPTPDSDEEEFVNSFLVKSGSASGLVAANDHPSSL 240  
QY 171 QNHARLRTPPPLSHAHTPNQHHAAASINSLNRGNFTPRSNPSPAPTDHLSLGEPPAGGAQ 230  
Db 241 QNHRLRTPPPLPHAHTPNQHHAAASINSLNRGNFTPRSNPSPAPTDHLSLGEPPAGSAQ 300  
QY 231 EPAHAQENWLLNSNIPLETRNLGKQPFGLTQDNLIEMDILGASRHDGAYS DGHFLFKPG 290  
Db 301 EPTHAQDNWVLNSKIPVETRNLGKQPFGLTQDNLIEMDIFSASRRDGAYS DGHFFFKPG 360  
QY 291 GTSPLFCTTSPGYPLTSTVYSPPRPLPRSTFARPAFNLKPKSKYCNWKCAALS AIVIS 350  
Db 361 GTSPLFCTTSPGYPLTSTVYSPPRPLPRSTFARPAFNLKPKSKYCNWKCAALS AILIS 420  
QY 351 ATLVI LLAYFVAMHLFGLNWHLQPMEG--QMYEITEDTASSWPVPTDVSLYPSGGTGLET 408  
Db 421 ATLVI LLAYFVAMHLFGLNWHLQPMEGQMOMEITEDTASSWPVPTDVSLYPSGGTGLET 480  
QY 409 PDRKGKGTTEGKPSFEPPEDSFIDSGEIDVGRRASQKIPPGTFWRSQVFI DHPVHLKFN 468  
Db 481 PDRKGKGAEGKPSLFPEDSFIDSGEIDVGRRASQKIPPGTFWRSQVFI DHPVHLKFN 540  
QY 469 SLGKAALVGIYGRKGLPPSHTQDFVELLDGRRLLTQEARSLGTPRQSRGTVPSSSHET 528  
Db 541 SLGKAALVGIYGRKGLPPSHTQDLDFVELLDGRRLLTQEARSLGTPRQSRGTVPSSSHET 600  
QY 529 GFIQYLDSGIWHLAFYNDGKSEVWSFLT TTAIESVDNCPSNCYGNGDCISGTC HCFILGFL 588  
Db 601 GFIQYLDSGIWHLAFYNDGKSEVWSFLT TTAIESVDNCPSNCYGNGDCISGTC HCFILGFL 660  
QY 589 GPDGGRASCPVLCSGNGQYMKGRCLCHSGWKGAEC DVPTNQCIDVACSNHGTCTGTCTIC 648  
Db 661 GPDGGRASCPVLCSGNGQYMKGRCLCHSGWKGAEC DVPTNQCIDVACSSHGTCTIMGTCTIC 720  
QY 649 NPGYKGESCEEVDCHMDPTCSGRGV CVRGECHCFVWGWTNCETPRATCLDQC SGHGTFLP 708  
Db 721 NPGYKGESCEEVDCHMDPTCSSRGV CVRGECHCSVGWGTNCETPRATCLDQC SGHGTFLP 780  
QY 709 DTGLCSDPSWTGHDCSI EICAADCGGHGV CVVGTGTCRCE DGWMAACDQ RACHPRCAEHG 768  
Db 781 DTGLCNCDPSTGHDCSI EICAADCGGHGV CVVGTGTCRCE DGWMAACDQ RACHPRCAEHG 840  
QY 769 TCRDGKCECSPGWNGEHTCTIAHYLD R VVKEGCPGLCNGNGRCTL DLNGWHCV CQLGWRGA 828  
Db 841 TCRDGKCECTPGWNGEHTCTI-----EGCPGLCNGNGRCTL DLNGWHCV CQLGWRGT 891







Db	1662	LYNFTYSGDLSSITDKNKNRVSIRRDSTGLPLWLMGPDGQTFWFTMGTNNAKSVAAQ	1721
Qy	1667	GHELAMTYHGNSGLLATKSNENGWTFPYEYDSFGRLTNVFTPTGQVSSFRSDTSSVHV	1726
Db	1722	GQEIAMTYHGSSGLLATKSNEDGWSTFYEDNYGRLTNVFTPTGRVSSYRTDSDSTVRV	1781
Qy	1727	QVETSSKDDVTITTNLSASGAFYTLLOQOVNRNSYYIGADGSLRLLLANGMEVALQTEPHL	1786
Db	1782	QTEGSKNEDITVTTNLSASGTFYTLMQDVKNSSYYIGDGLSLRLVLANGMEVSLHTEPHL	1841
Qy	1787	LACTVNPVTGKRNVTLPIDNGLNLVEWRQRKEAQGVTVFGRRRLRVHNRNLLSLDFDRV	1846
Db	1842	LSGTVNPTISKRNVTLPIDNGLNLVEWRQRKEAQGVTVYGRRLRVHNRNLLSMDFDRV	1901
Qy	1847	TRTEKIYDDHRKFTLRILYDQAGRPSLWSPSSRLNGVNVTVSPGGYIAGIQRGIMSERME	1906
Db	1902	TRTEKVYDDHRKFTLRIHVDHAGRPTLWAPSSRLNGVNVTVSPGGHIAGIQRGTMSVRME	1961
Qy	1907	YDQAGRITSRIFADGKTWSYTYLEKSMVLLLLHSQRQYIFEFDKNDRLSSVTMPNVARQTL	1966
Db	1962	YDQNGRITSKIFADGKWSYTYLEKSMVLLLYSQRQYIFEFDKNDRLSSVTMPNVARQTL	2021
Qy	1967	ETIRSVGYRNIYQPPEGNASVIOQFTEDGHLHTFYLGTGRRVIYKYGKLSKLAETLYD	2026
Db	2022	ETTRSIGYRNTYRPEGNATVLQDSEDLQLLQTIHQGTGRRVIYKYGKLSRLLEIYD	2081
Qy	2027	TTKVSFTYDETAGMLKTINLQNEGETCTIRYQIGPLIDRQIFRFTTEEGMVNAREFDNYD	2086
Db	2082	TTTRIAFSYDESAGMLKTVGLQSEGFACITIRYQIGPLIDRQIFRFSSEGMVNAREFDNYD	2141
Qy	2087	NSFRVTSMQAVINETPLPIDLYRYDDVSGKTEQFGKFGVIYDINQIITTAVMTHTKHFD	2146
Db	2142	NSFRVTSMQAVINETPLPIDLYRYDDVSGKTEQFGKFGVIYDINQIITTAVMTHTKHFD	2201
Qy	2147	AYGRMKEVQYEIFRSLMYMTVQYDNMGRVVKKELKVGYPVANTTRYSEYDADGQLQTVS	2206
Db	2202	AYGRVKEVQYEIFRSLMYMMVQDFNMGRVVAKELKVGYPVANTTRYAYEYDADGQLQVVS	2261
Qy	2207	INDKPLWRYSYDLNGNLHLLSPGNSARLTPLRYDIRDRITRLGDVQYKMDDEDGFLRQGG	2266
Db	2262	INDKPLWRYSYDLNGNLHLLSPGNSARLTPLRYDIRDRITRLGDVQYRLDEDEDGFLRQGN	2321
Qy	2267	DIFEYNSAGLLIKAYNRAGSWSVRYRYDGLGRRVSSKSSHHLQFFYADLTNPTKVTHL	2326
Db	2322	DFFEYNSAGLLVKTYNKVGWTKYRYDGLGRRVSSRSTQGHHLQFFYADLSSPTRVTHM	2381
Qy	2327	YNHSSSEITSLYDYLQHLFAMELSSGDEFYIACDNIGTPLAVFSGTGLMIKQILTYAYG	2386
Db	2382	YNHSSSEITSLYDYLQHLFAMELSSGDEFYVACDNIGTPLAVFSGAGLMIKQILHTAFG	2441
Qy	2387	EIYMDTNPNFQIIGYHGGLYDPLTKLVHMGRRDYDVLAGRWTSPDHCLKHLSSSNVMP	2446
Db	2442	EVYLDSPFSQLVIGYQGGLYEPLTKLVHMGRRDYDVLAGRWTTPDHDIRKRLNSDNIVP	2501
Qy	2447	FNLYMFKNNPISNSQDIKCFMTDVNSWLLTTFGQLHNVTIPGYPKPDMDAMEPSYELIHT	2506
Db	2502	FNLYMFKNNPLSNSQETKCYMTDVNSWLVTFGQLYNVIPGYRKPVTDAMEPSYELVHT	2561
Qy	2507	QMKTOEWDNSKSILGVQCEVQKQKAFVTLERFDQLYGSTITSCQAQPKTKKFASSGVF	2566
Db	2562	QIKTOEWDSTKSVLGVQCEVQRLKSFVRLERFGQIYSASDSGCPPTPLHTLTFATGTSLF	2621
Qy	2567	GKGVKFAKDGRTVTDIISVANEDGRRVAAILNHAHYLENLHFTIDGVDTHYFVKGPSE	2626
Db	2622	GKGVKVAIREGRVEADIISLANEDGRRIAVALDKASYLQDLHFTIAGLDTHYFVKSGLVE	2681
Qy	2627	GDLAJLGLSGRRRTLENGVNVTVSQINTVLNGRTRRYTDIQLQYGALCLNTRYGTTLDEE	2686
Db	2682	GDLSLLGMTVGQRTLETGVNVTVSQVMVLGRRSRRTIDIQMQYGTLSLNVRYGSSVDEE	2741
Qy	2687	KARVLELARQAVRQAWAREQQRLREGEGLRAWTEGEKQQVLSTGRVQGYDGFVISVE	2746

Db	2742	KRVVLELARQAVATAWAHERHRLRQEGEGSRAWTDGERQQLLSSGRVQGYEGFYIVSVD	2801
Qy	2747	QYPELSDSANNIHFMROSEMGRR	2769
Db	2802	QFPELTDNINNHFWRQTEMGRR	2824
RESULT 4			
Q9WTS6_MOUSE			
ID	Q9WTS6_MOUSE PRELIMINARY;	PRT;	2715 AA.
AC	Q9WTS6;		
DT	01-NOV-1999 (TrEMBLrel. 12, Created)		
DT	01-NOV-1999 (TrEMBLrel. 12, Last sequence update)		
DT	01-MAR-2004 (TrEMBLrel. 26, Last annotation update)		
DE	Ten-m3.		
GN	Name=Odz3; Synonyms=ten-m3;		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;		
OC	Muridae; Murinae; Mus.		
OX	NCBI_TaxID=10090;		
RN	[1]		
RP	NUCLEOTIDE SEQUENCE.		
RC	STRAIN=Balb/c; TISSUE=Brain;		
RA	Oohashi T., Zhou X., Feng K., Richter B., Moergelin M., Perez M.T.,		
RA	Su W., Chiquet-Ehrismann R., Rauch U., Faessler R.;		
RT	"Mouse Ten-m/Odz is a new family of dimeric type II transmembrane		
RT	proteins expressed in many tissues.";		
RL	J. Cell Biol. 0:0-0(1999).		
DR	EMBL; AB025412; BAA77398.1; -; mRNA.		
DR	HSSP; P00750; 1TPG.		
DR	Ensembl; ENSMUSG00000031561; Mus musculus.		
DR	MGI; MGI:1345183; Odz3.		
DR	InterPro; IPR000742; EGF_2.		
DR	InterPro; IPR006209; EGF_like.		
DR	InterPro; IPR006210; IEGF.		
DR	InterPro; IPR001258; NHL.		
DR	InterPro; IPR009471; Ten_N.		
DR	InterPro; IPR006530; YD.		
DR	Pfam; PF00008; EGF; 2.		
DR	Pfam; PF01436; NHL; 6.		
DR	Pfam; PF05593; RHS_repeat; 6.		
DR	Pfam; PF06484; Ten_N; 1.		
DR	SMART; SM00181; EGF; 7.		
DR	TIGRFAMS; TIGR01643; YD_repeat_2x; 5.		
DR	PROSITE; PS00022; EGF_1; 8.		
DR	PROSITE; PS01186; EGF_2; 7.		
DR	PROSITE; PS50026; EGF_3; 5.		
SQ	SEQUENCE 2715 AA; 303063 MW; 598F46A77334C2E1 CRC64;		
Query Match 68.7%; Score 10227; DB 2; Length 2715;			
Best Local Similarity 66.7%; Pred. No. 0;			
Matches 1864; Conservative 370; Mismatches 457; Indels 102; Gaps 19;			
Qy	1	MDVKERPYSRLTR-RRDAERRYTSSSADSEEGKAP-QKSYSSSETLKAYDQD-ARLAYG	57
Db	1	MDVKERPYSRLTKSRREKERRYTNSSADNEECRVPTQKSYSSSETLKAFDHYSRLLYG	60
Qy	58	SRVKDIVPQEAEEFCRTGANFTLRELGLEEYTPPHGTLYRTDIGLPQCYSMGAGSDADM	117
Db	61	NRVKDLVHREADEYTRQGNFTLRQLGVCEATRRRGVAFCAEMGLPHRGYSISAGSDADT	120
Qy	118	EADTVLSPHEPVLWGRSTRSGRSSCLSSRANSNLTLTDTHEH--TETDHPGGLQNHA	174
Db	121	ENEAVMSPEHAMRLWGRGVKSGRSSCLSSRSNSALTTLTDTHEHNSDSESEQPSNNPGQP	180
Qy	175	RLRTPPPPLSHAHTPNQHHAAASINSLNRGNFTPRSNPSPAPTDHLSLGEPPAGQAQ----	230
Db	181	TLQPLPP--SHKQHPAQHH-PSITSLNRNSLTNRRNQSPAP-----PAALPAELQTT	229
Qy	231	-EPAHAQENWLLNSNIPLETNRLGKQPFGLTQDNLIEMDILGASRHDGAYS DGHFLFKP	289
Db	230	PESVOLQDSWVLGSNVPLESR-----HFLFKT	256

Qy	290	G-GTSPLEFCTTSPGYPLTSSTVYSPPPRPLPRSTFARPAFNLKKPSKYCNWKCAALSAIV	348	Qy	1366	GTMIRRIDQNGIISTLLGSNDLTSARPLSCDSVMDISQVRLEWPTDLAINPMDNSLYVLD	1425
Db	257	GTGTTPLFSTATPGYTMASGSVYSPPTRPLPRNTLSRSAFKFKSSKYCSWRECTALCAVG	316	Db	1318	GTMIRKVDQNGIISTLLGSNDLTSARPLTCDTSMHISQVRLEWPTDLAINPMDNSIYVLD	1377
Qy	349	ISATLVILLAYFVAMHLFGLNWHLOPMEGQMYE---ITEDTASSWPVPPTDVSLYPSGGTG	405	Qy	1426	NNVLQISENHQVRIVAGRPMHCQVPGIDHFLLSKVAIHATLESATALAVSHNGVLYIAE	1485
Db	317	VSVLLAILLSYFIAMHLFGLNWHLQQTENDTFFENGKVNSDT-----VPTNTVSLPSG---	368	Db	1378	NNVLQITENRQVRIAAGRPMHCQVPGVE--YPVGKHAVQTTLESATAIAVSYSGLYITE	1436
Qy	406	LETPDRKKGTTTEGKPSFFPEDSFIDSGEIDVGRRASQKIPPGTFWRSQVFIIDHPVHLK	465	Qy	1486	TDEKKINRQVTTSGEISLVAGAPSGCDKNDANCDCFSGDDGYAKDAKLNTPSSSLAVC	1545
Db	369	-----DNGKLGGFTHENNTIDSGELDIGRRAIQEVPPGIFWRSQLEFIDQPQFLK	417	Db	1437	TDEKKINRQVTTDGEISLVAGIPSECDCKNDANCDCYQSGDGYAKDAKLNAPSSLAAS	1496
Qy	466	FNVSLGKAALVGIYGRKGLPPSHTQFDFVELLDGRLLTQEARSLGTPPROSGRTVPPSS	525	Qy	1546	ADGELYVADLGNIRIRFIRKXKPFNLNTQNNYELSSPIDQELYLFDTTGKHLTYQSLPTGD	1605
Db	418	FNISLQKDALIGVYGRKGLPPSHTQYDFVELLDGSRLLIAREQRNLVESERAGRQARSVL	477	Db	1497	PDGTLYIADLGNIRIRAVSKNKPLLNSMNFYEVASPTDQELYIFDINGTHQYTVSLVTGD	1556
Qy	526	HETGFIQYLDSGIWHLAFYNDGKESEVVSFLTATAIESVDNCPNSCYGNGDCISGTCHCFL	585	Qy	1606	LYNFTYTGDDITLITDNNGNMNVRRDSTGMPWLWVPDQVYVWVTMTGNSALKSVTT	1665
Db	478	HEAGFIQYLDSGIWHLAFYNDGKNPEQVSFNTIVIESVVCEPRNCHGNGECVSGTCHCFP	537	Db	1557	LYNFSYSNDNDVTAVTDSNGNTLRIRRDPNRPVVRVSPDNQVILWTIGTNGCLKSMTA	1616
Qy	586	GFLGPDCCRASCVPVLCSGNQYMKGRCLCHSGWKGAECDVPTNQCIDVACSNHGTCTIGT	645	Qy	1666	QGHELAMMTYHGNSGLLATKSNENGWTTTFEYDVSFGRLTNVTFFTGOVSSFRSDTSSVH	1725
Db	538	GFLGPDCSRACPVLCSGNQYSKGRCLCFSGWKGTGTECDVPTTQCIDPQCGRGICIMGS	597	Db	1617	QGLELVFTYHGNSGLLATKSDETGWTTFDFYDSEGRLTNVTFFTGVVTLHGDMDKAIT	1676
Qy	646	CICNPGYKGESCEEVDCMDPTCSGRGVCVRGECHECFVGWGGTNCETPRATCLDQCSGHGT	705	Qy	1726	VQVETSSK-DDVTITTNLSASGAFYTLQDQVRNSYIIGADGSLRLLLANGMEVALQTEP	1784
Db	598	CACNSGYKGENCEEADCLDPCGSNHGVCIHGECHCNPGWGGSNCEILKTMCADQCSGHGT	657	Db	1677	VDIESSSREEDVSITSNLSSIDSFYTMVQDQLRNSYQIGYDGLSRIFYASGLDSHYQTEP	1736
Qy	706	FLPDTGLCSCDPSWTGHDCSIIEICAADCGHGVCVGFTCRCEDGWMGAACDORACHPRCA	765	Qy	1785	HLLAGTVNPTVGKRNVTLPIDNGLNLVEWORKEQARGQVTVFGRRLRVHNRNLLSLDFFD	1844
Db	658	YLQESGSCTCDPNWTGDCSNEICSVDCSGSHGVCMGSCRCCEEGWTGPACNORACHPRCA	717	Db	1737	HVLAGTANPTVAKRNMTLPGENGQNLVEWFRKEQAQKVNVFGRKLRVNGRNLLSVDFD	1796
Qy	766	EHGTCRDGKCECSPGWNGEHCTIAHYLDRVVKEGCPGLCNGNGRCTLDLNGWHVCQQLGW	825	Qy	1845	RVTRTEKIYDDHRKFTLRILYDQAGRPSLWSPSSRLNGVNVTVSPGGYIAGIQRGIMSER	1904
Db	718	EHGTCKDCKECSQGWNGEHCTIAHYLDKIVKEGCPGLCNSNGRCTLDQNGWHVCQPGW	777	Db	1797	RTTKTEKIYDDHRKFLRLRIAYDTSGHPTLWLPSSKLMVNVTVSYSTGQIASIQRTSEK	1856
Qy	826	RGAGCDTSMETACGDSKNDGDGLVDCMDPDCCLOPLCHINPLCLGSPNPLDIQETQVP	885	Qy	1905	MEYDQAGRITSRIFADGKTWSYTYLEKSMVLLLHHSORQYIFEFDKNDRLSSVTMPNVARQ	1964
Db	778	RGAGCDVAMETLCTDSKDNEDGGLIDCMDPDCCLOSSCQNPYCRGLPDPQDIISQSLQT	837	Db	1857	VDYDSQGRIVSRVFADGKTWSYTYLEKSMVLLLHHSORQYIFEYDMWDRLSAITMPSVARH	1916
Qy	886	VSQONLHSFYDRIKFLVGRDSTHIIIPGENPFDGGHACVIRGOVMTSDGTPLVGVNISFVN	945	Qy	1965	TLETIRSVGYRNIYQPPEGNASVIOQDFTEDGHLLHHTFYLGTGRRRVYKYKLSKLAETL	2024
Db	838	PSQAAKSFYDRISFLIGSDSTHVLPGESPFNKSLASVIRGOVLTAADGTPLIGVNVVSFLH	897	Db	1917	TMQTIRSIGYRNIYPPESPESNASIITDYNEEGLLQTAFLGTSRRRVLFKYRROTRLSEIL	1976
Qy	946	NPLFGYTIISQDGSFDLVNKGISIIILRFERAPFITOSHTLWLPWDRFFVMETIIMRHEE	1005	Qy	2025	YDTTKVSFTYDETAGMLKTNLQNEGFTCTIRYQIGPLIDRQIFRFTTEEGMVNARFDYN	2084
Db	898	YSEYGYTITRQDGMFDLVANGASLTLVFRSPFLTQYHTVWIPWNVYVMDTLWMKKEE	957	Db	1977	YDSTRVSFTYDETAGVLKTVNLQSDGFICTIRYQIGPLIDRQIFRFSDEGMVNARFDYS	2036
Qy	1006	NEIPSCDLSNFARNPVVSPSLTSFASSCAEKGPVPEIQALQEEISISGCKMRLSYLS	1065	Qy	2085	YDNSFRVTSMQAVINETPLPIDLYRYDDVSGKTEQFGKFGVYYDINOIITTAVMTHTKH	2144
Db	958	NDIPSCDLSGFVRPSPPIIVSSPLSTFFRSPEDSPIIPETQVLHEETIPGTDLKLSYLS	1017	Db	2037	YDNSFRVTSMQGVINETPLPIDLYQFDDISGKVEQFGKFGVYYDINOIISTAVMTYTKH	2096
Qy	1066	SRTPGYKSVLRISLTHPTIPENLMKVHLMVAVEGRLEFRKWFAAAPDLSYFYIWDKTDVYN	1125	Qy	2145	FDAYGRMKEVQYEIFRSLMYWMTVOYDNMGRVVKELKVGPYANTTRYSEYEDADGQLQT	2204
Db	1018	SRAAGYKSVLKITMTQAVIPENLMKVHLMVAVVGRLFQKWFPPASPNLAYTFIWDKTDAYN	1077	Db	2097	FDAHGRIKEIQYEIFRSLMYWITIQYDNMGRVTKREIKIGPFANTTKYAYEYDVGQLQT	2156
Qy	1126	QKVFLGSEAFVSVGYEYESCDLILWEKRTTVLQYEBIDASKLGGWSLDKHHALNIQSGI	1185	Qy	2205	VSINDKPLWRYSYDLNGNLHLLSPGNSARLTPLRYDIRDRITRLGDVQYKMDDEDGFLRQR	2264
Db	1078	QKVYGLSEAVVSVGYEYESCLDLTLWEKRTAVLQGYELDASNMGWTLDKHHVLDVQNGI	1137	Db	2157	VYLNKIMWRYNYDLNGNLHLLNPSSSARLTPLRYDLDRITRLGDVQYRLDEDDGFLRQR	2216
Qy	1186	LHKNGENQFVSQPPVIGSIMNGRRRRSISCPSCNGLADGNKLLAPVALTCGSDGSLYV	1245	Qy	2265	GGDIFEYNSAGLLIKAYNRAGSWSVRYRYDGLGRRRVSSKSSHHLQFFYADLTNPTKVT	2324
Db	1138	LYKNGENQFISQPPVVSIMNGRRRRSISCPSCNGQADGNKLLAPVALACGIDGSLYV	1197	Db	2217	GTEIFEYSSKGLLTRVYSKSGWTVIYRYDGLGRRRVSSKTSLGQHLQFFYADLTYPTRIT	2276
Qy	1246	GDFNYIRRIFPSGNVTNILELRNKDFRHSHPAHKYVLATDPMGSAVFLSDSNSRVFVKI	1305	Qy	2325	HLYNHSSSEITSLYYDLQGHLFAMELSSGDEFYIACDNIGTPLAVFSGTGLMIKQILYTA	2384
Db	1198	GDFNYVRRIFPSGNVTSVLELRNKDFRHSNPAHRYVLATDPVTGDLVYSDTNTRRIYRP	1257	Db	2277	HVYNHSSSEITSLYYDLQGHLFAMEISSGDEFYIASDNTGTPLAVFSSNGLMLKQTYTA	2336
Qy	1306	KSTVVVKDLVKNSEVVAGTGDQCLPFDDTRCGDGGKATEATLTNPRGITVDKFGGLYFVD	1365	Qy	2385	YGEIYMDTNPNFQIIIGYHGGLYDPLTKLVHMGRDDYDLAGRWTSPDHLMKHLSSSNV	2444
Db	1258	KSLTGAKDLTKNAEVVAGTGEQCLPFDEARCGDGGKGAVEATLMSPKGMAIDKNGLLYFVD	1317	Db	2337	YGEIYFDSNVDFQLVIGFHGGLYDPLTKLIHFGERDYLILAGRWTTPDIEIWKRI-GKDP	2395
				Qy	2445	MPFNLYMFKNNNPISNSQDIKCFMTDVNSWLLTFCFQLHNVIPGYPKPMDAMBESYELI	2504

Db 2396 APFNLYMFRNNPNPASKIHDKVQYITDVNSWLVTFGFHLHNAIPGFPVPKFDLTSPSYELV 2455  
Qy 2505 HTQMKTQEWDNKSKILGVQCEVQQLKAFVTLERFDQLYGSTITSCQAPKTKK----- 2558  
Db 2456 ----KSQWEDVPPIFGVQQQVARQAKAFSLGLKMAEV-----QVSRKAKAGAEQSW 2502  
Qy 2559 --FASSGSVFQKGVKFAKDGRTTDDIISVANEDGRRVAAILNHAHYLENLHFTIDGVDT 2616  
Db 2503 LWFAIVKSLIGKVMKLVAVSQGRVQTNVLNIANEDCIKVA AVLNNAFYLENLHFTIEGKDT 2562  
Qy 2617 HYFVKPGPSEGLAILGLSGRRRTLENGVNVTVSQINTVLNGRTRRYTDIQLQYGALCLN 2676  
Db 2563 HYFIKTTTTPESDLGLRLTSGRKALENGINVTVSQSTTVVNGRTRRFADVEMQFGALALH 2622  
Qy 2677 TRYCTTLDDEKARVLELARQRAVRQAWAREQOORLREGEEGLRAWTEGEKQOVLSTGRVQG 2736  
Db 2623 VRYGMTLDEEKARILEQARQALARAWAREQOORVRDGEGARLWTEGEKROLLSAGKVQG 2682  
Qy 2737 YDGFVFISVEQYPELSDSANNIHFMRQSEMGR 2769  
Db 2683 YDGYVVLVSEQYPELADSANNIQFLRQSEIGKR 2715

RESULT 5

Q4RFP1\_TETNG PRELIMINARY; PRT; 2500 AA.  
AC Q4RFP1;  
DT 13-SEP-2005 (TrEMBLrel. 31, Created)  
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)  
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)  
DE Chromosome 16 SCAF15113, whole genome shotgun sequence.  
GN ORFNames=GSTENG0035234001;  
OS Tetraodon nigroviridis (Green puffer).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;  
OC Tetraodontidae; Tetraodontidae; Tetraodon.  
OX NCBI\_TaxID=99883;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA Jaillon O., Aury J.-M., Brunet F., Petit J.L., Stange-Thomann N.,  
RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,  
RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,  
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,  
RA Anthouard V., Jubin C., Castellani V., Katinka M., Vacherie B.,  
RA Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,  
RA Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,  
RA Parra G., Lardier G., Chapelle C., McKernan K.J., McEwan P., Bosak S.,  
RA Kellis M., Volff J.N., Guigo R., Zody M.C., Mesirov J.,  
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,  
RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,  
RA Wincker P., Lander E.S., Weissbach J., Roest Crollius H.;  
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals  
RT the early vertebrate proto-karyotype.";  
RL Nature 431:946-957(2004).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RG Genoscope; Whitehead Institute Centre for Genome Research;  
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.  
CC -1- CAUTION: The sequence shown here is derived from an  
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
CC preliminary data.  
DR EMBL; CAAE01015113; CAG12791.1; -; Genomic DNA.  
SQ SEQUENCE 2500 AA; 279277 MW; 61D18EB6E655376E CRC64;  
  
Query Match 67.8%; Score 10095.5; DB 2; Length 2500;  
Best Local Similarity 65.2%; Pred. No. 0;  
Matches 1875; Conservative 262; Mismatches 255; Indels 485; Gaps 16;  
  
Qy 1 MDVKERPYSRLTRRRDAERRYTTSSADSEEGKAPQKYSSTETLKAYDQDARLAYGSRV 60  
Db 1 MEVKERPYSRLTARQDTEHRYTTSSADSEDGKANPKYSSTETLKAFDHDSDRMAYGSRV 60

Qy 61 KDIVPQEAEEFCRTGANFTLRELGLBEEVTPPHGTLRYTDTIGLPQCGYSMGAGSDADMEAD 120  
Db 61 KEMVHHEVDEFSRQGVDFSLRNLGFGEALPSHVATYRSDMGLPHRDYSVSAGSDPDTETD 120  
Qy 121 TVLSPEHPVRLWGRS-TRSGRSSCLSSRANSNLTLTDTTEHENTE----- 163  
Db 121 GIMSPEHAVRLWGRSNTKSGRSSCLSSRANSNLTLTDTTEHENTENAYQYTRICLQLKCDV 180  
Qy 164 -----TDHPGGL----- 170  
Db 181 FYIRHHLVKSHGPPPLHCSSASSSPVEQLPYPPPSIAANESQGGLLGNSAAQPAQDSDES 240  
Qy 171 -----QNHARLRTPPPLSHAHTP-NQHHAASINSL 200  
Db 241 EFGPNSFLVKTGSGNLYTPATAAAEEGAFQNHSLRTPPLPLSHSHSPSHQHHAASINSL 300  
Qy 201 NRGNFTPRSNPSPAPTDHSLSGEPPAGGAQEPAPHAQENWLLNSNIPLETRNLGKQPFLLGT 260  
Db 301 NRSNYTQRSNPSPAPTDSSVPPEGPA--SQDSVSVDQNWLLNSNIPLETRNIAKQSLET 358  
Qy 261 LQDNLIEMDILGASRHDGAYS DGHFLFKPGGTSPLFCTTSPGYPLTSTVYSPPPRPLPR 320  
Db 359 LQDNLIEMDILASSGRDASVNDGQFLFKPGGTSPLYCTTSPGYPLTSTVYSPPPRPLPR 418  
Qy 321 STFARPAFNLKKPSKYCNWKCAALS AIVISATLVILLAYFVAMHLFGLNHLQPMEGQMY 380  
Db 419 NTFSRPAFSLKKPYKHCNWKCAALSAILISVMLLFLLAYFIAMHLFGLNHLQPVQRQMY 478  
Qy 381 EITEDTASSWPVPTDVSLYPSGGTGLETPDRKKGTTGKPPSSFFPEDSFIDSGEIDVGR 440  
Db 479 QLSEDNNTSGLPFPTDLVSVPVNTGLVIPERRGK--DDSKLDSLFDDSYIDMGEIDVGR 536  
Qy 441 RASQKIPPGTFWRSQVFI DHPVHLKFNVSLGKALVGIYGRKGLPPSHTQDFVELLDGR 500  
Db 537 KVTQIIPPGVFWRSQVFI DHPMYVKNVSLSKDALVGIYGRRLPPSHTQDFVELLDGR 596  
Qy 501 RLLTQEARSLGTPQRSRGTVPPSSSHETGFIQLDLSGIWHLAFYNDGKSESEVVSFLTTAI 560  
Db 597 RLLVQDIRVEGPAAMQORGLIPITTHDTGFIQYNDSGIWHLAIYNDGKETETVSFLTAT 656  
Qy 561 ESDVNCPSNCYGNDCISGTCHFCFLGFLGPDCCGRASCPVLCSGNGQYMKGRCLCHSGWK 620  
Db 657 DSIDDCPSNCFMNGDCIAGKCHFCFLGFKGPDCCGRAACPVLCSGNGQYLKGRCMCHSGWK 716  
Qy 621 AECDVPTNQCIDVACSNHGTCTGTICINPGYKESCEEVD CMDPTCSGRGVCVRGECHC 680  
Db 717 SECDVPTNQCIDIACSNHGTCTGTICINPGYKENCEEVD CMDPTCSGRGVCVRGECHC 776  
Qy 681 FVGWGTNCETPRATCLDQC SGHGTFLPDTGLCSDP SWTGHDCSIEICAADCGHGVCV 740  
Db 777 FVGWGGSGCESPRASCMDCQSGHGAFLADTGTCDPNTWTHDCSTEICAADCGHGVCV 836  
Qy 741 GGTCCRCEDGWMGAACDQACHPRCAEHGTCRDGKCECSPGWNGEHCTIAHYLDRVVKEGC 800  
Db 837 SGSCRCDDGWMGSGCDQACHPRCNEHGTCKDGKCECSPGWNGEHCTIAHYLDKVVKEGC 896  
Qy 801 PGLCNGNGRCTLDLNGWHVCQLGWRGAGCDTSMETACGDSKONDGDGLVDCMPDCCCLQ 860  
Db 897 PGLCNGNGRCTLGNNGMYCVCQLGWRGTGCDTSMETACTDVKDNDGDGLVDCMPDCCCLQ 956  
Qy 861 PLCHINPLCLGSPNPLDIIQETQVPVSQQNLHSPYDRIKFLVGRDSTHIIIPGENPFDGGH 920  
Db 957 ATCHTTALCVGSPDPLDIIQETQLSSTQSKLQTFYERVRFLVGRDSTHVI PGVNPFDG-- 1014  
Qy 921 ACVIRQVMTSDGTPLVGVNISFVNNPLFGYTIISRQDGSFDLVTNGGISIILRPERAPFI 980  
Db 1015 ----- 1014  
Qy 981 TQEHTLWLPWDRFFVFMETIIMRHEENEIPSCDLSNFARPNPVPVSPSLTSFASSCAEKGP 1040  
Db 1015 ----- 1014



QY 1041 IVPEIQALQEEISISGCKMRLSYLSSRTPGYKSVLRISLTHPTIPFNLMKVHLMVAVEGR 1100  
Db 1015 -----KTAGYKSLLRVTTLTHSTIPFNLMKVHLMVAVEGR 1048  
QY 1101 LFRKWFAAAPDLSYFIWDKTDVYNQKVFGLSEAFVSUVGYEYESCPDLILWEKRTTVLQG 1160  
Db 1049 LFRKWFAAPNLSYDFVMDKADVYSQKVYGLSEVFVSUVGYEYESCPDFILWEKRAAVLQG 1108  
QY 1161 YEIDASKLGWSLQKHALNIQSGILHKNGENQFVSQQPPVIGSIMGNRRRSISCPSC 1220  
Db 1109 YETTASKLGWTVDKHALNIQSGILHMNGENVFISQQPPVIGSVMGNRRRSISCPSC 1168  
QY 1221 NGLADGNKLLAPVALTCGSDGSLYVGDFNYIRIIPPSSGNVTNILELR--NKDFRHSHPA 1278  
Db 1169 NGLADGNKLLAPVALACGSDGSLYVGDFNYVRRIFTTGNVTSVLELRFCTSMFASEH--- 1225  
QY 1279 HKYYLATDPMGAVFLSDNSRRVFKIKSTVVVKDLV---KNSEVVA---GTGDQCLPFD 1332  
Db 1226 -----LVVSVEDTSRLPLRCHSRVAYIWLCCASARSEICTFFFEFCACVCLPY- 1272  
QY 1333 DTRCGDGGKATEATLNPRGITVDKFLIYFVDGTMIRRIDQNGIISTLGSNDLTSARP 1392  
Db 1273 ---C-----CITVDKYGVIFFDGTMIRRIDQNGIISTLLGFNDLTSARP 1314  
QY 1393 LSCDSVMDISQVRLEWPTDLAINPMDNSLYVLDNNVVLQISENHQVRIVAGRPMHCQVPG 1452  
Db 1315 LSCDAVMDISQVRLEWPTDLAVSPLDNSLYVLDNNVVLQISENHQVRIVAGRPIHCQVPG 1374  
QY 1453 IDHFLLSKVAIHATLESATALAVSHNGVLVYIAETDEKKINRIRQVTTSGEISLVAGAPSG 1512  
Db 1375 IDHFIMSKVAIHATLESANALAVSHTGILYIAESDEKKINRVQ----- 1418  
QY 1513 CDCKNDANCDCFSGDDGYAKDAKLNTPSSLAVCADGELYVADLGNIRIRFIRKNKPFLLNT 1572  
Db 1419 ----- 1418  
QY 1573 QNMYELSSPIDQELYLFDTTGKHLYTQSLPTGDYLYNFYTYTGDGDIITLITDNNGNMNVNR 1632  
Db 1419 QN-----EKHIITR----- 1427  
QY 1633 RDSTGMPLWLVPDGVVYVWTMGNTSALKSVTTQGHELAMWTYHGNSGLLATKSNENGWT 1692  
Db 1428 ----- 1427  
QY 1693 TFYEYDSFGRLTNVTFTPGQVSSFRSDTSSVHVQVETSSKDDVTITTNLSASGAFYTL 1752  
Db 1428 ----YDSYGRLTNVTYPTGQVSSYRTDADSSVRIQTEGSNKENITVTTNLSASGTFYTL 1483  
QY 1753 QDQVRNSYIIGADGSLRLLLANGMEVALQTEPHLLAGTVNPTVGRNVTLPIDNGLNLVE 1812  
Db 1484 QDQVRNSYFIGLDGSLRLVLANGMEVSLHTEPHLLAGTIIPTVSKRNITLIDNGLNLVE 1543  
QY 1813 WRQRKEAQARGQVTVFGRRLRVHNRNLLSLDFDVRTRTEKIYDDHRKFTLRILYDQAGRPS 1872  
Db 1544 WRQRKEAQARGQVTVYGRRLRVHNRNLLSLDFDRITRTEKVDYDDHRKFTLRHYDHAGRPT 1603  
QY 1873 LWSPSSRLNGVNVITYSPGGYIAGIQRGIMSERMEYDQAGRITSRIFADGKTWSYTYLEKS 1932  
Db 1604 LWAPSSRLNGVNVITYSPGGNVAGIQRGTMSVRMEYDQGRITSQIFADGKSWTYTYLEKS 1663  
QY 1933 MVLILLHSQRQYIFEFDKNDRLSSVTMPNVARQTLETIRSVGYRYNIYQPPEGNASVIQDF 1992  
Db 1664 MVLILLYSQRQYIFEFDKNDRLSSVTMPNVARHTLETSRISIGYRRTTYQPPEGNASVLQDY 1723  
QY 1993 TEDGHLLHTFYLGTGRRRVIYKYGKLSKLAETLYDTTKVSYFTYDETAGMLKTINLQNEGFT 2052  
Db 1724 SEEGQLLTLYLGTGRRRVTYKYGKIAKLLEMLYDTTRIGFPYDELGTMLKTINLQSEGFT 1783  
QY 2053 CTIRYRQIGPLIDRQIFRFTBEGMVNARFDYNYDNSFRVTSMQAVINETPLPIDLYRYDD 2112  
Db 1784 CTVRYRQIGPLIDRQIFRFSEBGMVNARLDYVYDNSFRVTSMQAVINETPLPIDLYRYDD 1843  
QY 2113 VSGKTEQFGKFGVIYYDINQIITTAVMTHTKHFDAYGRMKEVQYEIFRSLMYWMTVQYDN 2172

Db 1844 VSGKTEQFGKFGVIYYDINQIITTAVMTHTKHFDAYGRVKEVQYEIFRSLMYWMTVQYDN 1903  
QY 2173 MGRVVKELKVGPYANTTRYSEYDADGQLQTVSINDKPLWRYSYDLNGLHLLSPGNSA 2232  
Db 1904 MGRVVAKELKVGPYANTTRYTYEYDADGQLQVVSINDKPLWRYSYDLNGLHLLSPGNSA 1963  
QY 2233 RLTPLRYPDIRDITRLGDVQYKMDDEGFLRQGGDIFEYNSAGLLIKAYNRAGSWSVRYR 2292  
Db 1964 RLTPLRDNRDITRLGDVQYRMDDEGFLKQRGNDYFEYNSAGLLVRVYNKVSGWSIQYR 2023  
QY 2293 YDGLGRRVSSKSSHHLQFFYADLTNPTKVTHLYNHSSEITSLYYDLQGHLFAMELSS 2352  
Db 2024 YDGLGRRVSSRSSIGHHLQFFYADLSSPTRITHMYNHSSEIASLYYDLQGHLFAMELSS 2083  
QY 2353 GDEFYIACDNIGTPLAVFSGTGLMIKQILYTAIGEYIMDTNPNFQIIGYHGGLYDPLTK 2412  
Db 2084 GDEFYVACDNIGTPLAVFSGAGIMIKQILHTAFGEVYLDTNPSFQLIIGYQGGLYEPLSR 2143  
QY 2413 LVHMGRRDYDVLAGRWTSPDHELWKHLSSSNVMPFNLYMFKNNNPISNSODIKCFMTDVN 2472  
Db 2144 LVHMGKRDYDVLAGRWTTPNLEIWKRLNSKHIAPFNMYMFKNNPLSNNEBIKCYMTDVN 2203  
QY 2473 SWLLTFGFLHNVIPGYPKPMDMAMEPSVELIHTQMKTQEWDNKSILGVQCEVQKQLKA 2532  
Db 2204 SWLVTFGFLYNVIPGYHKPNTESMEPSVELVRTQIKTQEW DSTKSLLGVCQEVQRQLKA 2263  
QY 2533 FVTLERFDQYLGSTITSCQAPKTKKFASCSGVFGKGVKFALKDGRVTTDIISVANEDGR 2592  
Db 2264 FVKLERFGQIYGAKSAGCPQTETKHIFATWGSIFGKGVKFAIREGRVSTDIISLANEDGR 2323  
QY 2593 RVAAILNHAHYLENLHFTIDGVDTHTYFVKPGPSEGDLAILGLSGRRRTLENGVNVTVSQI 2652  
Db 2324 RMAAVLNDFAFYLEHLHFTVAGMDTHYFVKMGVPEGDSLIGMTVGQRTTLETGVNVTVSQV 2383  
QY 2653 NTVLNGRTRRYTDIQLQYGALCLNTRYGTTILDEEKARVLELARQRAVRQAWAREQRLRE 2712  
Db 2384 NAVLNGRTRRITDIQLQYGTLYLNTRYGSSVDEEKARILEMARQRAVTAWARERQLRD 2443  
QY 2713 GEEGLRAWTEGEKQOQVLSTGRVQGYDGFVFVISVEQYPELSDSANNIHFMRQSEMGR 2769  
Db 2444 GEEGSRWTGEKQOQLLGSQVQGYDGYVYVSVDPYPELADSVNNIHFMRQTEMGR 2500

RESULT 6

Q804R1 BRARE

ID Q804R1\_BRARE PRELIMINARY; PRT; 2192 AA.

AC Q804R1;

DT 01-JUN-2003 (TrEMBLrel. 24, Created)

DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)

DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

DE Odd Oz/ten-m homolog 4 (Fragment).

GN Name=odz4; ORFNames=odz4-001;

OS Brachydanio rerio (zebrafish) (Danio rerio).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;

OC Cyprinidae; Danio.

OX NCBI\_TaxID=7955;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RA Babbage A.;

RL Submitted (DEC-2004) to the EMBL/GenBank/DBJ databases.

DR EMBL; AL807754; CAD61260.1; -; Genomic\_DNA.

DR HSSP; P16109; 1FSB.

DR Ensembl; ENSDARG00000006161; Danio rerio.

DR ZFIN; ZDB-GENE-990714-20; odz4.

DR InterPro; IPR000742; EGF\_2.

DR InterPro; IPR006209; EGF\_like.

DR InterPro; IPR006210; IEGF.

DR InterPro; IPR001258; NHL.

DR InterPro; IPR006530; YD.

DR Pfam; PF01436; NHL; 5.

DR Pfam; PF05593; RHS\_repeat; 5.







Db 1124 VHKNGENMFISQPPVISTMMGNQHQRVSCSNCNGLNALNSKLFAPVALTSGPDGSVYI 1183

Qy 1246 GDFNYIRRIFFPSGNVTNILELRNCKDFRHSHPAHKYIYLATDPMGAVFLSDSNSRRVFKI 1305

Db 1184 GDFNFVRRIFPSGNSIGILELRNRDTRHSTSPAHKYIYLAVDPVESLYLSDTNRTRYKA 1243

Qy 1306 KSTVVVKDLVKNSEVVAGTGDQCLPFDDTRCGDGGKATEATLTNPRGITVDKFGLIYFVD 1365

Db 1244 KSLIETKDLAKVNDVVAGTGDQCLPFQDSHCGDGGKASEASLNSPRGITIDKHGFIYFVD 1303

Qy 1366 GTMIRRIDQGLIISTLLGSNDLTSARPLSCDSVMDISQVRLEWPTDLAINPMDNSLYULD 1425

Db 1304 GTMIRKIDENGWITTIIGSNGLTSTQPLSCDSGMDITQVRLEWPTDLTVNPLDNSLYULD 1363

Qy 1426 NNVLQISENHQVRIIVAGRPMHCQVPGIDHFLLSKVAIHATLESATALAVSHNGVLYIAE 1485

Db 1364 NNIVLQISESRRVRIIAGRPICHQVPGIDHFIVSKVAIHSTLESARAIIVSHSGIPYIRE 1423

Qy 1486 TDEKKINRIQVTTSGEISLVAGAPSGCDCKNDANCDCFSGDGYAKDAKLTNTPSSLAVC 1545

Db 1424 TDERKINRIQVTTNGEISIIAGAPSDCDCKIDPNCDCFSGDGYAKDAKLKAPSSLAVS 1483

Qy 1546 ADGELYVADLGNIRIRFIRKNKPFNTQNMVELSSPIDQELYLFDTTGKHLYTQSLPTGD 1605

Db 1484 PDDTLYVADLGNIRIRAVSRNKAHLSDTNMYEIASPADQELQFTINGTHLHTLNLITRD 1543

Qy 1606 YLYNFTYTGDGITLITDNNGMNVNRDSTGMPLWLVPDGVYVWVTMGTSNALKSVTT 1665

Db 1544 YIYNFTYSGEDVATITSSNGNSVHIRDTSGLPLVWVPPGGQVYWLTISSNGVLKRVA 1603

Qy 1666 QGHELAMTYHNGSGLLATKSNENGWTFYEDYDFGRLTNVTPTGQVSSFRSDTSSVH 1725

Db 1604 QGYNALMTYPGNTGLLATKSDENGWTFVYEDYSDGHLTNATPPTGEVSSFHSDVEKLTR 1663

Qy 1726 VQVETSSKDDVTITTNLSASGAFYTLQDQVRNSYYIGADGSLRLLLLANGMEVALQTEPH 1785

Db 1664 VELDTSNENMVMTATNFSATSTIYTLKQDNTQNIYRVSPDGLRVTFASGMEITLNTPEH 1723

Qy 1786 LLAGTVNPTVGRNVTLPIDNLGLNVLEWRQKEQARGQTVFGRRRLRVHNRNLLSDPDR 1845

Db 1724 ILAGVVSPTLGKCNISLPGEHNSNLIEWRQRREQTKGNISTFERRLRAHNRNLLSIDFDH 1783

Qy 1846 VTRTEKIYDDHRKFTLRILYDQAGRPSSLWSPSSRLNGVNVTVSPGGYIAGIQIGIMSERM 1905

Db 1784 VTRTGKIYDDHRKFTLRIMYDQTGRPLWSPISKYNEVNITYSHSGLVYTIQRTWTEKM 1843

Qy 1906 EYDQAGRITSRIFADGKTWSYTYLEKSMVLLLLHSQRQYIEFFDKNDRLSSVTMPNVARQT 1965

Db 1844 EYDPSGNIISRTWADGKIWSYTYLEKSMVLLLLHSQRRYIEFYDQSDYLLSVTMPSMVRHA 1903

Qy 1966 LETIRSVGYRNIYQPPEGNASVIOQDFTEDGHLHLHTFYLGTRRRVIYKYGKLSKLAETLY 2025

Db 1904 LQTMLSVGYRNIYTPPDSGAAFIQDVTRDGRLLQTLYPGTGRRVLYKYSKQSRLEILY 1963

Qy 2026 DTTKVSFTYDETAGMLKTINLQNEGFTCTIRYRQIGPLIDRQIFRFTTEGMVNARFDYNY 2085

Db 1964 DTTQVTFYEESGVIKTIHMHDFICTIRYRQTGPLIGRQIFRFSEEGLVNARFDYSY 2023

Qy 2086 DNSFRVTSMQAVINETPLPIDLYRYDDVSGKTEQFGKFGYIYDINQIITTAVMTHTKHF 2145

Db 2024 -NNFRVTSMQAMINETPLPIDLYRYVDVSGRTEQFGKFSYINYDLNQVITTTVMKHTKIF 2082

Qy 2146 DAYGRMKEVQYEIFRSLMYWMTVOYDNMGRVVKELKVGYPYANTTRYSYEYDADGLOQTV 2205

Db 2083 SANGQVIEVQYEILKSIAYWMTIQYDNMGRMVICDIRVGDANITRYFYEYDRDGGLOQTV 2142

Qy 2206 SINDKPLWRYSYDLNGLNHLHLLSPGNSARLTPLRYDIRDRITRLGDVOYKMDGEDGFLRQG 2265

Db 2143 SVNDKTQWRYSYDLNGLNINLLSHGNSARLTPLRYDLDRDIRTLGEIQYKMDGEDGFLRQG 2202

Qy 2266 GDIFEYNSAGLLIKAYNRAGSVRYRYDGLGRRVSSKSSHHLQFFYADLTNPTKVTH 2325

Db 2203 NEIFEYNSGLLNKAYNKVSGWTVQYCYDGLGRRVASKSSLGOHLQFFYADLSNPIRVTH 2262

Qy 2326 LYNHSSEITSLYDLQGHLFAMELSSSGDEFYIACDNIGTPLAVFSGTGLMIKIQILYTAY 2385

Db 2263 LYNHSSEITSLYDLQGHLIAMELSSGEEYYVACDNTGTPLAVFSSRGQVIKEILYTPY 2322

Qy 2386 GEIYMDTNPNFQIIIGYHGGLYDPLTKLVHMGRRDYDLVLAGRWTSPDHKLWKLSSSNVM 2445

Db 2323 GEIYQDTPDFQVVGIFGHGLYSLTKLVHLGORDYVIAGRWTTPNHHIWKHLNAV-PQ 2381

Qy 2446 PFNLYMFKNNPNISNODIKCFMTDVNSWLLTFGFOLHNVIPGYPKPMDAMEPSYELIH 2505

Db 2382 PFNLYSFENYYPVGRIQDVAKYTTDIGSWLELFGQLHNVLPGFPKPEIALETYELLQ 2441

Qy 2506 TOMKTOEWDNSKSILGVQCEVQOLKAFVTLERFDQLYGSTITSCQQAPKTKKFASSGSV 2565

Db 2442 LQTKTOEWDPGKTIIGIQCELOKQLRNFISLDQLPMTPRYSDGKCYEGVKQPRFAAIPSV 2501

Qy 2566 FGKGVKFALKDGRVTTDIISVANEDGRRVAAILNHAHYLENLHFTIDGVDTHYFVKPGPS 2625

Db 2502 FGKGIKFAIKOGIVTADIIGVANEDSRRIAAILNNAHYLENLHFTIEGRDTHYFIKLGSL 2561

Qy 2626 EGDLAAILGLSGRRTLENGVNVTVSQINTVLNGTRRRYTDIQLQYGALCLNTRYGTTLDE 2685

Db 2562 EEDLSLIGNTGRRILENGVNVTVSQMTSVINGTRRRFADIQLQHGALCFNVRYGTTVEE 2621

Qy 2686 EKARVLELARQAVRQAWAREQQRLREGEGLRAWTEGEKQQVLSTGRVQGYDGFFFVISV 2745

Db 2622 EKNHVLEVARQRAVAQAWTKQRRRLQEGEGIRAWTDGEKQQLLNTGRVQGYDGYFVLSV 2681

Qy 2746 EOYPELSDSANNIHFMRQSEMGR 2769

Db 2682 EOYLELSDSANNIHFMRQSEIGRR 2705

RESULT 8

Q5NBW7 MOUSE

ID Q5NBW7 MOUSE PRELIMINARY; PRT; 2765 AA.

AC Q5NBW7;

DT 01-FEB-2005 (TrEMBLrel. 29, Created)

DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)

DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)

DE Odd Oz/ten-m homolog 2 (Drosophila).

GN Name=Odz2; ORFNames=RP23-41F14.1-002;

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;

OC Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RA Holt K.;

RL Submitted (FEB-2005) to the EMBL/GenBank/DBSJ databases.

RN [2]

RP NUCLEOTIDE SEQUENCE.

RA Oliver K.;

RL Submitted (FEB-2005) to the EMBL/GenBank/DBSJ databases.

RN [3]

RP NUCLEOTIDE SEQUENCE.

RA Pelan S.;

RL Submitted (FEB-2005) to the EMBL/GenBank/DBSJ databases.

RN [4]

RP NUCLEOTIDE SEQUENCE.

RA Matthews L.;

RL Submitted (FEB-2005) to the EMBL/GenBank/DBSJ databases.

RN [5]

RP NUCLEOTIDE SEQUENCE.

RA Bird C.;

RL Submitted (FEB-2005) to the EMBL/GenBank/DBSJ databases.

DR EMBL; AL713915; CAI35945.1; -; Genomic\_DNA.

DR EMBL; AL713919; CAI35942.1; -; Genomic\_DNA.

DR EMBL; AL713956; CAI35934.1; -; Genomic\_DNA.

DR EMBL; BX000433; CAI35947.1; -; Genomic\_DNA.

DR EMBL; BX539311; CAI36038.1; -; Genomic\_DNA.



Db 1301 IYRVKSLSGAKDLAGNSEVWAGTGEQCCLPFDEARCGDGGKAVDATLMSPRGIAVDKNGLM 1360

Qy 1362 YFVDGTMIRRIDQNGIISTLLGSNDLTSARPLSCDSVMDISOVRLEWPTDLAINPMDNSL 1421

Db 1361 YFVDATMIRKVDQNGIISTLLGSNDLTAVRPLSCDSSMDVAQVRLEWPTDLAVNPMDNSL 1420

Qy 1422 YVLDNNVVLOISENHQVRIVAGRPMHCQVPGIDHFLLSKVAIHATLESATALAVSHNGVL 1481

Db 1421 YVLENNVILRITENHQVSIAGRPMHCQVPGID-YLSKLAIHSALESASAIAISHTGVL 1479

Qy 1482 YIAETDEKKINRIQVTTSGEISLVAGAPSGCDCKNDANCDFCGDDGYAKDAKLNTPSS 1541

Db 1480 YITETDEKKINRLRQVTTNGEICLLAGASDCDCKNDVNCICYSGDDAYATDAILNSPSS 1539

Qy 1542 LAVCADGELYVADLGNIRIRFIRKNKPFNTQNMVELSSPIDOELYLFDTTGKHLYTQSL 1601

Db 1540 LAVAPDGTIYIADLGNIRIRAVSKNKPVLNAFNQYEAASPEQEELYVFNADGIHQYTVSL 1599

Qy 1602 PTGDYLYNFTYTGDDITLITDNNGNMNVRRDSTGMPLWLVPDQVYVWVTMGTSALK 1661

Db 1600 VTGEYLYNFTYSADNDVTELIDNNGNSLKIRRDSSGMPRHLLMPDNQIITLTVGTNGGLK 1659

Qy 1662 SVTTQGHELAMTYHGNSGLLATKSNENGWTTTFEYDYSFGRLLTNVTFPTGOVSSFRSDTD 1721

Db 1660 AVSTQNLELGLMTYDGTGTLATKSDETGTTTFDYDHEGRLTNVTRPTGVVTSLHREME 1719

Qy 1722 SSVHVQVETSSK-DDVTITTNLSASGAPYTLLOQOVNRNSYIYGADGSLRLLLLANGMEVAL 1780

Db 1720 KSITIDIENSRDDDDVTITNLSSEASYTVQDOVRNSYQLCNCNGTLRVMYANGMAVSF 1779

Qy 1781 QTEPHLLAGTVNPTVGKRNVTLPIDNGLNLVWQRKEQARQOVTVFGRRRLRVHNRNLLS 1840

Db 1780 HSEPHVLAGTITPTIGRCNISLPMENGLNSIEWRLRKEQIKGKVTFIGRKLRVHGRNLLS 1839

Qy 1841 LDFDRVTRTEKIYDDHRKFTLRILYDQAGRPSLWSPSSRLNGVNVITYSPGGYIAGIQRGI 1900

Db 1840 IDYDRNIRTEKIYDDHRKFTLRIIYDQVGRPFLWLPSSGLAANVSYFFNGRLAGLQGA 1899

Qy 1901 MSERMEYDQAGRITSRIFADGKTWSYTYLEKSMVLLLHRSQRYIFEFDKXNDRLSSVTMPN 1960

Db 1900 MSERTDIDKQGRIVSRMFADGKWSYSYLDKSMVLLLQSQRYIFEYDSSDRLHAVTMP 1959

Qy 1961 VARQTLETIRSVGYRNIYQPPEGNASVIQDFTEDGHLHLTFYLGTRRRVIYKYGKLSKL 2020

Db 1960 VARHSMSTHTSIGYIRNIYNPPESNASVIFYSDDGRILKTSFLGTGRQVIFYKYGKLSKL 2019

Qy 2021 AETLYDTTKVSFTYDETAGMLKTLNLQNEGFTCTIRYROIGLPLIDRQIFRFTTEGMVNAR 2080

Db 2020 SEIYVDSSTAVTFGYDETTGVLKMNVLQSGGFSCTIRYRKVPLVDKQIYRFSEEGMINAR 2079

Qy 2081 FDYNY-DNSFRVTSMQAVINETPLIDLYRYDDVSGKTEQFGKFGVIYYDINQIITTAVM 2139

Db 2080 FDYTYHNSFRIASIKPVISETPLPVDLYRYDEISGKVEHFGKFGVIYYDINQIITTAVM 2139

Qy 2140 THTKHFDAYGRMKEVQYEIFRSLMYWMTVQYDNMGRVVKKELKVGPYANTTRYSEYDAD 2199

Db 2140 TLSKHFDTHGRIKEVQYEMFRSLMYWMTVQYDSMGRVIRKRELKGPYANTTKTYDYDGD 2199

Qy 2200 GQLQTVSINDKPLWRYSYDLNGLHLSPGNSARLTPLRYDIRDRITRLGDVQYKMWDEDG 2259

Db 2200 GQLQSAVANDRPTWRYSYDLNGLHLNPGNSARLMPLRYDLRDRITRLGDVQYKIDDDG 2259

Qy 2260 FLRQGGDIFEYNSAGLLIKAYNRAGSWSVRYRYDGLGRRVSSKSSHSHLQFFYADLTN 2319

Db 2260 YLCQGSDFEYNSKGLLTRAYNKASGWSVQRYRYDGVGRRASYKTNLGHHLQVYFYSDLHN 2319

Qy 2320 PTKVTHLYNHSSEITSLSYVDLQGHLFAMELSSGDEFYIACDNIGTPLAVFSGTGLMIKQ 2379

Db 2320 PTRITHVYNHSNSEITLSYVDLQGHLFAMESSSGEEYVVASDNTGTPLAVFSINGLMIKQ 2379

Qy 2380 ILYTAYGEIYMDTNPNFQIIIGYHGGLYDPLTKLVHMGRRDYDLAGRWTSPDHELWKHL 2439

Db 2380 LQYTAYGEIYYDSNPDFQMVIGFPHGGLYDPLTKLVHFTQRDYDVLAGRWTSPDYTMWRNV 2439

Qy 2440 SSSNVMPFNLYMFKNNNPISNQDIKCFMTDVNSWLLTFFGQLHNVIPGYPKPMDMAMEP 2499

Db 2440 GKPEA-PFNLYMFKNNNPISNELDLKNYVTDVKSWLVMFQGQLSNIIPGFPRAXMYFVPP 2498

Qy 2500 SYELIHTQMTQEWDNSKILGVQCEVQKQKAFVTLERFDQLYGSTIITSCQQAPKTKK- 2558

Db 2499 PYELSESQAS-----ENGQLITGVQOTTERHNOAFALB-----GOVITKKLHASIREKA 2548

Qy 2559 ---PASSGSVFGKGVKPFALKDGRVTTDIIISVANEDGRRVAAILNHAHYLENLHFTIDGVD 2615

Db 2549 GHWFATTTPIIGKGINFAIKEGRVTTGVSSIASEDSRKVASVLNNAYYLDKMHYSIEGKD 2608

Qy 2616 THYFVKPGPSEGDLAJLGLSGRRRTLENGVNVTVSQINTVLNGRTRRRYTDIQLQYGALCL 2675

Db 2609 THYFVKIGAADGDLVTLGTTIGRKVLESGVNVTVSQPTLLVNGRTRRRFTNIEFYQYSTLLL 2668

Qy 2676 NTRYG---TTLDEEKARVLELARQRAVRQAWAREQQRLREGEGLRAWTEGEKQQLSTG 2732

Db 2669 SIRYGLTPDTLDEEKARVLDQARQALGTAWAKEQQKARDGREGSRLWTEGEKQQLSTG 2728

Qy 2733 RVQGYDGGFFVISVEQYPELSDSANNIHFMRQSEMGRR 2769

Db 2729 RVQGYEGYVLPVEQYPELADSSNIQFLRQNEMGKR 2765

RESULT 9

Q5NBW8\_MOUSE

ID Q5NBW8\_MOUSE PRELIMINARY; PRT; 2764 AA.

AC Q5NBW8;

DT 01-FEB-2005 (TremBLrel. 29, Created)

DT 01-FEB-2005 (TremBLrel. 29, Last sequence update)

DT 10-MAY-2005 (TremBLrel. 30, Last annotation update)

DE Odd Oz\ten-m homolog 2 (Drosophila).

GN Name=Od2; ORFNames=RP23-41F14.1-001;

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;

OC Muroidea; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;

RN [1]\_

RP NUCLEOTIDE SEQUENCE.

RA Holt K.;

RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.

RN [2]

RP NUCLEOTIDE SEQUENCE.

RA Oliver K.;

RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.

RN [3]

RP NUCLEOTIDE SEQUENCE.

RA Pelan S.;

RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.

RN [4]

RP NUCLEOTIDE SEQUENCE.

RA Matthews L.;

RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.

RN [5]

RP NUCLEOTIDE SEQUENCE.

RA Bird C.;

RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.

DR EMBL; BX000433; CAI35946.1; -; Genomic\_DNA.

DR EMBL; AL645912; CAI35083.1; -; Genomic\_DNA.

DR EMBL; AL713919; CAI35941.1; -; Genomic\_DNA.

DR EMBL; AL713915; CAI35944.1; -; Genomic\_DNA.

DR EMBL; AL713956; CAI35933.1; -; Genomic\_DNA.

DR EMBL; BX539311; CAI36037.1; -; Genomic\_DNA.

DR EMBL; BX000433; CAI35933.1; JOINED; Genomic\_DNA.

DR EMBL; BX539311; CAI35933.1; JOINED; Genomic\_DNA.

DR EMBL; AL645912; CAI35946.1; JOINED; Genomic\_DNA.

DR EMBL; AL713919; CAI35946.1; JOINED; Genomic\_DNA.

DR EMBL; BX539311; CAI35946.1; JOINED; Genomic\_DNA.

DR EMBL; AL645912; CAI36037.1; JOINED; Genomic\_DNA.

DR EMBL; AL713919; CAI36037.1; JOINED; Genomic\_DNA.





Db 1420 YVLENNVILRITENHQVSIAGRPMHCQVPGID-YLSKLAHSALESASAIASHTGVL 1478

Qy 1482 YIAETDEKKINRIRQVTTSGEISLVAGAPSGCDCKNDANCDFCSGDGYAKDAKLNTPSS 1541

Db 1479 YITETDEKKINRLRQVTTNGEICLLAGAAASDCDCCKNDVNCICYSGDDAYATDAILNSPSS 1538

Qy 1542 LAVCADGELYVADLGNIRIFIRKKNPFLNTQNMVELSSPIDQELYLFDTTGKHLYTQSL 1601

Db 1539 LAVAPDGTIYIADLGNIRIRAVSKNKPVLNAFNQYEAASPEQELYVFNAIDGHIQYTVSL 1598

Qy 1602 PTGDYLYNFTYTGDGDIITLITDNNGMVNVRRDSTGMPLWLVPDGVVYVWMTGMTNSALK 1661

Db 1599 VTGEYLYNFTYSADNDVTELIDNNGNSLKIRRDSSGMPRHLLMPDNQIITLTVGTNGGLK 1658

Qy 1662 SVTTQGHELAMTYHNGSGLLATKSNENGWTTFEYDYSFGRLLTNVTFPTGQVSSFRSDTD 1721

Db 1659 AVSTQNLELGLMTYDGNLGLATKSDETGWITTFDYDHEGRLTNVTRPTGVVTSLHREME 1718

Qy 1722 SSVHVQVETSSK-DDVTITTNLSASGAFYTLQDQVRNSYIIGADGSLRLLLLANGMEVAL 1780

Db 1719 KSITIDIENSRRDDVTITNLSSEASYTVVQDQVRNSYQLCNGNGLRVMYANGMAVSF 1778

Qy 1781 QTEPHLLAGTVNPTVGKRNVTLPIDNGLNLVWRQKEQARGQVTVFGRRLRVHNRNLLS 1840

Db 1779 HSEPHVLAGTITPTIGRCNISLPMENGLNSIEWRLKEQIKGVKTIIFGRKLRVHGRNLLS 1838

Qy 1841 LDfDRVTRTEKIYDDHRKFTLRILYDQAGRPSLWSPSSRLNGVNVTVSPGGYIAGIQRGI 1900

Db 1839 IDYDRNIRTEKIYDDHRKFTLRiYDQVRPPLWLPSSGLAAVNSVFFNGRLAGLQRG 1898

Qy 1901 MSERMEYDQAGRITSRIFADGKTWSYTYLEKSMVLLLSQRQYIFEPDKNDRLSSVTMPN 1960

Db 1899 MSERTDIDKQGRIVSRMFADGKWSYSYLDKSMVLLLQSQRQYIFEYDSSDRLHAVTMPS 1958

Qy 1961 VARQTLLETIRSVGVYRNIYQPPEGNASVIOPTFEDGHLLHTFYLGTRRVVIKYKGLSKL 2020

Db 1959 VARHSMSTHTSIGIYRNIYNPPESNASVIFYDSDGRILKTSFLGTGRQVFKYKGLSKL 2018

Qy 2021 AETLYDTTKVSFTYDETAGMLKTINLQNEGFTCTIRYRQIGPLIDRQIFRFTEEGMVNAR 2080

Db 2019 SEIYVDSTAVTFGYDETGGVLKQVNLQSGFSC TIRYRKVGPLVDKQIYRFSEEGMINAR 2078

Qy 2081 FDYNY-DNSFRVTSMQAVINETPLPIDLYRDDVSGKTEQFGKFGVIYYDINQIITTAVM 2139

Db 2079 FDYTYHDNSFRIASIKPVISETPLPVDLYRYDEISGKVEHFGKFGVIYYDINQIITTAVM 2138

Qy 2140 THTKHFEDAYGRMKEVQYEIFRSLMYWMTVQYDNMGRVVVKELKVGPYANTTRYSYEYDAD 2199

Db 2139 TLSKHFDTHGRIKEVQYEMFRSLMYWMTVQYDSMGRVIRKRELKLGPIYANTTKYTYDYDGD 2198

Qy 2200 GOLQTVSINDKPLWRYSYDLNGLNHLHLLSPGNSARLTPLRYDIRDRITRLGDVQYKMDSDG 2259

Db 2199 GOLQSAVANDRPTWRYSYDLNGLNHLNPGNSARLMPLRYDLRDRITRLGDVQYKIDDDG 2258

Qy 2260 FLRQRGGDIFEYNSAGLLIKAYNRAGSWVRVRYDGLGRRVSSKSSHHLQFFYADLTN 2319

Db 2259 YLCQRGSDIFEYNSKGLLTRAYNKASGWSVQYRYDGVGRRASYKTNLGHLLQYFYSDLHN 2318

Qy 2320 PTKVTHLYNHSSEITSLSYYDLQHLFAMELSSGDEFYIACDNIGTPLAVFSGTGLMIKQ 2379

Db 2319 PTRITHVYNHNSSEITSLSYYDLQHLFAMESSSGEEYVVASDNTGTPLAVFSINGLMIKQ 2378

Qy 2380 ILYTAYGEIYMDTNPNFQIIGYHGGLYDPLTKLVHMGRRDYDVLAGRWTSPDHELWKHL 2439

Db 2379 LQYTAYGEIYYDSNPDFQMVGIFHGGLYDPLTKLVHFTQRDYDVLAGRWTSPDYTMWRNV 2438

Qy 2440 SSSNVMPENLYMFKNNNPISNSQDIKCFMTDVSWSLLTFGQLHNVIPGYPKPDMADAMEP 2499

Db 2439 GKEPA-PENLYMFKNNNPLSNELDLKNYVTDVKSWLVMFGQLSNIIIPGFPRAKMYFVPP 2497

Qy 2500 SYELIHTQMKTQEWDNKSIILGVQCEVQQLKAFVTLERFDQLYGSTITSCQQA PKTK- 2558

Db 2498 PYELSESQAS-----ENGQLITGVQQTTERHNOAFLALE-----GQVITKKLHASIREKA 2547

Qy 2559 ---PASSGSVFGKGVKFAKDGKRVTTDIIISVANEDGRRVAAAILNHAHYLENLHFTIDGVD 2615

Db 2548 GHWFATTTPIIGKGIMFAIKRGRVTTGVSSIASEDSRKVASVLNNAYYLDKMHYSIEGKD 2607

Qy 2616 THYFVKPGPSEGLAILGLSGGRRRTLENGVNVTVSQINTVLNGRTRRYTDIQLQYGALCL 2675

Db 2608 THYFVKIGAADGDLVTLGTTIGRKVLESGVNVTVSQPTLLVNGRTRRFTNIEFOYSTLLL 2667

Qy 2676 NTRYG---TTLDEEKARVLELARQAVRQAWAREQORLREGEGLRAWTEGEKQOVLSTG 2732

Db 2668 SIRYGLTPDRTLDEEKARVLDQARQALGTAWAKEQQKARDGREGSRLWTEGEKQQLSTG 2727

Qy 2733 RVQGYDGFVFISVEQYPELSDSANNIHFMRSQSEMGR 2769

Db 2728 RVQGYEGYVLPVEQYPELADSSSNIQFLRQONEMGKR 2764

RESULT 10

Q9DER5\_CHICK

ID Q9DER5\_CHICK PRELIMINARY; PRT; 2802 AA.

AC Q9DER5;

DT 01-MAR-2001 (TrEMBLrel. 16, Created)

DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)

DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

DE Teneurin-2 (Fragment).

GN Name=TEN2;

OS Gallus gallus (Chicken).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;

OC Gallus.

OX NCBI\_TaxID=9031;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RX MEDLINE=20581705; PubMed=11146505;

RX DOI=10.1002/1097-0177(2000)999:9999<:AID-DVDY1084>3.0.CO;2-B;

RA Tucker R.P., Chiquet-Ehrismann R., Chevrton M., Martin D., Hall R.J.,

RA Rubin B.P.;

RT "Teneurin-2 is expressed in tissues that regulate limb and somite

RT pattern formation and is induced in vitro and in situ by FGF8.";

RL Dev. Dyn. 220:27-39(2001).

DR EMBL; AJ279031; CAC09416.1; -; mRNA.

DR HSSP; P00750; 1TPG.

DR Ensembl; ENSGALG0000001768; Gallus gallus.

DR InterPro; IPR000742; EGF 2.

DR InterPro; IPR006209; EGF\_like.

DR InterPro; IPR006210; IEGF.

DR InterPro; IPR001258; NHL.

DR InterPro; IPR009471; Ten\_N.

DR InterPro; IPR006530; YD\_.

DR Pfam; PF00008; EGF; 2.

DR Pfam; PF01436; NHL; 6.

DR Pfam; PF05593; RHS\_repeat; 5.

DR Pfam; PF06484; Ten\_N; 1.

DR SMART; SM00181; EGF; 6.

DR TIGRFAMs; TIGR01643; YD\_repeat\_2x; 5.

DR PROSITE; PS00022; EGF\_1; 8.

DR PROSITE; PS01186; EGF\_2; 7.

DR PROSITE; PS50026; EGF\_3; 5.

KW EGF-like domain.

FT CHAIN <1 >2802 teneurin-2.

FT NON\_TER 1

FT NON\_TER 2802 2802

SQ SEQUENCE 2802 AA; 310746 MW; B1FBC2C84EDFA4B3 CRC64;

Query Match 64.6%; Score 9616.5; DB 2; Length 2802;

Best Local Similarity 61.3%; Pred.No. 0;

Matches 1775; Conservative 411; Mismatches 491; Indels 217; Gaps 27;

Qy 1 MDVKERKPYRSLTRRR-DAERRYTSSSADSEEGKAP-QKSYSSSETLKAYDQDARLAYGS 58

Db 1 MDIKRR-HRSLTRGRCGKECRYTSSSLDSEDCRVPQAQKSYSSSETLKAYGHDTRMHYGN 59





Db 2140 LPVDLYRYDEISGKVEHFGKFGVIYYDINQIITTAWMTLSKHFDTHGRIKEVQYEMFRSL 2199  
QY 2163 MYWMTVOYDNMGRVVKKELKVGYPYANTTRYSEYEDADGQLQTVSNDKPLWRYSYDLNGN 2222  
Db 2200 MYWMTVOYDSMGRVTKRELKLGYPYANTTKYTYDYDGDGQLQSVAVNDRPTWRYSYDLNGN 2259  
QY 2223 LHLLSPGNSARLTPPLYDIRDIRITRLGDVQYKMEDEGFLRQRGDIFEYNSAGLLIKAYN 2282  
Db 2260 LHLLNPGNSVRLMPLRYDLRDRITRLGDIPIYKIDDDGFLCQSGDVFEYNSKGLLTRAYN 2319  
QY 2283 RAGSWSVRYRYDGLGRRVSSKSSHSHLQFFYADLTNPTKVTHLYNHSSEITSLYYDLQ 2342  
Db 2320 KANGWNVQRYDGLGRRASCKTNLGHHLQVYFADLHNPTRVTHVYNHSSEITSLYYDLQ 2379  
QY 2343 GHLFAMELSSGDEFIACDNIGTPLAVFSGTGLMIKQILYTAYPEYMDTNPNFQIIGY 2402  
Db 2380 GHLFAMESSSGEYVVASDNTGTPLAVFSINGLMIKOLQYTAYPEIYYDSNPDFQLVIGF 2439  
QY 2403 HGGLYDPLTKLVHMGRRDYDVLAGRWTSPDHELWKHLSSSNVMPNLYMFKNNPISNSQ 2462  
Db 2440 HGGLYDPLTKLVHFTQRDYDVLAGRWTSPDYTMWKNIGREPA-PFNLYMFKSNNPLSNEL 2498  
QY 2463 DIKCFMTDVNSWLLTFGFLQHNVIPGYPKPDMDAMEPSYELIHTQMKTQEWDNKSILGV 2522  
Db 2499 DLKQYVTVDKSWLVMFGFLQSLNIIIPGFPRAKMYFVSPPYEL----TESQACENGQLITGV 2554  
QY 2523 QCEVQKQLKAFVTLERFDQLYSTIITSQQAPKTKK- ---FASGSGVFGKGVKFALKDGR 2578  
Db 2555 QOTTERHNQAFVALE-----GVISKRLHASIREKAGHWFATSPPIIGKIMFAVKKGR 2608  
QY 2579 VTTDIISVANEDGRRVAAILNHAHYLENLHFTIDGVDTHYFVKPSPSEGDLAILGLSGGR 2638  
Db 2609 VTTGISSIATDSDRKIASVLNSAHYLEKMHYSIEGKDTHYFVKIGSADSLVTLAMTSGR 2668  
QY 2639 RTLENGVNVTVSQINTVLNGRTRRYTDIQLQYGALCLNTRYG---TTLDEEKARVLELAR 2695  
Db 2669 KVLDSGVNVTVSQPTLLINGRTRRFTNIEFQYSTLLINIRYGLTADTLDEEKARVLDQAR 2728  
QY 2696 QRAVRQAWAREOQRLREGEGLRAWTEGKQOVLSTGRVQGYDGFVISVEQYPELSDSA 2755  
Db 2729 QRALGSAWAKEQKARDGREGSRVWTDGKQQLLNTGRVQGYEGYVLPVEQYPELADSS 2788  
QY 2756 NNHFMRQSEMGRR 2769  
Db 2789 SNIQFLRQNEMGKR 2802

RESULT 11  
Q9WTS5\_MOUSE  
ID Q9WTS5\_MOUSE PRELIMINARY; PRT; 2764 AA.  
AC Q9WTS5;  
DT 01-NOV-1999 (TrEMBLrel. 12, Created)  
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Ten-m2.  
GN Name=Odz2; Synonyms=ten-m2;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=Balb/c; TISSUE=Brain;  
RA Oohashi T., Zhou X., Feng K., Richter B., Moergelin M., Perez M.T.,  
RA Su W., Chiquet-Ehrismann R., Rauch U., Faessler R.;  
RT "Mouse Ten-m/Odz is a new family of dimeric type II transmembrane  
RT proteins expressed in many tissues.";  
RL J. Cell Biol. 0:0-0(1999).  
DR EMBL; AB025411; BAA77397.1; -; mRNA.  
DR HSSP; P35555; 1EMN.  
DR Ensembl; ENSMUSG00000049336; Mus musculus.

DR MGI;1345184; Odz2.  
DR GO; GO:0016021; C:integral to membrane; TAS.  
DR InterPro; IPR000742; EGF\_2.  
DR InterPro; IPR006209; EGF\_like.  
DR InterPro; IPR006210; IEGF.  
DR InterPro; IPR001258; NHL.  
DR InterPro; IPR009471; Ten\_N.  
DR InterPro; IPR006530; YD\_.  
DR Pfam; PF00008; EGF\_3.  
DR Pfam; PF01436; NHL; 6.  
DR Pfam; PF05593; RHS\_repeat; 5.  
DR Pfam; PF06484; Ten\_N; 1.  
DR SMART; SM00181; EGF; 7.  
DR TIGRFAMS; TIGR01643; YD\_repeat\_2x; 5.  
DR PROSITE; PS00022; EGF\_1; 8.  
DR PROSITE; PS01186; EGF\_2; 7.  
DR PROSITE; PS50026; EGF\_3; 4.  
SQ SEQUENCE 2764 AA; 306465 MW; 73BA3D916D0F0344 CRC64;  
  
Query Match 64.6%; Score 9610.5; DB 2; Length 2764;  
Best Local Similarity 61.9%; Pred. No. 0;  
Matches 1769; Conservative 418; Mismatches 489; Indels 181; Gaps 28;  
  
QY 1 MDVKERKPYRSLTRRR-DAERRYTSSSADSEEGKAP-QKSYSSSETLKAYDQDARLAYGS 58  
Db 1 MDVKDORR-HRSLTRGRCGKECRYTSSSLDSDCRVPTQKSYSSSETLKAYDHSRMHYGN 59  
  
QY 59 RVKDIVPQEAEEFCRTGANFTLRELGLLEEVTPPHGTLTYRTDIGLPQCGYSGMAGSDADME 118  
Db 60 RVTDLVHRESDEFSRQGTNFTLAELGICEPS-PHRSGYCSMDGMILHQYSLSTGSDADSD 118  
  
QY 119 ADTVLSPEHPVRLWGRSTRSGRSSCLSSRANSNLTLTDEHENTETDHPG----- 168  
Db 119 TEGGMSPEHAIRLWGRGIKRRSSSGLSSRENSALTLTDSNENKSDDDNGRPIPTSSSS 178  
  
QY 169 -----G 169  
Db 179 LLPSAQLPSSHNPVPVSCOMPLLDSENTSHQIMDTNPDEEFSPNSYLLRACSGPQQASSG 238  
  
QY 170 LQNH---ARLRTPPPLSHAHTPNQHHAASINSLNRGNFTPRSN----PSPAPTDHSLSG 222  
Db 239 PPNHHSQSTLRPLPP-PHNHTLSHHH-SSANSLNRSNLNRRSQIHAPAPAPND--LAT 294  
  
QY 223 EPPAGGAQEPHAQENWLLNSNIPLETRNLGKQPFGLTQDNLIEMDILGASRHDGAYSD 282  
Db 295 TP-----ESVQLQDSWVLNSNVPLETR----- 316  
  
QY 283 GHFLFK-PGGTSPLFCTTSPGYPLTSTVYSPPPRPLRSTFARPAFNLKKPSKYNWKC 341  
Db 317 -HFLFKTSSGSTPLFSSSSPGYPLTSGTVYTPPPRLLPRNTFSRKAFKLKKPSKYCSWK 375  
  
QY 342 AALSAIVISATLVLLAYFVAMHLFGLNWHLPMEGQMVEITEDTASSWPVPTDVSLYPS 401  
Db 376 AALSAIAAALLLAILLAYFIAMHLGLNWLQLPADGHTF--NNGVRTGLPGNDDVATVPS 433  
  
QY 402 GGTGLETPDRKKGKGTTEGKPSSFPPEDSFIDSGEIDVGRRASQKIPPGTFWRSQVFIDHP 461  
Db 434 GGK-----VPWSL--KNSSIDSGEAEVGRRTVQEVPPGVFWRSQIHISQP 476  
  
QY 462 VHLKFNVSLGKAALVGIYGRKGLPPSHQTPDFVELLDGRRLLLTQEARSLGTPRQSRGTV 521  
Db 477 QFLKFNISLGKDALFGVIYIRRGLPSPSHAQYDFMERLDGK-----EKWSVVESPRRRSIQ 531  
  
QY 522 PPSSHETGFIQYLDSGIWHLAFYNDGKESEVVSFLTTAIESVDNCPSCNYGNGDCISGTC 581  
Db 532 TLVQNEAVFVQYLDVGLWHLAFYNDGKDKEMVSFNTVVLDVQDCPRNCHNGECVSGLC 591  
  
QY 582 HCFLGLGPDCCGRASCPVLCSGNGQYMKGRCLCHSGWKGAECDVPTNQCIDVACSNHGTC 641  
Db 592 HCFPGFLGADCAKAACPVLCSGNGQYSKTCQCYSGWKGAECDVPMNQCIDPSCGGHGSC 651  
  
QY 642 ITGTICINPGYKGESCEEVD CMDPTCSGRGVCVRGECHCFVGGWGTNCETPRATCLDQCS 701

Db 652 IDGNCVCAAGYKGEHCEEVDCLDPTCSSHGVCVNGECLCSPGWGGLNCELARVQCPDQCS 711

Qy 702 GHGFELPDTGLCSCDPSWTGHDCSIEICAADCGGHGVCVGGTCRCEDGMMGAACDQRACH 761

Db 712 GHGYLPSGLCSCDPNMWGPCSV-VCSVDCGTHGVGIGACRCEEWTGAACDQRVCH 770

Qy 762 PRCAEHGTCRDGKCECSPGWNGEHCTIAHYLDRVVKEGCPGLCNGNGRCTLDLNGWHCVC 821

Db 771 PRCTEHGTCDKGCECREGNGEHCTI-----DGCPLCNGNGRCTLGQNSWQVCV 821

Qy 822 QLWRGAGCDTSMETACGDSKXNDGDGLVDCMDPDCCLOPLCHINPLCLGSPNPLDIIQE 881

Db 822 QTWRGPGCNVAMETSCADNKDNEGDLVDCLDPDCCLOSACQNSLLCRGSRDPLDIIQQ 881

Qy 882 TQVPVSQQNLHSFYDRIKFLVGRDSTHIIIPGENPFDGGHACVIRGOVMTSDGTPLVGVI 941

Db 882 GQ--TDWPAVKSFYDRIKLLAGKDSTHIIPGDNPFNSLSVLIRGOVVTMDGTPLVGVI 939

Qy 942 SFVNNPLFGYTISRQDGSFDLVTNGGISIIILRFERAPITQEHTLWLPWDRFFVNETIIM 1001

Db 940 SFVKYPKYGYTITRQDGTFDLIANGGSALTLLHFERAPMSQERTVWLPWNSFYAMDTLVM 999

Qy 1002 RHENEIPSCDLSNFARNPVVSPSLTSFASSCAEKGPVPEIQALQEEISISGCKMRL 1061

Db 1000 KTEENSIPSCDLSGFVRPDPIIISPLSTFFSASPASNPIVPETQTVLHEEIELPGTNVKL 1059

Qy 1062 SYLSSRTPGYKSVLRISLTHPTIPFNLMKVHLMVAVEGLFRKWFAAAPDLSYFIWDKT 1121

Db 1060 RYLSRRTAGYKSKLLKITMTQSTVPLNLRVHLMVAVEGHLFQKSFQASPNLAYFIWDKT 1119

Qy 1122 DVYNQVFLGSEAFVSUGYEVESCPDDLILWEKRTTVLQGYEIDASKLGWSLDKXHALNI 1181

Db 1120 DAYGQRVYGLSDAVSVGFYETCPSLILWEKRTALLOGFELDPNLSGGWSLDKXHTLNV 1179

Qy 1182 QSGILHKGNGENQFVSQQPPVTGSIIMGNGRRRSISCPSCNGLADGNKLLAPVALTCGSDG 1241

Db 1180 KSGILHKGTTGENQFLTQQPAIITSIMGNGRRRSISCPSCNGLAEGNKLLAPVALVGIDG 1239

Qy 1242 SLVYGFBNYIRRIFFPSGNVTNILELRNKDFRHSHPAHKYKYLATDPMMSGAVFLSDSNSRR 1301

Db 1240 SLVGFBNYIRRIFFPSRNVTSIELRNKEFKHSNPGHKYKYLAVDPVTGSLYVSDTNSRR 1299

Qy 1302 VFKIKSTVVVKDLVKNSEVVAGTGDQCLPFDDTRCGDGGKATEATLTNPRGITVDKFGLI 1361

Db 1300 IYRVKLSGAKDLAGNSEVVAGTGEQCCLPFDEARCGDGGKAVDATLMSPRGIAVDKNGLM 1359

Qy 1362 YFVDGTWIRRIDQNGIISTLLGSNDLTSARPLSCDSVMDISQVRLEWPTDLAINPMDNSL 1421

Db 1360 YFVDATMIRKVDQNGIISTLLGSNDLTAVRPLSCDSSMDVAQVRLEWPTDLAVNPMDNSL 1419

Qy 1422 YVLDDNNVYLQISENHQVRIVAGRPMHCQVPGIDHFLLSKVAIHATLESATALAVSHNGVL 1481

Db 1420 YVLENNVILRITENHQVSIAGRPMHCQVPGID-YLSLSKLAHSALESASAIASHTGVL 1478

Qy 1482 YIAETDEKKINRIRQVTTSGEISLVAGAPSGCDCKNDANCDFSGDDGYAKDAKLNTPSS 1541

Db 1479 YITETDEKKINRLRQVTTNGEICLLAGAASDCCKNDVNCICYSGDDAYATDAILNSPSS 1538

Qy 1542 LAVCAGELYVADLGNIRIRFIRKNKPFNLTONMYELSSPIDQELYLFDDTTGKHLYTQSL 1601

Db 1539 LAVAPDGTIYIADLGNIRIRAVSKNKPVLNAFNQYEAASPGEQLYVFNADGIHQYTVSL 1598

Qy 1602 PTGDYLVNFTYTGDDITLITDNGNMVNVRDSTGMPLWLVPDGOVYVWVTMTGITSALK 1661

Db 1599 VTGEYLVNFTYSADNDVTELDIDNNGNSLKIRRDSSGMPRHLLMPDNQIITLTVGTNGGLK 1658

Qy 1662 SVTTQGHELAMTYHGNSGLLATKSNENGWTTFFEYDSFGRLTNVTFPTGOVSSFSRSDTD 1721

Db 1659 AVSTQNLELGLMTYDGTGLLATKSDGTWTTFYDYDHEGRLTNVTRPTGVVTSLHREME 1718

Qy 1722 SSVHVQVETSSK-DDVTITTNLSAGAFYTLLODQVRNSYVIGADGSLRLLLANGMEVAL 1780

Db 1719 KSITIDIENSRDDDVITITNLSVVEASYTVVQDQVRNSYQLCNNGTLRVMYANGMAVSF 1778

Qy 1781 QTEPHLLAGTVNPTVGKRNVTLPIDNGLNLVVEWRQKEOARGQVTVFGRRLRVHNRNLLS 1840

Db 1779 HSEPHVLAGTPTIGRCNISLPMENGLNSIEWRLRKEQIKGKVTIFGRKLRVHGRNLLS 1838

Qy 1841 LDFDRVTRTEKIYDDHRKFTLRILYDQAGRPSLWSPSSRLNGVNVTVSPGGYIAGIQRG 1900

Db 1839 IDYDRNIRTEKIYDDHRKFTLRILYDQVGRPFLWLPSSGLAAVNVSYFFNGRLAGLQGA 1898

Qy 1901 MSERMEYDQAGRITSRIFADGKTWSYTYLEKSMVLLLLHSQRQYIFEFDKNDRLSSVTMPN 1960

Db 1899 MSERTDIDKQGRIVSRMFADGKVMWSYSLDKSMVLLLQSORQYIFEYDSSDRLHAVTMS 1958

Qy 1961 VARQTLETIRSVGYRNIYQPPEGNASVQDFTEDGHLHLHTFYLGTGRRVIYKYGKLSKL 2020

Db 1959 VARHSMSTHTSIGYIRNIYNPPESNASVIFYDSDGRILKTSFLGTGRQVYKYGKLSKL 2018

Qy 2021 AETLYDITTKVSFTYDETAGMLKTIINLQNEGFTCTIRYQIGPLIDRQIFRPTEEGMVNAR 2080

Db 2019 SEIVYDSTAVTFGYDETGVLMKNVLOSGGFSCTRIYKVGPLVDKQIYRPFSEEGMINAR 2078

Qy 2081 FDYNY-DNSFRVTSMQAVINETPLPIDLYRYDDVSGKTEQFGKFGVIYDINQIITTAVM 2139

Db 2079 FDYTYHDNSFRIASIKPVISETPLPVDLYRYDEISGKVEHFGKFGVIYDINQIITTAVM 2138

Qy 2140 THTKHFDAYGRMKEVQYEIFRSLMYWMTVOYDNMGRVVKELKVGPIYANTRYSYEYDAD 2199

Db 2139 TLSKHFDTHGRIKEVQYEMFRSLMYWMTVOYDSMGRVVKRELKLGPIYANTKYTYDYDGD 2198

Qy 2200 GOLQTVSINDKPLWRYSYDLNGLNHLLSPGNSARLTPLRYDIRDRITRLGDVQYKMDDEDG 2259

Db 2199 GOLQSVAVNDRPTWRYSYDLNGLNHLNPGNSARLMLPRLYDRIDRLDRITRLGDVQYKIDDDG 2258

Qy 2260 FLRQRGGDIFEYNSAGLLIKAYNRAGSWSYRYRYDGLGRRVSSKSSHSHLQFFYADLTN 2319

Db 2259 YLCQRGSDIFEYNSKGLLTRAYNKASGWSVQYRYDGVGRRASYKTNLGHHLQYFYSDLHN 2318

Qy 2320 PTKVTHLYNHSSEITSLYDYLQHLFAMELSSGDEFYIACDNIGTPLAVFSGTGLMIKQ 2379

Db 2319 PTRITHVYNHSNEITSLYDYLQHLFAMESSSGEEYVVASDNTGTPLAVYSINGLMIKQ 2378

Qy 2380 ILYTAYGEIYMDTNPNFQIIIGYHGGLYDPLTKLVHMGRRDYDVLAGRWTSPDHELWKHL 2439

Db 2379 LOYTAYGEIYDSDNPDFQMVIGFHGGLYDPLTKLVHFTQRDYDVLAGRWTSPDYTMWRNV 2438

Qy 2440 SSSNVMPFNLYMFKNNNPISNSQDIKCFMTDVSNSWLLTFGFLQHLNVIIPGYKPDMDAMEP 2499

Db 2439 GKEPA-PFNLYMFKNNNPLSNELDKNYVTDVKSWLVMFGFQLSNIIPGFPRAKMYFVPP 2497

Qy 2500 SYELIHTQMKTOEWDNSKSIILGVQCEVQKQLKAFVTLERFDQLYGSTITSCQOAPKTKK- 2558

Db 2498 PYELSESQAS----ENGQLITGVQQTTERHNQAFLALE-----GQVITKKLHASIREKA 2547

Qy 2559 ---FASSGSVFGKGVKFALKDGRVTTDIISVANEDGRRVAAILNHAHYLENLHFTIDGVD 2615

Db 2548 GHWFATTTPIIGKIMFAIKEGRVTTGVSSIASEDSRKVASVLNNAYYLDKMHSIEGKD 2607

Qy 2616 THYFVKPGPSEGDALAILGLSGRRRTLENGVNVTVSQINTVLNGRTRRYTDIQLQYGALCL 2675

Db 2608 THYFVKIGAADGDLVTLGTGTIGRKVLESGVNVTVSQPTLLVNGRTRRFTNIEFYSTLLL 2667

Qy 2676 NTRYG---TTLDEEKARVLELARQAVRQAWAREQORLREGEEGLRAWTEGEKQOVLSTG 2732

Db 2668 SIRYGLTPTDLDEEKARVLDQAGQALGTAWAKEQQKARDGREGSRLWTEGEKQOOLLSTG 2727

Qy 2733 RVQYDGGFFVISVEQYPELSDSANNIHFMRQSEMGR 2769

Db 2728 RVQYEGYVYVLPVEQYPELADSSNIQFLRQNEMGKR 2764

RESULT 12  
Q9WTS4\_MOUSE  
ID Q9WTS4\_MOUSE PRELIMINARY; PRT; 2731 AA.





Qy	1466	TLESATALAVSHNGVLYIAETDEKINRIRQVTTSGEISLVAGAPSGCDCKNANDCDFS	1525
Db	1430	TLESARAI SVSHGSLFLIAETDERKNRIQVTTNGEISIIAGAPTDCDCIKIDPNCDFCS	1489
Qy	1526	GDDGYAKDAKLNTPSSSLAVCADGELYVADLGNIRIRFIRKKNKPFLLNTQNMYSSELSSPIDQE	1585
Db	1490	GDDGYAKDAKAKAPSSSLAVSPDGTLYVADLGNVRIRTIISKNAHLNDMNLYEIASPADQE	1549
Qy	1586	LYLFDFTTGKHLTYQSLPTGDYLYNFETYTGDDITLITDNNGNMNVRRDSTGMPLWLVP	1645
Db	1550	LYQFTVNGTHLHTMNLITRDYVYNFTYNAEGDLGAI TSSNGNSVHIRRDAGGMPLWLVP	1609
Qy	1646	DGOVYVMTGNTSALKSVTTQGHELAMMTYHGNSGLLATKSNENGWTTFFEYDSFGRLTN	1705
Db	1610	GGQVYWLTISSNGVLKRVSQAQYNLALMTYPGNTGLLATKSNENGWTTVVEYDPEGHLTN	1669
Qy	1706	VTFTPGOVSSFRSDTSSVHVQVETSSKDDVTITTNLSASGAFYTL LQDQVRNSVYIGAD	1765
Db	1670	ATFPTGEVSSFHSDLEKLT KVALDTSNRENVLMSTNLTATSTIYILKQENTQSTYRVSPD	1729
Qy	1766	GSLRLLANGMEVALQTEPHLLAGTVNPTVGKRNVTLPIDNGLNLVEWRQKEAQGVTT	1825
Db	1730	GSLRVTFASGMEINLSSEPHILAGAVNPTLGKCNISLPGEHANLIEWRQKEQNKGNVS	1789
Qy	1826	VFGRRLRVHNRNLLSLDFRVTRTEKIIDHRKFTLRILYDQAGRPSLWSPSSRLNGVNV	1885
Db	1790	AFERRLRAHNRNLLSIDFDMTRTGKIYDDHRKFTLRILYDQGRPILWSPVSRVNEVNI	1849
Qy	1886	TYSPGGYIAGIQGIMSERMEYDQAGRITSRIFADGKTWSYTYLEKSMVLLLHRSQRQYIF	1945
Db	1850	TYSPSGLVTFIQRTGWNEKMEYDQSGKIIISRTWADGKIWSYTYLEKSMVLLLHRSQRRIYF	1909
Qy	1946	EFDKNDRLSSVTMPNVARQTLETIRSVGYRYRNIYQPPEGNASVTIQDFTEDGHLLHTFYLG	2005
Db	1910	EYDQSDCLLSVTMPMSVHRHSLQTMLSVGYYRNIYTPPDSSTSFQDYSRDRLLQTLHLG	1969
Qy	2006	TGRRVIYKYGKLSKLAETLYDTTKVSFTYDETAGMLKTNLQNEGFTCTIYRQIGPLID	2065
Db	1970	TGRRVLKYKYTKQARLSEILYDTTQVTLTYEESGVIKTIHLMHDGFICTIYRQTGPLIG	2029
Qy	2066	RQIFRFTTEGMVNARFDYNDNSFRVTSMQAVINETPLPIDLYRDDVSGKTEQFGKGV	2125
Db	2030	RQIFRSEGLVNARFDYSY -NNFRVTSMQAVINETPLPIDLYRYVDVSGRTEQFGKFSV	2088
Qy	2126	IYYDINQIITTAVMTHTKHFDAYGRMKEVQYEIIFRSLMYWMTVOYDNMGRVVKELKVGP	2185
Db	2089	INYDLNQVITTTVMKHTKIFNANGQVIEVQYEILKAIAYWMTIQYDNMGRMVICDIRGV	2148
Qy	2186	YANTTRYSYEYDADGLOQTVSINDKPLWRSYDNLGNLHLLSPGNSARLTPLRYDIRDRI	2245
Db	2149	DANITRYFYEYDADGLOQTVSVNDKIQWRSYDNLGNINLLSHGNSARLTPLRYDLDRDI	2208
Qy	2246	TRLGDVQYKXNDEDDGFLRQGGDIFEYNSAGLLIKAYNRAGSWSVRYRYDGLGRRVSSKSS	2305
Db	2209	TRLGEIQYKXNDEDDGFLRQGRNDIFEYNSNGLLQKAYNKVSGWTVQYYYDGLGRRVASKSS	2268
Qy	2306	HSHLQFFYADLTNPTKVTHLYNHSSEITSLYYDLQGHLPANELSSGDEFYIACDNIGT	2365
Db	2269	LGQHLQFFYADLANPIRVTHLYNHTSABITSLYYDLQGHLIAMELSSGEEYYVACDNMGT	2328
Qy	2366	PLAVFSGTGLMIKQILYTAYGEIYMDTNPNFQIIIGYHGGLYDPLTKLVHMGRRDYDVLA	2425
Db	2329	PLAVFSSRGQVIKEILYTPYGDYIYHDTYDPFEVIGFHGGLYDFTKLVLHLGQRDYDVVA	2388
Qy	2426	GRWTSPDHELWKHLSSSNVM--PENLYMFKNNPNISNSODIKCFWMTDVNSWLLTFGFQLH	2483
Db	2389	GRWTTPNHHIWKQL---NLLPKPFNLYSFENNPVVGKIQDVAKYTTDGTWLELFGFQLH	2445
Qy	2484	NVIPGYPKPDMDAMEPSYELIHTQMTQEWDNKSILGVQCEVQQLKAFVTLERFDQLY	2543
Db	2446	NVLPGFPKPELENMELTYELLQLOTKTQEWDPGKMILGIQCELOQLRNFISLDQLPMTP	2505

Qy	2544	GSTITSCQQAPKTKKPASSGSVFGKGVKFKALDKDGRVTTDIIISVANEDGRRRAAILNHAHY	2603
Db	2506	QYNEGRCLGGKQPRFAAVPSVFGKGIKFAIKEGIVTADIIGVANEDSRRLAAILNNAHY	2565
Qy	2604	LENLHFTIDGVDTHYVVKPGPSEGD LAILGLSGGRRTLENGVNVTVSQINTVLNGRTRRY	2663
Db	2566	LENLHFTIEGRDTHYFIKLGSLSEEDLV LIGNTGRRILENGVNVTVSQMTSVLNGRTRRF	2625
Qy	2664	TDIQLQYGALCLNTRYGTTLDDEEKARVLELARQRAVRQAWAREQQORLREGEGLRAWTEG	2723
Db	2626	ADIQLQHGALCFNIRYGTVEEEKNVHLEMARQAVAQAWTQEQRRLQEGEGEGRVWTEG	2685
Qy	2724	EKQVLSTGRVQGYDGFFVISVEQYPELSDSANNIHFMRQSEMGRR	2769
Db	2686	EKQLLGTGRVQGYDGYFVLSVEQYLELSDSANNIHFMRQSEIGRR	2731
RESULT 13			
Q9R1K2_RAT			
ID	Q9R1K2_RAT	PRELIMINARY;	PRT; 2765 AA.
AC	Q9R1K2;		
DT	01-MAY-2000	(TremBLrel. 13, Created)	
DT	01-MAY-2000	(TremBLrel. 13, Last sequence update)	
DT	01-MAR-2004	(TremBLrel. 26, Last annotation update)	
DE	Neurestin alpha.		
GN	Name=Od2;		
OS	Rattus norvegicus (Rat).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;		
OC	Muridae; Murinae; Rattus.		
OX	NCBI_TaxID=10116;		
RN	{1}		
RP	NUCLEOTIDE SEQUENCE.		
RC	STRAIN=Sprague Dawley; TISSUE=Olfactory bulb;		
RX	MEDLINE=99350226; PubMed=10419693; DOI=10.1006/dbio.1999.9310;		
RA	Otaki J.M., Firestein S.;		
RT	"Neurestin: putative transmembrane molecule implicated in neuronal development.";		
RT	Dev. Biol. 212:165-181(1999).		
RL	EMBL; AF086607; AAD47383.1; -; mRNA.		
DR	HSSP; P00750; ITPG.		
DR	Ensembl; ENSRNOG00000011151; Rattus norvegicus.		
DR	RGD; 727907; Od22.		
DR	InterPro; IPR000742; EGF_2.		
DR	InterPro; IPR006209; EGF_like.		
DR	InterPro; IPR006210; IEGF.		
DR	InterPro; IPR001258; NHL.		
DR	InterPro; IPR009471; Ten_N.		
DR	InterPro; IPR006530; YD.		
DR	Pfam; PF00008; EGF; 3.		
DR	Pfam; PF01436; NHL; 6.		
DR	Pfam; PF05593; RHS_repeat; 5.		
DR	Pfam; PF06484; Ten_N; 1.		
DR	SMART; SM00181; EGF; 7.		
DR	TIGRFAMS; TIGR01643; YD_repeat_2x; 5.		
DR	PROSITE; PS00022; EGF_1; 8.		
DR	PROSITE; PS01186; EGF_2; 7.		
DR	PROSITE; PS50026; EGF_3; 4.		
SQ	SEQUENCE 2765 AA; 306569 MW; 6748D70D5FFD8F0E CRC64;		
Query Match 64.5%; Score 9601; DB 2; Length 2765;			
Best Local Similarity 61.8%; Pred. No. 0;			
Matches 1767; Conservative 422; Mismatches 488; Indels 180; Gaps 27;			
Qy	1	MDVKERKPYRSLTRRR-DAERRY TSSSADSEEGKAP-QKSYSSSETLKAYDQDARLAYGS	58
Db	1	MDVKDRR-HRSLTRGRCKECRYTSSSLDSEDCRVFTQKSYSSSETLKAYDHD SRMHYGN	59
Qy	59	RVKDIVPQEAEEFCRTGANFTLRELGLEEVTTPPHGTYLRTDIGLPQC GYSMGAGSDADME	118
Db	60	RVTDLVHRESDEF SRQGANFTLAE L GICEPS-PHRSGYCSDMGILHQGYS LSTGSDADSD	118
Qy	119	ADTVLSPEHPVRLWGRSTRSGRSSCLSSRANSNLTLTDTHEHENTETDHPG-----	168









Db 2326 VFSSRGQVIKEILYTPYGDYHDTYPDFQVVIIFHGSLYDFTLTKLVHLGORDYDVWAGRW 2385

QY 2429 TSPDHELWKHLSSSNVM--PFNLYMFKNPNPISNSODIKCFMTDVNSWLLTFGFLHNVI 2486

Db 2386 TTPNHIIWKQL--NLLPKFPNLYSFENYYPVGKIQDVAKYTTDIRSWLELFGFLHNVL 2442

QY 2487 PGYPKPDMDAMEPSYELIHTQMKTQEWDNKSKILGVCQEVQKQKAFVTLERFDQLYGST 2546

Db 2443 PGFPKPELENLELTYYELLRLQTKTQEWDPGKTIILGTQCELQKQLRNFISLDQLPMTPRYN 2502

QY 2547 ITSQQAQPKTKKFASSGSVFGKGVKFALKDGRVTTDIISVANEDGRRVAAILNHAHYLEN 2606

Db 2503 DGRLEGGKQRFAAVPSVFGKGIKFAIKDGIVTADIIGVANEDSRRLAAILNNAHYLEN 2562

QY 2607 LHFTIDGVDTHYFVKPGPSEGDLAAILGLSGRRRTLENGVNVTVSQINTVLNGRTRRYTDI 2666

Db 2563 LHFTIEGRDTHYFIKLSLEEDLVLI GNTGGRRILENGVNVTVSQMTSVLNGRTRRPADI 2622

QY 2667 QLQYGALCLNTRYGTTLDEEKARVLELARQAVRQAWAREQORLREGEGGLRAWTEGEKQ 2726

Db 2623 QLQHGALCFNIRYGTTVBEKQHVLEIARQRAVAQAWTKQRRLQEGEGEGIRAWTEGEKQ 2682

QY 2727 QVLSTGRVQYDGFVFISVEQYPELSDSANNIHFMRQSEMGRR 2769

Db 2683 QLLSTGRVQYDGYFVLVSEQYLELSDSANNIHFMRQSEIGRR 2725

RESULT 15

Q9UKZ4\_HUMAN

ID Q9UKZ4\_HUMAN PRELIMINARY; PRT; 2725 AA.

AC Q9UKZ4;

DT 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

DE Tenascin-M1.

GN Name=ODZ1; Synonyms=TNM1;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;

OC Homo.

OX NCBI\_TaxId=9606;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RX MEDLINE=20025749; PubMed=10556288; DOI=10.1093/hmg/8.13.2407;

RA Brandau A., Schuster V., Weiss M., Hellebrand H., Fink F.M.,

RA Kreczy A., Friedrich W., Strahm B., Niemeyer C., Belohradsky B.H.,

RA Meindl A.;

RT "Epstein-Barr virus-negative boys with non-Hodgkin lymphoma are

RT mutated in the SH2D1A gene, as are patients with X-linked

RT lymphoproliferative disease (XLP).";

RL Hum. Mol. Genet. 8:2407-2413(1999).

DR EMBL; AF100772; AAF04723.1; -; mRNA.

DR HSSP; P01135; 1MOX.

DR Ensembl; ENSG00000009694; Homo sapiens.

DR HGNC; HGNC:8117; ODZ1.

DR GO; GO:0005576; C:extracellular region; TAS.

DR GO; GO:0008201; F:heparin binding; TAS.

DR GO; GO:0006955; P:immune response; TAS.

DR GO; GO:0008285; P:negative regulation of cell proliferation; TAS.

DR GO; GO:0007399; P:neurogenesis; TAS.

DR InterPro; IPR000742; EGF\_2.

DR InterPro; IPR006209; EGF\_like.

DR InterPro; IPR006210; IEGF.

DR InterPro; IPR001258; NHL.

DR InterPro; IPR000209; Pept\_s8\_s53.

DR InterPro; IPR009471; Ten\_N.

DR InterPro; IPR006530; YD.

DR Pfam; PF00008; EGF; 2.

DR Pfam; PF01436; NHL; 6.

DR Pfam; PF05593; RHS\_repeat; 6.

DR Pfam; PF06484; Ten\_N; 1.

DR SMART; SM00181; EGF; 6.

DR TIGRFAMS; TIGR01643; YD\_repeat\_2x; 5.

DR PROSITE; PS00022; EGF\_1; 8.

DR PROSITE; PS01186; EGF\_2; 7.

DR PROSITE; PS50026; EGF\_3; 5.

DR PROSITE; PS00136; SUBTILASE\_ASP; UNKNOWN 1.

SQ SEQUENCE 2725 AA; 304894 MW; 6F383E64C1B2E1B1 CRC64;

Query Match 63.8%; Score 9501; DB 2; Length 2725;

Best Local Similarity 62.0%; Pred. No. 0;

Matches 1737; Conservative 404; Mismatches 550; Indels 112; Gaps 17;

QY 1 MDVKERKPYRSILTR-RRDAERRYTSSSADSEEGKAPQKYSYSSSETLKAYDQDARLAYGS- 58

Db 1 MEQTDCKPYQPLPKVKHEMDLAYTSSSEDESDGRKPRQSYNSRETLHEYNQELRMNYSQ 60

QY 59 --RVKDIVPQEA-EFCRTGANFTLRELGLEEVTTPPHGTLYRTDI-GLPQCGYSMGAGSD 114

Db 61 SRKRKEVEKSTQEMEFCEHTSLC-----SGYQTDHMSVSRHGYQLEMGS 106

QY 115 ADMEADTVLSPEHPVRLWGRSTRSGRSSCLSSRANSNLTLTDEHENTETDHPGGLQ--- 171

Db 107 VDTETGAASPDHALRMWIRGMKSEHSSCLSSRANSALSLTDTDHER-KSDGENGFKFSP 165

QY 172 -----NহারLR--TPPPPLSHAHTPNQHHAASINSLNRGNFTPRS 209

Db 166 VCCDMEAQAGSTQDVQSSPHNQFTFRPLPPPPPPHACTCARKPPPAADSLQRRSMTTRS 225

QY 210 NPSAPPTDHSLSGEPAGGAQEPAAHQENWLLNSNIPLETRNLGKQPFLGTLQDNLIEMD 269

Db 226 QPSA-----APAPPTSTQDSVHLHNSVNLNSNIPLETR----- 259

QY 270 ILGASRHDGAYSDGHFLFKPG-GTSPLFCTTSPGYPLTSTVYSPPPRPLPRSTFARPAF 328

Db 260 -----HSLFKHSGSSAIFSAASQNYPLTNTVYSPPPRPLPRSTFSRPAF 305

QY 329 NLKPKSKYCNWKCAALSAIVISATLVILLAYFVAMHFLGLNWHLQPMEGQMYEITEDTAS 388

Db 306 TFNKPYRCCNWKCTALSATAITVTLALLAVIAVHLFGLTWQLQPVGELYANGVSKGN 365

QY 389 SWPVPTDVSLYPSGGTGLETPDRKGKGTTECKPSSFFPEDSFIDSGEIDVGRRASQKIPP 448

Db 366 RGTESMDTTYSPIGKVKSDKSEK-----VFQKGRAIDTGEVDIGAQMOTIPP 414

QY 449 GTFWRSQVFIDHPVHLKFNVSGLKAALVGIYGRKGLPPSHTQDFVELLDGRLLTQEAR 508

Db 415 GLFWRFQITIHPIYLKFNISLAKDSLGLIYGRNIPPTHTQDFVKLMDGKQLVKQDSK 474

QY 509 SLEGTPRQSRGTVPSSSHETGFIQYLDSGIWHLAFYNDGKSEVVSFLTTAIESVDNCPS 568

Db 475 GSDDTQHSPRNLILTSLQETGFIYMDQGPWLAFYNDGKQMEQVFLTTAIEMDDCST 534

QY 569 NCYNGGDCISGTCFLGFLGPDCCRASCPLVCSGNGQYMKGRCLCHSGWKGAECDDVPTN 628

Db 535 NCNGNGECISGHCHCFPGFLGPDCCARDSCPVLCGGNGEYKGHCVCRHGWKGPECDVPEE 594

QY 629 QCIDVACSNHGTCTGTICNPGYKGESCEEVDMDPTCSGRGVCVRGECHCFVGWGGTN 688

Db 595 QCIDPTCFGHGTCIMGVICVPGYKGEICEEEDCLDPMCSNHGICVKGECHCSTGMGGVN 654

QY 689 CETPRATCLDQCSGHGTFLPDPTGLCSDPSWTGHDCSIICAADCGGHGVCVGTCRCED 748

Db 655 CETPLPVCQEQCSCGHGTFLLDAGVCSDDPKWTGSDCSTELCTMECGSHGVCSGICQCEE 714

QY 749 GWMGAACDQACHPRCAEHGTCRDGKCECSPGWNGEHCTIAHYLDRVVKEGCGPLCNGNG 808

Db 715 GWVGPTCEERSCHSHCTEHGQCKDGKCECSPGEGDHCTIAHYLD-AVRDGCGLCFGNG 773

QY 809 RCTLDLNGWHCVQLGWRGAGCDTSMETACGSKDNDGDGLVDCMDPDCCLQLCHINPL 868

Db 774 RCTLDQNGWHCVQVGSWGTGCNVVMEMLCGDNLNDGDGLTDCVDPDCCQSNICYISPL 833

QY 869 CLGSPNPLDIIQETQVPVVSQQNLHSFYDRIKFLVGRDSTHIIIPGENPFDGGHACVIRGOV 928

Db 834 CQGSPPDLIIQQSOTLFSQHTSRLFYDRIKFLIGKDSHTHVIPPEVSFDSRRACVIRGOV 893

Qy	929	MTSDGTPLVGVNISFVNNPLFGYTIISRQDGSFDLVNTGGISIIILRERAPPITQEHTLWL	988
Db	894	VAIDGTPLVGVNVSLHHSDYGFTISRQDGSFDLVAIGGISVILIFDRSPFLPEKRTLWL	953
Qy	989	PWDRFFVMETIIMRHEENEIPSCDLSNFARPNPVVSPSPLTSFASSCAEKGPVPEIQAL	1048
Db	954	PWNQFIVVEKVTMQRVVSDPPSCDISNFISPNPVLPSPLTSFGGSCPGRGTIVPELQVV	1013
Qy	1049	QEEISISGCKMRLSYLSSRTPGYKSVLRISLTHPTIPFNLMKVHLMVAVEGRLFRKWFAA	1108
Db	1014	QEEIPIPSSFVRLSYLSSRTPGYKTLRLILLTHSTIPVGMIKVHLTVAVEGRLTQKWFPA	1073
Qy	1109	APDLSYYFIWKTDVYNQKVFLSEAFVSVCYEYESCPDLILWEKRTTVLQGYEIDASKL	1168
Db	1074	AINLVYTFAWNKTDIYGQKVWGLAEALVSVGYEYETCPDFILWEQRTVVVLQGFEMDASNL	1133
Qy	1169	GWSLDKHHALNQSILHKNGENQFVSQQPPVIGSIMGNRRRSISPCSCNGLADGNK	1228
Db	1134	GDWSLNXHHILNPQSGIIHKNGENMFISQQPPVISTIMGNHQRSVACTNCNGPAHNKK	1193
Qy	1229	LLAPVALTCGSDGLYVGFNFYIRRIFFSGNVTNILELRNKDFRHSHPAHKYLLATDPM	1288
Db	1194	LFAPVALASPGDSVYVGFNFVRRIRFPSCNSVSILEL-----STSPAHHYYLAMDPV	1246
Qy	1289	SGAVFLSDSNRRVEKIKSTVVVKDLVKNSEVVAGTGDQCLPFDTRCGDGGKATEATLT	1348
Db	1247	SESLYLSDTNTRKVKYKLSLVETKOLSKNFEVWAGTGDQCLPFDQSHCGDGRASEASLN	1306
Qy	1349	NPRGITVDKFLYFVDGTMIRRIDQNGIISTLLGSNDLTSARPLSCDSVMDISQVRLEW	1408
Db	1307	SPRGITVDRHGFIYFVDGTMIRKIDENAVITTVIGSNGLTSTQPLSCDSGMDITQVRLEW	1366
Qy	1409	PTDLAINPMDNSLYVLDNNVVLQISENHQVRIVAGRPMHCQVPGIDHFLLSKVAIHATLE	1468
Db	1367	PTDLAVNPMDNSLYVLDNNIVLQISENRRVRIIAGRPIHCQVPGIDHFLVSKVAIHSTLE	1426
Qy	1469	SATALAVSHNGVLYIAETDEKKINRIRQVTTSGEISLVAGAPSGCDCKNDANCDCFSGDD	1528
Db	1427	SARAI SVSHSGLLFI AETDERKVNRIQQVTNGEIIYIIAGAPTCDCIDKIDPNCDCFSGDG	1486
Qy	1529	GYAKDAKLNTPSSLAVCADGELYVADLGNIRIRFIRKNKPFNTQNMYELSSPIDQELYL	1588
Db	1487	GYAKOAKMKAPSSLAVSPDGTLYVADLGNVRIRTI SRNQAHLNDMNIYEIASPADQELYQ	1546
Qy	1589	FDTTGKHLYTQSLPTGDYLYNFTYTGDDITLITDNNGNMNVRRDSTGMPLWLVPDQG	1648
Db	1547	FTVNGTHLNLITRDYVYNFTYNSEGLGALITSSNGNSVHIRRDAGGMPLWLVPDGGQ	1606
Qy	1649	VYWVTMGTSALKSVTTQGHELAMMTYHGNSGLLATKSNENGWTTFFEYDSFGRLTNVTF	1708
Db	1607	VYWLTISSNGVLKRVSAQGYNPALMTYPGNTGLLATKSNENGWTTVVEYDPEGHLTNATF	1666
Qy	1709	PTQVSSFRSDTSSVHVQVETSSKDDVTITTNLSAGAFYTLLODQVRNSYYIGADGSL	1768
Db	1667	PTGEVSSFHSDLEKLTKVELDTSNRENVLMTNLATATSTIYILKQENTQSTYRVNPDGSL	1726
Qy	1769	RLLLANGMEVALQTEPHLLAGTVNPTVKRNVTLPIDNGLNLVEWRQKEQARGQVTVFG	1828
Db	1727	RVTFASGMEIGLSSEPHILAGAVNP TLGKCNISLPGEHNNANLIEWRQKEQNKGNVSAFE	1786
Qy	1829	RRLRVHNRNLLSLDFDRVTRTEKIYDDHRKFTLRILYDQAGRPSLWSPSSRLNGVNTYS	1888
Db	1787	RRLRAHNRNLLSIDFDHITRTGKIYDDHRKFTLRILYDQTRPILWSPVSRYNNEVNTYS	1846
Qy	1889	PGYIAGIQGIMSERMEYDQAGRITSRIFADGKTWSYTYLEKSMVLLLLHSQRQYIFEPD	1948
Db	1847	PSGLVTFIQRTWNEKMEYDQSGKII SRTWADGKIWSYTYLEKSMVLLLLHSQRRIPEYD	1906
Qy	1949	KNDRLSSVTMPNPNVARQTLETIRSVGYRNIYQPPPEGNASVIQDFTEDGHLLHTFYLGTGR	2008
Db	1907	QSDCLLSVTMPBSMVRHSLQTMLSVGYYRNIYTPPDSSTSFIDYSRDRGLLQTLHLGTGR	1966
Qy	2009	RVIYKYGKLSKLAETLYDTTKVSFTYDETAGMLKTINLQNEGFTCTIRYRQIGPLIDRQI	2068
Db	1967	RVLKYTKQARLSEVLDTTQVTLTYEESSGVIKTHLMHDGFICTIRYRQTGPLIGRQI	2026
Qy	2069	FRFTEEGMVNARFDYNDNSFRVTSMQAVINETPLPIDLYRYDDVSGKTEQFGKFGVIYY	2128
Db	2027	FRFSEGLVNARFDYSY-NNFRVTSMQAVINETPLPIDLYRYVDVSGRTEQFGKFSVINY	2085
Qy	2129	DINQIITTAVMTHTKHFDAYGRMKEVQYEIFRSLMYMTVOYDNMGRVVKKELKVGPYAN	2188
Db	2086	DLNQVITTTVMKHTKJFSANGQVIEVQYIELKATAWMTIOYDNVGRHGNMCIRVGVDAN	2145
Qy	2189	TTRYSEYDADGQLQTVSINDKPLWRYSYDLNGLHLLSPGNSARLTPLRYDIRDRITRL	2248
Db	2146	ITRYFYEDADGQLQTVSVNDKTQWRYSYDLNGDINLLSHGKSARLTPLRYDLDRITRL	2205
Qy	2249	GDVQYKMDGDFLRQRGDIFEYNSAGLLIKAYNRAGSWSVRYRYDGLGRRVSSKSSHSH	2308
Db	2206	GEIQYKMDGDFLRQRGNDIFEYNSNGLLQKAYNKASGWTVOYYYDGLGRRVASKSSLGQ	2265
Qy	2309	HLQFFYADLTNPTKVTHLYNHSSEITSLYYDLQGHLFAMELSSGDEFYIACDNIGTPLA	2368
Db	2266	HLQFFVDATANPIRVTHLYNHTSSEITSLYYDLQGHLIAMELSSGEEYYVACDNTGTPLA	2325
Qy	2369	VFSGTGLMIKQIILYTAYGEIYMDTNPNFQIILGIVHGGLYDPLTKLVHMGRRDYDVLAGR	2428
Db	2326	VFSSRGQVIKEILYTPGDIYHDTYDPFOVILGIVHGGLYDFTLTKLVHLGQRDYDVVAGR	2385
Qy	2429	TSPDHELWKHLSSSNVM--PFNLYMFKNPNPISNSQDIKCFMTDVNSWLLTFGFQLHNVI	2486
Db	2386	TTAYHHIWKQL---NLLPKPFNLYSFENNYPVGKIQDVAKYTTDIRSWLELFGFQLHNVL	2442
Qy	2487	PGYPKPDMDAMEPSYELIHTQMKTOEWDNKSILGVQCEVQKQKAFVTLERFDQLYGST	2546
Db	2443	PGFPKPELENLELTYELLRLQTKTQEWDPGKTI LGIQCELOKQLRNFISLDQLPMTPRYN	2502
Qy	2547	ITSCQQAPKTKKFASSGSVFGKVKFALKDGRVTTDII SVANEDGRRVAAILNHAHYLEN	2606
Db	2503	DGRCLEGGKQPRFAAVPSVFGKIKFAIKDGI VTADIIGVANEDSRRLAAILNNAHYLEN	2562
Qy	2607	LHFTIDGVDTHYFVKPGPSEGDLA IILGSLGGRRTLENGVNVTVSQINTVLNGRTRRYTDI	2666
Db	2563	LHFTIEGRDTHYFIKLSLEEDLVLIGNTGRRILENGVNVTVSQMTSLNGRTRRFADI	2622
Qy	2667	QLQYGALCLNTRYGTTLDEEKARVLELARQRAVRQAWAREQQORLREGEEGLRAWTEGEKQ	2726
Db	2623	QLQHGALCFNIRYGTTVEEKNHVLEIARQRAVAQAQWTKEQORRLOEGEEGIRAWTEGEKQ	2682
Qy	2727	QVLSTGRVQGYDGFVVISVEQYPELSDSANNIHFMRQSEMGRR	2769
Db	2683	QLLSTGRVQGYDGFVLSVEQYLELSDSANNIHFMRQSEIGRR	2725

Search completed: December 11, 2005, 04:48:10  
Job time : 254 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 11, 2005, 04:48:17 ; Search time 157 Seconds  
(without alignments)  
7369.232 Million cell updates/sec

Title: US-10-029-020-14  
Perfect score: 14887  
Sequence: 1 MDVKERKPYRSLTRRRDAER.....ELSDSANNIHFMRQSEMGR 2769

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA Main:\*  
1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep:\*  
2: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep:\*  
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4: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep:\*  
5: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep:\*  
6: /cgn2\_6/ptodata/1/pubpaa/US11\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	14887	100.0	2769	4 US-10-383-201-44	Sequence 44, Appl
2	14887	100.0	2769	4 US-10-029-020-14	Sequence 14, Appl
3	14748.5	99.1	2758	4 US-10-467-535-10	Sequence 10, Appl
4	14610	98.1	2775	4 US-10-383-201-56	Sequence 56, Appl
5	14529	97.6	2771	3 US-09-808-602-82	Sequence 82, Appl
6	14529	97.6	2771	3 US-09-800-198-70	Sequence 70, Appl
7	14406.5	96.8	2794	4 US-10-042-865-2	Sequence 2, Appli
8	10227	68.7	2715	4 US-10-042-865-52	Sequence 52, Appl
9	10227	68.7	2715	4 US-10-029-020-51	Sequence 51, Appl
10	10221	68.7	2721	4 US-10-038-854-38	Sequence 38, Appl
11	10201	68.5	2725	4 US-10-038-854-36	Sequence 36, Appl
12	9888.5	66.4	2628	4 US-10-038-854-40	Sequence 40, Appl
13	9856	66.2	2613	4 US-10-038-854-42	Sequence 42, Appl
14	9616.5	64.6	2802	3 US-09-808-602-81	Sequence 81, Appl
15	9616.5	64.6	2802	3 US-09-800-198-69	Sequence 69, Appl
16	9616.5	64.6	2802	4 US-10-072-012-489	Sequence 489, App
17	9610.5	64.6	2764	3 US-09-808-602-80	Sequence 80, Appl
18	9610.5	64.6	2764	3 US-09-800-198-68	Sequence 68, Appl
19	9610.5	64.6	2764	4 US-10-072-012-487	Sequence 487, App
20	9610.5	64.6	2764	5 US-10-631-467-1514	Sequence 1514, Ap
21	9601	64.5	2765	3 US-09-808-602-84	Sequence 84, Appl
22	9601	64.5	2765	3 US-09-800-198-72	Sequence 72, Appl
23	9601	64.5	2765	4 US-10-072-012-488	Sequence 488, App
24	9584	64.4	2725	4 US-10-029-020-52	Sequence 52, Appl
25	9584	64.4	2725	4 US-10-408-765A-1687	Sequence 1687, Ap
26	9536	64.1	2733	3 US-09-808-602-8	Sequence 8, Appli
27	9536	64.1	2733	3 US-09-800-198-8	Sequence 8, Appli

28	9530.5	64.0	2724	3 US-09-808-602-13	Sequence 13, Appl
29	9530.5	64.0	2724	3 US-09-800-198-13	Sequence 13, Appl
30	9501	63.8	2725	4 US-10-295-027-928	Sequence 928, App
31	9501	63.8	2725	5 US-10-723-860-4102	Sequence 4102, Ap
32	9418	63.3	2759	4 US-10-072-012-144	Sequence 144, App
33	9314	62.6	2633	4 US-10-144-194A-82	Sequence 82, Appl
34	9314	62.6	2633	5 US-10-491-566-82	Sequence 82, Appl
35	9303	62.5	2590	4 US-10-072-012-490	Sequence 490, App
36	9145	61.4	2346	4 US-10-072-012-491	Sequence 491, App
37	8874	59.6	2551	4 US-10-144-194A-80	Sequence 80, Appl
38	8874	59.6	2551	5 US-10-491-566-80	Sequence 80, Appl
39	8059.5	54.1	2144	5 US-10-723-860-2303	Sequence 2303, Ap
40	6774	45.5	1769	5 US-10-723-860-4494	Sequence 4494, Ap
41	6389.5	42.9	1737	3 US-09-808-602-83	Sequence 83, Appl
42	6389.5	42.9	1737	3 US-09-800-198-71	Sequence 71, Appl
43	6258.5	42.0	1688	4 US-10-144-194A-113	Sequence 113, App
44	6258.5	42.0	1688	5 US-10-491-566-113	Sequence 113, App
45	6258.5	42.0	1688	5 US-10-494-940-52	Sequence 52, Appl

ALIGNMENTS

RESULT 1

US-10-383-201-44  
; Sequence 44, Application US/10383201  
; Publication No. US20040029226A1  
; GENERAL INFORMATION:  
; APPLICANT: Alsobrook II, John et al.  
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHO  
; FILE REFERENCE: 21402-568A  
; CURRENT APPLICATION NUMBER: US/10/383,201  
; CURRENT FILING DATE: 2003-03-06  
; PRIOR APPLICATION NUMBER: 10/029020  
; PRIOR FILING DATE: 2001-12-19  
; PRIOR APPLICATION NUMBER: 60/365,984  
; PRIOR FILING DATE: 2002-03-20  
; PRIOR APPLICATION NUMBER: 60/372,022  
; PRIOR FILING DATE: 2002-04-12  
; PRIOR APPLICATION NUMBER: 60/389,143  
; PRIOR FILING DATE: 2002-06-14  
; PRIOR APPLICATION NUMBER: 60/391,779  
; PRIOR FILING DATE: 2002-06-26  
; PRIOR APPLICATION NUMBER: 60/410,755  
; PRIOR FILING DATE: 2002-09-13  
; PRIOR APPLICATION NUMBER: 60/412,957  
; PRIOR FILING DATE: 2002-09-23  
; PRIOR APPLICATION NUMBER: 10/051,874  
; PRIOR FILING DATE: 2002-01-16  
; PRIOR APPLICATION NUMBER: 60/366,928  
; PRIOR FILING DATE: 2002-03-22  
; PRIOR APPLICATION NUMBER: 10/055,877  
; PRIOR FILING DATE: 2002-01-22  
; NUMBER OF SEQ ID NOS: 155  
; SOFTWARE: CuraseqList version 0.1  
; SEQ ID NO 44  
; LENGTH: 2769  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-383-201-44

Query Match 100.0%; Score 14887; DB 4; Length 2769;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2769; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MDVKERKPYRSLTRRRDAERRYTTSSSADSEEGKAPOKSYSSSETLKAYDQDARLAYGSRV	60
Db	1	MDVKERKPYRSLTRRRDAERRYTTSSSADSEEGKAPOKSYSSSETLKAYDQDARLAYGSRV	60
QY	61	KDIVPQEAEEFCRTGANFTLRELGLEEVTPPHGTLYRTDIGLPQCGYSMGAGSDADMEAD	120
Db	61	KDIVPQEAEEFCRTGANFTLRELGLEEVTPPHGTLYRTDIGLPQCGYSMGAGSDADMEAD	120

QY	121	TVLSPEHPVRLWGRSTRSGRSSCLSSRANSNLTLTDTHEHENTETDHPGGLQNHARL RTPP	180
Db	121	TVLSPEHPVRLWGRSTRSGRSSCLSSRANSNLTLTDTHEHENTETDHPGGLQNHARL RTPP	180
QY	181	PPLSHAHTPNQHHAASINSLNRGNFTPRSNPSPAPT D H S L S G E P P A G G A Q E P A H A Q E N W L	240
Db	181	PPLSHAHTPNQHHAASINSLNRGNFTPRSNPSPAPT D H S L S G E P P A G G A Q E P A H A Q E N W L	240
QY	241	LNSNIPL E T R N L G K O P F L G T L Q D N L I E M D I L G A S R H D G A Y S D G H F L F K P G G T S P L F C T T S	300
Db	241	LNSNIPL E T R N L G K O P F L G T L Q D N L I E M D I L G A S R H D G A Y S D G H F L F K P G G T S P L F C T T S	300
QY	301	P G Y P L T S S T V Y S P P P R P L P R S T F A R P A F N L K K P S K Y C N W K C A A L S A I V I S A T L V I L L A Y F	360
Db	301	P G Y P L T S S T V Y S P P P R P L P R S T F A R P A F N L K K P S K Y C N W K C A A L S A I V I S A T L V I L L A Y F	360
QY	361	V A M H L F G L N W H L Q P M E G Q M Y E I T E D T A S S W P V P T D V S L Y P S G G T G L E T P D R K G K G T T E G K	420
Db	361	V A M H L F G L N W H L Q P M E G Q M Y E I T E D T A S S W P V P T D V S L Y P S G G T G L E T P D R K G K G T T E G K	420
QY	421	P S S F P P E D S F I D S G E I D V G R R A S Q K I P P G T F W R S Q V F I D H P V H L K F N V S L G K A A L V G I Y G	480
Db	421	P S S F P P E D S F I D S G E I D V G R R A S Q K I P P G T F W R S Q V F I D H P V H L K F N V S L G K A A L V G I Y G	480
QY	481	R K G L P S H T Q F D F V E L L D G R R L L T Q E A R S L E G T P R Q S R G T V P P S S H E T G F I Q I Y L D S G I W H	540
Db	481	R K G L P S H T Q F D F V E L L D G R R L L T Q E A R S L E G T P R Q S R G T V P P S S H E T G F I Q I Y L D S G I W H	540
QY	541	L A F Y N D K G E S E W S F L T T A I E S V D N C P S N C Y G N G D C I S G T C H C F L G F L G P D C G R A S C P V L	600
Db	541	L A F Y N D K G E S E W S F L T T A I E S V D N C P S N C Y G N G D C I S G T C H C F L G F L G P D C G R A S C P V L	600
QY	601	C S G N G O Y M K G R C L C H S G W K G A E C D V P T N Q C I D V A C S N H G T C I T G T C I C N P G Y K G E S C E E V	660
Db	601	C S G N G O Y M K G R C L C H S G W K G A E C D V P T N Q C I D V A C S N H G T C I T G T C I C N P G Y K G E S C E E V	660
QY	661	D C M D P T C S G R G V C V R G E C H C F V G W G T N C E T P R A T C L D Q C S G H G T F L P D T G L C S C D P S W T	720
Db	661	D C M D P T C S G R G V C V R G E C H C F V G W G T N C E T P R A T C L D Q C S G H G T F L P D T G L C S C D P S W T	720
QY	721	G H D C S I E I C A A D C G G H G V C V G G T C R C E D G W M G A A C D Q R A C H P R C A E H G T C R D G K C E C S P G	780
Db	721	G H D C S I E I C A A D C G G H G V C V G G T C R C E D G W M G A A C D Q R A C H P R C A E H G T C R D G K C E C S P G	780
QY	781	W N G E H C T I A H Y L D R V V K E G C P G L C N G N G R C T L D L N G W H C V C Q L G W R G A G C D T S M E T A C G D	840
Db	781	W N G E H C T I A H Y L D R V V K E G C P G L C N G N G R C T L D L N G W H C V C Q L G W R G A G C D T S M E T A C G D	840
QY	841	S K O N D G D L V D C M D P D C C L Q P L C H I N P L C L G S P N P L D I I Q E T Q V P V S Q Q N L H S F Y D R I K F	900
Db	841	S K O N D G D L V D C M D P D C C L Q P L C H I N P L C L G S P N P L D I I Q E T Q V P V S Q Q N L H S F Y D R I K F	900
QY	901	L V G R D S T H I I P G E N P P F D G G H A C V I R G Q V M T S D G T P L V G V N I S F V N N P L F G Y T I S R Q D G S F	960
Db	901	L V G R D S T H I I P G E N P P F D G G H A C V I R G Q V M T S D G T P L V G V N I S F V N N P L F G Y T I S R Q D G S F	960
QY	961	D L V T N G G I S I I L R F E R A P F I T Q E H T L W L P W D R F F V M E T I I M R H E E N E I P S C D L S N F A R P N	1020
Db	961	D L V T N G G I S I I L R F E R A P F I T Q E H T L W L P W D R F F V M E T I I M R H E E N E I P S C D L S N F A R P N	1020
QY	1021	P V V S P S P L T S F A S S C A E K G P I V P E I Q A L Q E I S I S G C K M R L S Y L S S R T P G Y K S V L R I S L T	1080
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Db	1081	H P T I P F N L M K V H L M V A V E G R L F R K W F A A A P D L S Y Y F I W D K T D V V N Q K V F G L S E A F V S V G Y	1140
QY	1141	E Y E S C P D L I L W E K R T T V L Q G Y E I D A S K L G W S L D K H H A L N I Q S G I L H K G N G E N Q F V S Q Q P	1200
Db	1141	E Y E S C P D L I L W E K R T T V L Q G Y E I D A S K L G W S L D K H H A L N I Q S G I L H K G N G E N Q F V S Q Q P	1200
QY	1201	P V I G S I M G N G R R R S I S C P S C N G L A D G N K L L A P V A L T C G S D G S L Y V G D F N Y I R R I F P S G N V	1260

Db	1201	P V I G S I M G N G R R R S I S C P S C N G L A D G N K L L A P V A L T C G S D G S L Y V G D F N Y I R R I F P S G N V	1260
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QY	1381	L L G S N D L T S A R P L S C D S V M D I S Q V R L E W P T D L A I N P M D N S L Y L D N N V V L Q I S E N H Q V R I	1440
Db	1381	L L G S N D L T S A R P L S C D S V M D I S Q V R L E W P T D L A I N P M D N S L Y L D N N V V L Q I S E N H Q V R I	1440
QY	1441	V A G R P M H C Q V P G I D H F L L S K V A I H A T L E S A T A L A V S H N G V L Y I A E T D E K K I N R I R Q V T T S	1500
Db	1441	V A G R P M H C Q V P G I D H F L L S K V A I H A T L E S A T A L A V S H N G V L Y I A E T D E K K I N R I R Q V T T S	1500
QY	1501	G E I S L V A G A P S G C D C K N D A N C D C F S G D D G Y A K D A K L N T P S S L A V C A D G E L Y V A D L G N I R I	1560
Db	1501	G E I S L V A G A P S G C D C K N D A N C D C F S G D D G Y A K D A K L N T P S S L A V C A D G E L Y V A D L G N I R I	1560
QY	1561	R F I R K N K P F L N T Q N M Y E L S S P I D Q E L Y L F D T T G K H L Y T Q S L P T G D Y L Y N F T Y T G D G D I T L	1620
Db	1561	R F I R K N K P F L N T Q N M Y E L S S P I D Q E L Y L F D T T G K H L Y T Q S L P T G D Y L Y N F T Y T G D G D I T L	1620
QY	1621	I T D N N G N M V N V R R D S T G M P L W L V V P D G Q V Y V W T M G T N S A L K S V T T Q G H E L A M M T Y H G N S G	1680
Db	1621	I T D N N G N M V N V R R D S T G M P L W L V V P D G Q V Y V W T M G T N S A L K S V T T Q G H E L A M M T Y H G N S G	1680
QY	1681	L L A T K S N E N G W T T F Y E Y D S F G R L T N V T F P T G Q V S S F R S D T D S S V H V Q V E T S S K D D V T I T T	1740
Db	1681	L L A T K S N E N G W T T F Y E Y D S F G R L T N V T F P T G Q V S S F R S D T D S S V H V Q V E T S S K D D V T I T T	1740
QY	1741	N L S A S G A F Y T L L Q D Q V R N S Y Y I G A D G S L R L L L A N G M E V A L Q T E P H L L A G T V N P T V G K R N V	1800
Db	1741	N L S A S G A F Y T L L Q D Q V R N S Y Y I G A D G S L R L L L A N G M E V A L Q T E P H L L A G T V N P T V G K R N V	1800
QY	1801	T L P I D N G L N L V E W R Q R K E Q A R G Q V T V F G R R L R V H N R N L L S L D F D R V T R T E K I Y D D H R K F T	1860
Db	1801	T L P I D N G L N L V E W R Q R K E Q A R G Q V T V F G R R L R V H N R N L L S L D F D R V T R T E K I Y D D H R K F T	1860
QY	1861	L R I L Y D Q A G R P S L W S P S S R L N G V N V T Y S P G Y I A G I O R G I M S E R M E Y D Q A G R I T S R I F A D	1920
Db	1861	L R I L Y D Q A G R P S L W S P S S R L N G V N V T Y S P G Y I A G I O R G I M S E R M E Y D Q A G R I T S R I F A D	1920
QY	1921	G K T W S Y T Y L E K S M V L L H S Q R Q Y I F E F D K N D R L S S V T M P N V A R Q T L E T I R S V G Y Y R N I Y Q	1980
Db	1921	G K T W S Y T Y L E K S M V L L H S Q R Q Y I F E F D K N D R L S S V T M P N V A R Q T L E T I R S V G Y Y R N I Y Q	1980
QY	1981	P P E G N A S V I Q D F T E D G H L L H T F Y L G T G R R V I Y K Y G K L S K L A E T L Y D T T K V S F T Y D E T A G M	2040
Db	1981	P P E G N A S V I Q D F T E D G H L L H T F Y L G T G R R V I Y K Y G K L S K L A E T L Y D T T K V S F T Y D E T A G M	2040
QY	2041	L K T I N L Q N E G F T C T I R Y R Q I G P L I D R Q I F R F T E E G M V N A R F D Y N D S F R V T S M Q A V I N E	2100
Db	2041	L K T I N L Q N E G F T C T I R Y R Q I G P L I D R Q I F R F T E E G M V N A R F D Y N D S F R V T S M Q A V I N E	2100
QY	2101	T P L P I D L Y R Y D D V S G K T E Q F G K F G V I Y Y D I N Q I I T T A V M T H T K H F D A Y G R M K E V Q Y E I F R	2160
Db	2101	T P L P I D L Y R Y D D V S G K T E Q F G K F G V I Y Y D I N Q I I T T A V M T H T K H F D A Y G R M K E V Q Y E I F R	2160
QY	2161	S L M Y W M T V Q Y D N M G R V V K K E L K V G P Y A N T T R Y S Y E Y D A D G Q L O T V S I N D K P L W R Y S Y D L N	2220
Db	2161	S L M Y W M T V Q Y D N M G R V V K K E L K V G P Y A N T T R Y S Y E Y D A D G Q L O T V S I N D K P L W R Y S Y D L N	2220
QY	2221	G N L H L S P G N S A R L T P L R Y D I R D R I T R L G D V Q Y K M D E D G F L R Q G G D I F E Y N S A G L L I K A	2280
Db	2221	G N L H L S P G N S A R L T P L R Y D I R D R I T R L G D V Q Y K M D E D G F L R Q G G D I F E Y N S A G L L I K A	2280
QY	2281	Y N R A G S W S V R Y R Y D G L G R R V S S K S S H H L Q F F Y A D L T N P T K V T H L Y N H S S E I T S L Y Y D	2340

Db 2281 YNRAGSWVRVRYDGLGRRVSSKSSHHLQFFYADLTNPTKVTHLYNHSSEITSLYYD 2340

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Db 2341 LQGHLFAMELSSGDEFYIACDNIGTPLAVFSGTGLMIKQILYTAYGEIYMDTNPNFQIII 2400

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Db 2401 GYHGGLYDPLTKLVHMGRRDYDVLAGRWTSPDHFWKHLSSSNVMPFNLYMFKNKNNPISN 2460

QY 2461 SQDIKCFMTDVNSWLLTFGFQLHNVIPGYPKPDMADAMPSYELIHTQMKTOEWDNSKSIL 2520

Db 2461 SQDIKCFMTDVNSWLLTFGFQLHNVIPGYPKPDMADAMPSYELIHTQMKTOEWDNSKSIL 2520

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Db 2521 GVQCEVQKQKAFVTLERFDQLYGSTITSCQQAPKTKKFASSGSVFGKGVKFALKDGRVT 2580

QY 2581 TDIISVANEDGRRVAAILNHAHYLENLHFTIDGVDTHYFVKPGPSEGD LAILGLSGRRRT 2640

Db 2581 TDIISVANEDGRRVAAILNHAHYLENLHFTIDGVDTHYFVKPGPSEGD LAILGLSGRRRT 2640

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Db 2641 LENGVNVTVSQINTVLNGRRTRYTDIQLQYGALCLNTRYGTTLDEEKARVLELARQAVR 2700

QY 2701 QAWAREQORLREGEGLRAWTEGEKQOVLSTGRVQGYDGFVVISVEQYPELSDSANNIHF 2760

Db 2701 QAWAREQORLREGEGLRAWTEGEKQOVLSTGRVQGYDGFVVISVEQYPELSDSANNIHF 2760

QY 2761 MRQSEMGR 2769

Db 2761 MRQSEMGR 2769

RESULT 2

US-10-029-020-14

; Sequence 14, Application US/10029020

; Publication No. US20040033971A1

; GENERAL INFORMATION:

; APPLICANT: Gangolli et al.

; TITLE OF INVENTION: Polypeptides and Nucleic Acids Encoding Same

; FILE REFERENCE: 21402-225

; CURRENT APPLICATION NUMBER: US/10/029,020

; CURRENT FILING DATE: 2001-12-19

; PRIOR APPLICATION NUMBER: 60/256,704

; PRIOR FILING DATE: 2000-12-19

; PRIOR APPLICATION NUMBER: 60/311,590

; PRIOR FILING DATE: 2001-08-10

; PRIOR APPLICATION NUMBER: 60/257,314

; PRIOR FILING DATE: 2000-12-20

; PRIOR APPLICATION NUMBER: 60/311,613

; PRIOR FILING DATE: 2001-08-10

; PRIOR APPLICATION NUMBER: 60/315,617

; PRIOR FILING DATE: 2001-08-29

; PRIOR APPLICATION NUMBER: 60/307,506

; PRIOR FILING DATE: 2001-07-24

; PRIOR APPLICATION NUMBER: 60/322,358

; PRIOR FILING DATE: 2001-09-14

; PRIOR APPLICATION NUMBER: 60/294,075

; PRIOR FILING DATE: 2001-05-29

; PRIOR APPLICATION NUMBER: 60/288,153

; PRIOR FILING DATE: 2001-05-02

; NUMBER OF SEQ ID NOS: 190

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 14

; LENGTH: 2769

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-029-020-14

Query Match 100.0%; Score 14887; DB 4; Length 2769;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 2769; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDVKERKPYRSLTRRRDAERRYTTSSADSEEGKAPQKSYSSSETLKAYDQDARLAYGSRV 60

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QY 61 KDIVPQEAEEFCRTGANFTLRELGLEEVTPPHGTLYRTDIGLPQCGYSMGAGSDADMEAD 120

Db 61 KDIVPQEAEEFCRTGANFTLRELGLEEVTPPHGTLYRTDIGLPQCGYSMGAGSDADMEAD 120

QY 121 TVLSPEHPVRLWGRSTRSGRSSCLSSRANSNLTLTDEHENTETDHPGGLQNHARLRTPP 180

Db 121 TVLSPEHPVRLWGRSTRSGRSSCLSSRANSNLTLTDEHENTETDHPGGLQNHARLRTPP 180

QY 181 PPLSHAHTPNQHHAAASINSLNRGNFTPRSNPSPAPTDHLSLSEPPAGGAQEPAAHAQENWL 240

Db 181 PPLSHAHTPNQHHAAASINSLNRGNFTPRSNPSPAPTDHLSLSEPPAGGAQEPAAHAQENWL 240

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Db 241 LNSNIPLETRNLGKQPFGLGTLODNLIEMDILGASRHDGAYS DGHFLFKPGGTSPLFCTTS 300

QY 301 PGYPLTSTVYSPPPRPLPRSTFARPAFLNKKPSKYCNWKCAALSAIVISATLVILLAYF 360

Db 301 PGYPLTSTVYSPPPRPLPRSTFARPAFLNKKPSKYCNWKCAALSAIVISATLVILLAYF 360

QY 361 VAMHLFGLNWLQPMEGQMYEITEDTASSWPVPTDVSLYPSGGTGLETPDRKGGTTEGK 420

Db 361 VAMHLFGLNWLQPMEGQMYEITEDTASSWPVPTDVSLYPSGGTGLETPDRKGGTTEGK 420

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Db 421 PSSFFPEDSFIDSGEIDVGRRASQKIPPGTFRSQVFIDHPVHLKENVSLGKAALVGIYG 480

QY 481 RKGLPPSHTQDFVELLDGRRLLTQEARSLGTPRQSRGTVPSSSHETGFIQYLDSGIWH 540

Db 481 RKGLPPSHTQDFVELLDGRRLLTQEARSLGTPRQSRGTVPSSSHETGFIQYLDSGIWH 540

QY 541 LAFYNDGKESEVVSFLTТАIESVDNCPNCGNGDCISGTCFLGLGPDCCGRASCPVL 600

Db 541 LAFYNDGKESEVVSFLTТАIESVDNCPNCGNGDCISGTCFLGLGPDCCGRASCPVL 600

QY 601 CSGNGQYMKGRCLCHSGWKGAECDVPTNQCIDVACSNHGTCITGTICINPGYKGESCEEV 660

Db 601 CSGNGQYMKGRCLCHSGWKGAECDVPTNQCIDVACSNHGTCITGTICINPGYKGESCEEV 660

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Db 661 DCMDPTCSGRGVCVRGECHCFVGWGGTNCETPRATCLDQCSGHGTFLPDTGLCSDPSWT 720

QY 721 GHDCSIEICAADCGGHGVCVGGTCRCEDGWMGAACDQACHPRCAEHGTCRDGKCECSPG 780

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QY 781 WNGEHCTIAHYLDRVVKEGCPGLCNGNGRCTLDLNGWHCVCOLGWRGAGCDTSMETACGD 840

Db 781 WNGEHCTIAHYLDRVVKEGCPGLCNGNGRCTLDLNGWHCVCOLGWRGAGCDTSMETACGD 840

QY 841 SKDNDGDLVDCMDPCCLQPLCHINPLCLGSPNPLDIIQETQVPVSQQNLHSFYDRIKF 900

Db 841 SKDNDGDLVDCMDPCCLQPLCHINPLCLGSPNPLDIIQETQVPVSQQNLHSFYDRIKF 900

QY 901 LVGRDSTHIIIPGENPFDGGHACVIRGOVMTSDGTPLVGNVISFVNNPLFGYTISRQDGSF 960

Db 901 LVGRDSTHIIIPGENPFDGGHACVIRGOVMTSDGTPLVGNVISFVNNPLFGYTISRQDGSF 960

QY 961 DLVTNGGISIIILRFERAPFITQEH TLWL PWD RFFVME TIIMRHEENEIPSCDLSNFARPN 1020

Db 961 DLVTNGGISIIILRFERAPFITQEH TLWL PWD RFFVME TIIMRHEENEIPSCDLSNFARPN 1020

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QY 1081 HPTIPFNLKVKHLMVAVEGRLEFRKWFAAAPDLSYYFIWDKTDVYNQKVFLSEAFVSGY 1140  
Db 1081 HPTIPFNLKVKHLMVAVEGRLEFRKWFAAAPDLSYYFIWDKTDVYNQKVFLSEAFVSGY 1140  
QY 1141 EYESCPDLILWEKRTTVLQGYEIDASKLGGWSLDKXHALNIQSGILHKNGENQFVSQOP 1200  
Db 1141 EYESCPDLILWEKRTTVLQGYEIDASKLGGWSLDKXHALNIQSGILHKNGENQFVSQOP 1200  
QY 1201 PVIIGSIMGNGRRRSISCPSCNGLADGNKLLAPVALTCGSDGSLYVGDFNYIRRIFFPSGNV 1260  
Db 1201 PVIIGSIMGNGRRRSISCPSCNGLADGNKLLAPVALTCGSDGSLYVGDFNYIRRIFFPSGNV 1260  
QY 1261 TNILELRNKDPRHSHSPAKEYLATDPMGAVFLSDSNSRRRVFKIKSTVVVKDLVKNSEV 1320  
Db 1261 TNILELRNKDPRHSHSPAKEYLATDPMGAVFLSDSNSRRRVFKIKSTVVVKDLVKNSEV 1320  
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Db 1321 VAGTGDQCLPFDDTRCGDGGKATEATLTNPRGITVDKFGLIYFVDGTMIRRIDQNGIIST 1380  
QY 1381 LLGSNDLTSARPLSCDSVMDISQVRLEWPTDLAINPMDNSLYVDNNVVVLQISENHQVRI 1440  
Db 1381 LLGSNDLTSARPLSCDSVMDISQVRLEWPTDLAINPMDNSLYVDNNVVVLQISENHQVRI 1440  
QY 1441 VAGRPMHCQVPGIDHFLLSKVAIHATLESATALAVSHNGVLYIAETDEKKINRIRQVTTTS 1500  
Db 1441 VAGRPMHCQVPGIDHFLLSKVAIHATLESATALAVSHNGVLYIAETDEKKINRIRQVTTTS 1500  
QY 1501 GEISLVAGAPSGCDCKNANDCFSGDDGYAKDAKLNTPSSILAVCADGELYVADLGNIRI 1560  
Db 1501 GEISLVAGAPSGCDCKNANDCFSGDDGYAKDAKLNTPSSILAVCADGELYVADLGNIRI 1560  
QY 1561 RFIRKNKPFINTQNMVELSSPIDQELYLFDTTGKHLYTQSILPTGDLYLNFTYTGDDITL 1620  
Db 1561 RFIRKNKPFINTQNMVELSSPIDQELYLFDTTGKHLYTQSILPTGDLYLNFTYTGDDITL 1620  
QY 1621 ITDNNGNMNVNRRDSTGMPLWLVPDQVYVWVTMGNTNSALKSVTTQGHELAMMTYHGN SG 1680  
Db 1621 ITDNNGNMNVNRRDSTGMPLWLVPDQVYVWVTMGNTNSALKSVTTQGHELAMMTYHGN SG 1680  
QY 1681 LLATKSNENGWTTFFEYDSFGRLTNVTFPTGQVSSFRSDTSSVHVQVETSSKDDVTITT 1740  
Db 1681 LLATKSNENGWTTFFEYDSFGRLTNVTFPTGQVSSFRSDTSSVHVQVETSSKDDVTITT 1740  
QY 1741 NLSASGAFYTLLODQVRNSYYIGADGSLRLLLLANGMEVALQTEPHLLAGTVNPTVGKRN V 1800  
Db 1741 NLSASGAFYTLLODQVRNSYYIGADGSLRLLLLANGMEVALQTEPHLLAGTVNPTVGKRN V 1800  
QY 1801 TLPIDNGLNLVEWRQORKEARGQVTVFGRRLRVHNRNLLSLDFDRVTRTEKIYDDHRKFT 1860  
Db 1801 TLPIDNGLNLVEWRQORKEARGQVTVFGRRLRVHNRNLLSLDFDRVTRTEKIYDDHRKFT 1860  
QY 1861 LRILYDQAGRPSLWSPSSRLNGVNVTVSPGGYIAGIQGIMSERMEYDQAGRITSRIFAD 1920  
Db 1861 LRILYDQAGRPSLWSPSSRLNGVNVTVSPGGYIAGIQGIMSERMEYDQAGRITSRIFAD 1920  
QY 1921 GKTWSYTYLEKSMVLLLLHSORQYIFEFDKNDRLSSVTMPNVAROTLETIRSVGYVRNIYQ 1980  
Db 1921 GKTWSYTYLEKSMVLLLLHSORQYIFEFDKNDRLSSVTMPNVAROTLETIRSVGYVRNIYQ 1980  
QY 1981 PPEGNASVIQDFTEDGHLHHTFYLGTGRRVIYKYGKLSKLAETLYDTTKVSFTYDETAGM 2040  
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Db 2041 LKTINLQNEGFTCTIRYRQIGPLIDRQIFRFTEEGMVNARFDYDNSFRVTSMQAVINE 2100  
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Db 2101 TPLPIDLYRYDDVSGKTEQFGKFGVIYYDINQIITTAVMTHTKHFDAYGRMKEVOYEIFR 2160

QY 2161 SLMYWMTVQYDNMGRVVKELKVGYPYANTTRYSEYDADGQLQTVSINDKPLWRYSYDLN 2220  
Db 2161 SLMYWMTVQYDNMGRVVKELKVGYPYANTTRYSEYDADGQLQTVSINDKPLWRYSYDLN 2220  
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Db 2221 GNLHLLSPGNSARLTPLRYDIRDRITRLGDVQYKMDDEDGFLRQGGDIFEYNSAGLLIKA 2280  
QY 2281 YNRAGSWSVRRYRVDGLGRRVSSKSSHSHLQFFYADLTNPTKVTHLYNHSSEITSLYYD 2340  
Db 2281 YNRAGSWSVRRYRVDGLGRRVSSKSSHSHLQFFYADLTNPTKVTHLYNHSSEITSLYYD 2340  
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Db 2341 LQGHLFAMELSSGDEFYIACDNIGTPLAVFSGTGLMIKQIILYTAYGEIYMDTNPNFQIII 2400  
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QY 2461 SQDIKCFMTDVNSWLLTFGFQLHNVIPGYPKPDMDAMEPSYELIHTQMKTOEWDNSKSIL 2520  
Db 2461 SQDIKCFMTDVNSWLLTFGFQLHNVIPGYPKPDMDAMEPSYELIHTQMKTOEWDNSKSIL 2520  
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QY 2761 MRQSEMGR 2769  
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RESULT 3  
US-10-467-535-10  
; Sequence 10, Application US/10467535  
; Publication No. US20040146970A1  
; GENERAL INFORMATION:  
; APPLICANT: YUE, Henry; YAO, Monique G.  
; APPLICANT: ISON, Craig H.; LU, Yan  
; APPLICANT: WARREN, Bridget A.; ELLIOTT, Vicki S.  
; APPLICANT: BAUGHN, Mariah R.; DING, Li  
; APPLICANT: XU, Yuming; GIETZEN, Kimberly J.  
; APPLICANT: TANG, Tom Y.; LAL, Preeti G.  
; APPLICANT: DUGGAN, Brendan M.; BURFORD, Neil  
; APPLICANT: LU, Dyung Aina M.; RICHARDSON, Thomas W.  
; APPLICANT: TRAN, Uyen K.; KHARE, Reena  
; APPLICANT: CHAWLA, Narinder K.  
; TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL GROWTH, DIFFERENTIATION, AND DEATH  
; FILE REFERENCE: PF-0903 USN  
; CURRENT APPLICATION NUMBER: US/10/467,535  
; CURRENT FILING DATE: 2003-08-08  
; PRIOR APPLICATION NUMBER: PCT/US02/03715  
; PRIOR FILING DATE: 2002-08-02  
; PRIOR APPLICATION NUMBER: US 60/268,111  
; PRIOR FILING DATE: 2001-02-09  
; PRIOR APPLICATION NUMBER: US 60/271,175  
; PRIOR FILING DATE: 2001-02-23  
; PRIOR APPLICATION NUMBER: US 60/274,503  
; PRIOR FILING DATE: 2001-03-08  
; PRIOR APPLICATION NUMBER: US 60/274,552

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; PRIOR FILING DATE: 2001-03-09
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PERL Program
; SEQ ID NO 10
; LENGTH: 2758
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No: 7488573CD1
US-10-467-535-10

Query Match      99.1%; Score 14748.5; DB 4; Length 2758;
Best Local Similarity 99.3%; Pred. No. 0;
Matches 2751; Conservative 0; Mismatches 7; Indels 11; Gaps 3;

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Db 61 KDIVPQEAEEFCRTGANFTLRELGLEEVTTPPHGTLVRTDIGNLPCQGYSMGAGSDADMEAD 120

QY 121 TVLSPEHPVRLWGRSTRSGRSSCLSSRANSNLTLTDTHEHENTETDHPGGLQNHARLRTPP 180
Db 121 TVLSPEHPVRLWGRSTRSGRSSCLSSRANSNLTLTDTHEHENTET--PGGLQNHARLRTPP 178

QY 181 PPLSHAHTPNQHHAAASINSLNRGNFTPRSNPSPAPTDHSLSGEPPAGGAQEPAAHQENWL 240
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QY 241 LNSNIPLERNLGKQPFGLTLQDNLIEMDILGASRHDGAYSFGHFLFKPGGTSPLFCCTS 300
Db 239 LNSNIPLERNLGKQPFGLTLQDNLIEMDILGASRHDGAYSFGHFLFKPGGTSPLFCCTS 298

QY 301 PGYPLTSSTVSPRRPLPRSTFARPAFNLKKPSKYCNWKAALSAIVISATLVILLAYF 360
Db 299 PGYPLTSSTVSPRRPLPRSTFARPAFNLKKPSKYCNWKAALSAIVISATLVILLAYF 358

QY 361 VAMHLFGLNWHLQPMEGOMYEITEDTASSWPVPTDVSLYPSGGTGLETPDRKKGKGTTEGK 420
Db 359 VKGHLF--NWHLQPMEGOMYEITEDTASSWPVPTDVSLYPSGGTGLETPDRKKGKGTTEGK 416

QY 421 PSSFFPEDSFIDSGEIDVGRASQKIPPGTFWRQSVFIDHPVHLKFNVSLGKAALVGIYG 480
Db 417 PSSFFPEDSFIDSGEIDVGRASQKIPPGTFWRQSVFIDHPVHLKFNVSLGKAALVGIYG 476

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Db 477 RKGLPPSHTQDFVELLDGRRLLTQEARSLGTPRQSRGTVPSPSSHETGFIQYLDSGIWH 536

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Db 537 LAFYNDGKESEVVSFLTTAIESVDNCPSNCYGNGDCISGTCHCFGLGFLGPCGGRASCPVL 596

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Db 597 CSGNGQYMKGRCLCHSGWKGAECVPTNQCIDVACSNHGTCTGTCTICNPGYKGESCEEV 656

QY 661 DCMDDPTCSGRGVCVRGECHCFVWGCGTNCETPRATCLDQCSGHGTFELPDTGLCSCDSPWT 720
Db 657 DCMDDPTCSGRGVCVRGECHCSVGWCGTNCETPRATCLDQCSGHGTFELPDTGLCSCDSPWT 716

QY 721 GHDCSIEICAADCGGHGVCVGGTCRCEDGWMGAACDQACHPRCAEHGTCRDGKCECPG 780
Db 717 GHDCSIEICAADCGGHGVCVGGTCRCEDGWMGAACDQACHPRCAEHGTCRDGKCECPG 776

QY 781 WNGEHCTIAHYLDRVVKEGCPGLCNGNGRCRTLNLNGWHVCQLGWRGAGCDTSMETACGD 840
Db 777 WNGEHCTIAHYLDRVVKEGCPGLCNGNGRCRTLNLNGWHVCQLGWRGAGCDTSMETACGD 836

QY 841 SKDNDGDLVDCMDPDCCCLQPLCHINPLCLGSPNPLDIIQETQVPVSVQQNLHSFYDRIKF 900
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Db 837 SKDNDGDLVDCMDPDCCCLQPLCHINPLCLGSPNPLDIIQETQVPVSVQQNLHSFYDRIKF 896

QY 901 LVGRDSTHIIIPGENPFDGGHACVIRGQVMTSDGTPLVGNVISFVNPLFGYTISRQDGSF 960
Db 897 LVGRDSTHIIIPGENPFDGGHACVIRGQVMTSDGTPLVGNVISFVNPLFGYTISRQDGSF 956

QY 961 DLVTNGGISIIILFERAPFITOEHTLWLPWDRFFVMEIIMRHEENEIPSCDLSNFARPN 1020
Db 957 DLVTNGGISIIILFERAPFITOEHTLWLPWDRFFVMEIIMRHEENEIPSCDLSNFARPN 1016

QY 1021 PIVSPSPLTSFASSCAEKGPVPEIQALQEEISISGCKMRLSYLSSRTPGYKSVLRISLT 1080
Db 1017 PIVSPSPLTSFASSCAEKGPVPEIQALQEEISISGCKMRLSYLSSRTPGYKSVLRISLT 1076

QY 1081 HPTIPFNLKVMHLMVAVEGRLEFRKWFAAAPDLSYFIWDKTDVYNQKVFGLSEAFVSVGY 1140
Db 1077 HPTIPFNLKVMHLMVAVEGRLEFRKWFAAAPDLSYFIWDKTDVYNQKVFGLSEAFVSVGY 1136

QY 1141 EYESCPDLILWEKRTTVLQGYEIDASKLGGWSLDKHALNIQSGILHKNGENQFVSQQP 1200
Db 1137 EYESCPDLILWEKRTTVLQGYEIDASKLGGWSLDKHALNIQSGILHKNGENQFVSQQP 1196

QY 1201 PVIGSIMGNRRRSISCPSCNGLADGNKLLAPVALTCGSDGLYVGDFNYIRRIFFPSGNV 1260
Db 1197 PVIGSIMGNRRRSISCPSCNGLADGNKLLAPVALTCGSDGLYVGDFNYIRRIFFPSGNV 1256

QY 1261 TNILELRNKDFRSHSPAHKYYLATDPMMSGAVFLSDSNSRRVFKIKSTVVVKDLVKNSEV 1320
Db 1257 TNILEL-----SHSPAHKYYLATDPMMSGAVFLSDSNSRRVFKIKSTVVVKDLVKNSEV 1309

QY 1321 VAGTGDQCLPFDDTRCGDGGKATEATLTNPRGITVDKFGLIYFVDGTMIRRIDQNGIIST 1380
Db 1310 VAGTGDQCLPFDDTRCGDGGKATEATLTNPRGITVDKFGLIYFVDGTMIRRIDQNGIIST 1369

QY 1381 LLGSNDLTSARPLSCDSVMDISQVRLEWPTDLAINPMDNSLYVLDDNNVVLQISENHQVRI 1440
Db 1370 LLGSNDLTSARPLSCDSVMDISQVHLEWPTDLAINPMDNSLYVLDDNNVVLQISENHQVRI 1429

QY 1441 VAGRPMHCQVPGIDHFLLSKVAIHATLESATALAVSHNGVLYIAETDEKKINIRQVTTTS 1500
Db 1430 VAGRPMHCQVPGIDHFLLSKVAIHATLESATALAVSHNGVLYIAETDEKKINIRQVTTTS 1489

QY 1501 GEISLVAGAPSGCCKNDANCDCFSGDDGYAKDAKLNTPSSLAVCADGELYVADLGNIRI 1560
Db 1490 GEISLVAGAPSGCCKNDANCDCFSGDDGYAKDAKLNTPSSLAVCADGELYVADLGNIRI 1549

QY 1561 RFIRKNKPFNLNTQMYELSSPIDQELYLFDTTGKHLYTQSLPTGDLYNFTYTGDGDIITL 1620
Db 1550 RFIRKNKPFNLNTQMYELSSPIDQELYLFDTTGKHLYTQSLPTGDLYNFTYTGDGDIITL 1609

QY 1621 ITDNNGNMNVRRDSTGMPLWLVPDQGVYVWVTMGTSNLSALKSVTTQGHELAMMTYHGNSG 1680
Db 1610 ITDNNGNMNVRRDSTGMPLWLVPDQGVYVWVTMGTSNLSALKSVTTQGHELAMMTYHGNSG 1669

QY 1681 LLATKSNENGWTTTFEYDSFGRLTNVTFTPTQGVSSFRSDTSSVHVQVETSSKDDVTITT 1740
Db 1670 LLATKSNENGWTTTFEYDSFGRLTNVTFTPTQGVSSFRSDTSSVHVQVETSSKDDVTITT 1729

QY 1741 NLSASGAFYTLQDQVRNSYYIGADGSLRLLLLANGMEVALQTEPHLLAGTVNPTVGKRN 1800
Db 1730 NLSASGAFYTLQDQVRNSYYIGADGSLRLLLLANGMEVALQTEPHLLAGTVNPTVGKRN 1789

QY 1801 TLPIDNGLNLVEWRQREKQARGQVTVFGRRLRVHNRNLLSLDFDVRTTEKIYDDHRKFT 1860
Db 1790 TLPIDNGLNLVEWRQREKQARGQVTVFGRRLRVHNRNLLSLDFDVRTTEKIYDDHRKFT 1849

QY 1861 LRILYDQAGRPSLWSPSSRLNGVNVITYSPGGYIAGIQRGIMSERMEYDQAGRITSRIFAD 1920
Db 1850 LRILYDQAGRPSLWSPSSRLNGVNVITYSPGGYIAGIQRGIMSERMEYDQAGRITSRIFAD 1909

QY 1921 GKTWSYTYLEKSMVLLLSQRQYIFEEFDKNDRLLSSWTMPNVARQTLETIRSVGYRNIIYQ 1980
Db 1910 GKTWSYTYLEKSMVLLLSQRQYIFEEFDKNDRLLSSWTMPNVARQTLETIRSVGYRNIIYQ 1899
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Db 1910 GKTWSYTYLEKSMVLLHSQRQYIFEFDKNDRLSVTPMPNVARQTILETIRSVGYRNIYQ 1969

QY 1981 PPEGNASVIQDFTEDGHLHLHTFYLGTGRRRVYKYGKLSKLAETLYDTTKVSFTYDETAGM 2040

Db 1970 PPEGNASVIQDFTEDGHLHLHTFYLGTGRRRVYKYGKLSKLAETLYDTTKVSFTYDETAGM 2029

QY 2041 LKTINLQNEGFTCTIRYRQIGPLIDRQIFRFTTEGMVNARFDYNDNSFRVTSMQAVINE 2100

Db 2030 LKTINLQNEGFTCTIRYRQIGPLIDRQIFRFTTEGMVNARFDYNDNSFRVTSMQAVINE 2089

QY 2101 TPLPIDLYRYDDVSGKTEQFGKFGVIYYDINQIITTAVMTHTKHFDAYGRMKEVQYEIFR 2160

Db 2090 TPLPIDLYRYDDVSGKTEQFGKFGVIYYDINQIITTAVMTHTKHFDAYGRMKEVQYEIFR 2149

QY 2161 SLMYWMTVQYDNMGRVVKKELKVGPYANTTRYSYEYDADGQLQTVSINDKPLWRYSYDLN 2220

Db 2150 SLMYWMTVQYDNMGRVVKKELKVGPYANTTRYSYEYDADGQLQTVSINDKPLWRYSYDLN 2209

QY 2221 GNLHLLSPGNSARLTPLRYDIRDRITRLGDVQYKMDGEDGFLRQRGDIFEYNSAGLLIKA 2280

Db 2210 GNLHLLSPGNSARLTPLRYDIRDRITRLGDVQYKMDGEDGFLRQRGDIFEYNSAGLLIKA 2269

QY 2281 YNRAGSWSVRYDGLGRRVSSKSSHHLQFFYADLTNPTKVTHLYNHSSEITSLYYD 2340

Db 2270 YNRAGSWSVRYDGLGRRVSSKSSHHLQFFYADLTNPTKVTHLYNHSSEITSLYYD 2329

QY 2341 LQGHLFAMELSSGDEFYIACDNIGTPLAVFSGTGLMIKQILYTAYGEIYMDTNPNFQII 2400

Db 2330 LQGHLFAMELSSGDEFYIACDNIGTPLAVFSGTGLMIKQILYTAYGEIYMDTNPNFQII 2389

QY 2401 GYHGGLYDPLTKLVHMGRDDYDVLAGRWTSPDHELWKHLSSSNVMPFNLYMFKNNPISN 2460

Db 2390 GYHGGLYDPLTKLVHMGRDDYDVLAGRWTSPDHELWKHLSSSNVMPFNLYMFKNNPISN 2449

QY 2461 SQDIKCFMTDVNSWLLTFGFQLHNVI PGYPKPDMDAMEPSYELIHTQMKTOEWDNSKIL 2520

Db 2450 SQDIKCFMTDVNSWLLTFGFQLHNVI PGYPKPDMDAMEPSYELIHTQMKTOEWDNSKIL 2509

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Db 2510 GVQCEVQQLKAFVTLERFDQLYGSTITSCQQAPKTKKFASGSGVFGKGVKFAKDGRT 2569

QY 2581 TDIISVANEDGRRVAAILNHAHYLENLHFTIDGVDTTHYFVKPGPSEGDLAILGLSGGRT 2640

Db 2570 TDIISVANEDGRRVAAILNHAHYLENLHFTIDGVDTTHYFVKPGPSEGDLAILGLSGGRT 2629

QY 2641 LENGVNVTVSQINTVLNGRTRRYTDIQLQYGALCLNTRYGTTLDDEKARVLELARQAVR 2700

Db 2630 LENGVNVTVSQINTVLNGRTRRYTDIQLQYGALCLNTRYGTTLDDEKARVLELARQAVR 2689

QY 2701 QAWAREQORLREGEGLRAWTEGEKQVLS TGRVOGYDGFVISVEQYPELSDSANNIHF 2760

Db 2690 QAWAREQORLREGEGLRAWTEGEKQVLS TGRVOGYDGFVISVEQYPELSDSANNIHF 2749

QY 2761 MRQSEMGR 2769

Db 2750 MRQSEMGR 2758

RESULT 4

US-10-383-201-56

; Sequence 56, Application US/10383201

; Publication No. US20040029226A1

; GENERAL INFORMATION:

; APPLICANT: Alsobrook II, John et al.

; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD

; FILE REFERENCE: 21402-568A

; CURRENT APPLICATION NUMBER: US/10/383,201

; CURRENT FILING DATE: 2003-03-06

; PRIOR APPLICATION NUMBER: 10/029020

; PRIOR FILING DATE: 2001-12-19

; PRIOR APPLICATION NUMBER: 60/365,984

; PRIOR FILING DATE: 2002-03-20

; PRIOR APPLICATION NUMBER: 60/372,022

; PRIOR FILING DATE: 2002-04-12

; PRIOR APPLICATION NUMBER: 60/389,143

; PRIOR FILING DATE: 2002-06-14

; PRIOR APPLICATION NUMBER: 60/391,779

; PRIOR FILING DATE: 2002-06-26

; PRIOR APPLICATION NUMBER: 60/410,755

; PRIOR FILING DATE: 2002-09-13

; PRIOR APPLICATION NUMBER: 60/412,957

; PRIOR FILING DATE: 2002-09-23

; PRIOR APPLICATION NUMBER: 10/051,874

; PRIOR FILING DATE: 2002-01-16

; PRIOR APPLICATION NUMBER: 60/366,928

; PRIOR FILING DATE: 2002-03-22

; PRIOR APPLICATION NUMBER: 10/055,877

; PRIOR FILING DATE: 2002-01-22

; NUMBER OF SEQ ID NOS: 155

; SOFTWARE: CuraSeqList version 0.1

; SEQ ID NO 56

; LENGTH: 2775

; TYPE: PRT

; ORGANISM: Homo sapiens

; US-10-383-201-56

Query Match 98.1%; Score 14610; DB 4; Length 2775;

Best Local Similarity 98.2%; Pred. No. 0;

Matches 2743; Conservative 2; Mismatches 6; Indels 42; Gaps 12;

QY 1 MDVKERKPYRSLTRRRDAERRY TSSADSEEGKAPOKSYSSSETLKAYDQDARLAYGSRV 60

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QY 61 KDIVPQEAEEFCRTGANFTLRELGLEEVTPPHGTLYRTDIGLPQCQGYSMGAGSDADMEAD 120

Db 61 KDIVPQEAEEFCRTGANFTLRELGLEEVTPPHGTLYRTDIGLPQCQGYSMGAGSDADMEAD 120

QY 121 TVLSPEHPVRLWGRSTRSGRSSCLSSRANSNLTLTDEHENTETDHPGGLQNHARLRTPP 180

Db 121 TVLSPEHPVRLWGRSTRSGRSSCLSSRANSNLTLTDEHENTETDHPGGLQNHARLRTPP 180

QY 181 PPLSHAHTPNQHHAAASINSLNRGNFTPRSNPSPAPTDHSLSGEPAGGAQEPAAHAQENWL 240

Db 181 PPLSHAHTPNQHHAAASINSLNRGNFTPRSNPSPAPTDHSLSGEPAGGAQEPAAHAQENWL 240

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Db 241 LNSNIPLERNLGKQPFLGTLDNLNLIEMDILGASRHDGAYSDGHFLFKPGTSPFLCFTTS 300

QY 301 PGYPLTSSTVYSPPPRPLPRSTFARPAFNLKKPSKYCNWKCAALSAIVISATLVILLAYF 360

Db 301 PGYPLTSSTVYSPPPRPLPRSTFARPAFNLKKPSKYCNWKCAALSAIVISATLVILLAYF 360

QY 361 VAMHLFGLNWHLQPMEGOMYEITEDTASSWPVPTDVSLYPSGGTGLETPDRKGKGTTEGK 420

Db 361 VAMHLFGLNWHLQPMEGOMYEITEDTASSWPVPTDVSLYPSGGTGLETPDRKGKGTTEGK 420

QY 421 PSSFFPEDSFIDSGEIDVRRASQKIPPGTFWRSQVFIHVPVHLKPNVSLGKAALVGIYG 480

Db 421 PSSFFPEASFIDSGEIDVRRASQKIPPGTFWRSQVFIHVPVHLKPNVSLGKAALVGIYG 480

QY 481 RKGLPPSHTQDFVELLDGRRLLTOEARSLEGTPRQSRGTVPSPSSHETGFIQYLDSGIWH 540

Db 481 RKGLPPSHTQDFVELLDGRRLLTOEARSLEGTPRQSRGTVPSPSSHETGFIQYLDSGIWH 540

QY 541 LAFYNDGKSEWVSFLTAAIESVDNCPSNCYNGDCISGTCCHCFLGFLGPDCCGRASCPVL 600

Db 541 LAFYNDGKSEWVSFLSP--ESVDNCPSNCYNGDCISGTCCHCFLGFLGPDCCGRASCPVL 598

QY 601 CSGNGQYMKGRCLCHSGWKGAECVPTNQCIDVACSNHGTCITGTICNPNPYKGESCEEV 660

Db 599 CSGNGQYMKGRCLCHSGWKGAECVPTNQCIDVACSNHGTCITGTICNPNPYKGESCEE- 657

QY 661 DCMDDPTCSGRGVCVRGECHCFVWGWTNCETPRATCLDQCSHGHTFLPDTGLCSCDPSWT 720



Db 658 DCMPTCSGRGVCVRECHCSVGWGTNCETPRATCLDQCSGHGTFLPDTGLCSCDPSWT 717  
Qy 721 GHDCSIEICAADCGGHGVCVGGTCRCEDGWMGAACDORACHPRCAEHGTCRDGKCECSPG 780  
Db 718 GHDCSIEICAADCGGHGVCVGGTCRCEDGWMGAACDORACHPRCAEHGTCRDGKCECSPG 777  
Qy 781 WNGEHCTI--AHYLDRVVK--EGCPGLCNGNGRCTLDLNGWHVCVQLGWRGAGCDTSMET 836  
Db 778 WNGEHCTIISLAHYLDRVVVKLSEGPCPLCNGNGRCTLDLNGWHVCVQLGWRGAGCDTSMET 837  
Qy 837 ACGDSKONDGGLVDCMDPDCCLQPLCHINPLCLGSPNPLDIIQETQVPVSOQNLSFYD 896  
Db 838 ACGDSKONDGGLVDCMDPDCCLQPLCHINPLCLGSPNPLDIIQETQVPVSOQNLSFYD 897  
Qy 897 RIKFLVGRDSTHIIIPGENPFDGGHACVIRQVMTSDGTPLVGVNISFVNNPLFGYTIISRQ 956  
Db 898 RIKFLVGRDSTHIIIPGENPFDGGHACVIRQVMTSDGTPLVGVNISFVNNPLFGYTIISRQ 957  
Qy 957 DGSFDLVTNGGIIILRFERAPFITOEHTLWL PWRFFVMETIIMRHEENEIPSCDLSNF 1016  
Db 958 DGSFDLVTNGGIIILRFERAPFITOEHTLWL PWRFFVMETIIMRHEENEIPSCDLSNF 1017  
Qy 1017 ARPNPVSPSPLTSFASSCAEKGPVPEIQALQBEISISGCKMRLSYLSRTPGYKSVLR 1076  
Db 1018 ARPNPVSPSPLTSFASSCAEKGPVPEIQALQBEISISGCKMRLSYLSRTPGYKSVLR 1077  
Qy 1077 ISLTHPTIPFNLMKVHLMVAVEGRLFRKWFAAAPDLSYFIWDKTDVYNQKVFGLSEAFV 1136  
Db 1078 ISLTHPTIPFNLMKVHLMVAVEGRLFRKWFAAAPDLSYFIWDKTDVYNQKVFGLSEAFV 1137  
Qy 1137 SVGEYESCPDLILWEKRTTVLQYEIDASKLGWSLDKHHALNIQS-GILHKNGENQF 1195  
Db 1138 SVGEYESCPDLILWEKRTTVLQYEIDASKLGWSLDKHHALNIQSGGILHKNGENQF 1197  
Qy 1196 VSQOPPVGSI MGNGRRRSISCPSCNGLADGNKLLAPVALTCGSDGSLYVGDFNYIRIF 1255  
Db 1198 VSQOPPVGSI MGNGRRRSISCPSCNGLADGNKLLAPVALTCGSDGSLYVGDFNYIRIF 1257  
Qy 1256 PSGNVTNILEL--RNKDFRSHSPA KYYLATDPMSCAVFLSDSNSRRRVFKISTVVVKD 1313  
Db 1258 PSGNVTNILELRVRNKDFRSHSPA KYYLATDPMSCAVFLSDSNSRRRVFKISTVVVKD 1317  
Qy 1314 LVKNSEWAGTGDCQLPFDDTRCGDGGKATEATLTNPR--GITVDKFGLIYFVDGTMIR 1370  
Db 1318 LVKNSEWAGTGDCQLPFDDTRCGDGGKATEATLTNPRGPPGITVDKFGLIYFVDGTMIR 1377  
Qy 1371 RIDQNGIISTLLGSNDLTSARPLSCDSVMDISQVR--LEWPTDLAINPMDNSLYVL DNN 1427  
Db 1378 RIDQNGIISTLLGSNDLTSARPLSCDSVMDISQVRQVHLEWPTDLAINPMDNSLYVL DNN 1437  
Qy 1428 VVLOISENHQVRI VAGRPMHCQVPGIDHFLLSKVAIHATLESATALAVSHNGVLYIAETD 1487  
Db 1438 VVLOISENHQVRI VAGRPMHCQVPGIDHFLLSKVAIHATLESATALAVSHNGVLYIAETD 1497  
Qy 1488 EKKINRI RQVTTSGEISLVAGAPSGCDCKNDANCDPFGDDGYAKDAKLNTPSSLAVCAD 1547  
Db 1498 EKKINRI RQVTTSGEISLVAGAPSGCDCKNDANCDPFGDDGYAKDAKLNTPSSLAVCAD 1557  
Qy 1548 GELYVADLGNIRIRFIRKNKPFNTQNMVELSSPIDQELYLFDTTGKHL YTSQSLPTGDYL 1607  
Db 1558 GELYVADLGNIRIRFIRKNKPFNTQNMVELSSPIDQELYLFDTTGKHL YTSQSLPTGDYL 1617  
Qy 1608 YNFTYTGDDITLITDNNGMVNVRRDSTGMPLWLVPDQGVVWVTMTGNSALKSVTTQG 1667  
Db 1618 YNFTYTGDDITLITDNNGMVNVRRDSTGMPLWLVPDQGVVWVTMTGNSALKSVTTQG 1677  
Qy 1668 HELAMMTYHGNSGLLATKSNENGWTTFFEYDSFGRLTNVTFPTQOVSSFRSDTDS SVHVQ 1727  
Db 1678 HELAMMTYHGNSGLLATKSNENGWTTFFEYDSFGRLTNVTFPTQOVSSFRSDTDS SVHVQ 1737  
Qy 1728 VETSSKDDVTITTNLSASGAFYTLLODQVRNSYYIGADGSLRLLLLANGMEVALQTEPHLL 1787  
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Db 1738 VETSSKDDVTITTNLSASGAFY---DQVRNSYYIGADGSLRLLLLANGMEVALQTEPHLL 1793  
Qy 1788 AGTVNPTVGRNVTLPIDNGLNLVEWRQKEAQGVTVFGRRLR---VHNRNLLSLDFD 1844  
Db 1794 AGTVNPTVGRNVTLPIDNGLNLVEWRQKEAQGVTVFGRRRLRVLQVHNRNLLSLDFD 1853  
Qy 1845 RVTRTEKIYDDHRKFTLRILYDQAGRPSLWSPSSRLNGVNVTYSPGGYIAGIQGIMSER 1904  
Db 1854 RVTRTEKIYDDHRKFTLRILYDQAGRPSLWSPSSRLNGVNVTYSPGGYIAGIQGIMSER 1913  
Qy 1905 MEYDQAGRITSRIFADGKTWSYTYLEKSMVLLLSHQRYIFEFDKNDRLSSTVMPNVARQ 1964  
Db 1914 MEYDQAGRITSRIFADGKTWSYTYLEKAGV-----EFDKNDRLSSTVMPNVARQ 1962  
Qy 1965 TLETIRSVGYRNIYQPPEGNASVIQDFTEDGHLLHTFYLGTGRRRIYKYGKLSKLAETL 2024  
Db 1963 TLETIRSVGYRNIYQPPEGNASVIQDFTEDGHLLHTFYLGTGRRRIYKYGKLSKLAETL 2022  
Qy 2025 YDTTKVSFTYDETAGMLKTINLQNEGFTCTIRYRQIGPLIDRQIFRFTBEGMVNARFDYN 2084  
Db 2023 YDTTKVSFTYDETAGMLKTINLQNEGFTCTIRYRQIGPLIDRQIFRFTBEGMVNARFDYN 2082  
Qy 2085 YDNSFRVTSMQAVINETPLPIDLYRYDDVSGKTEQFGKFGVIYYDINQIITTAVMTHTKH 2144  
Db 2083 YDNSFRVTSMQAVINETPLPIDLYRYDDVSGKTEQFGKFGVIYYDINQIITTAVMTHTKH 2142  
Qy 2145 FDAYGRMKEVQYEIFRSLMYMTVQYDNMGRVVVKELKVGPYANTTRYSEYDADGQLQT 2204  
Db 2143 FDAYGRMKEVQYEIFRSLMYMTVQYDNMGRVVVKELKVGPYANTTRYSEYDADGQLQT 2202  
Qy 2205 VSINDKPLWRYSYDLNGNLHLLSPGNSARLTPLRYDIRDRIITRLGDVQYKMDGDFLRQR 2264  
Db 2203 VSINDKPLWRYSYDLNGNLHLLSPGNSARLTPLRYDIRDRIITRLGDVQYKMDGDFLRQR 2262  
Qy 2265 GGDIFEYNSAGLLIKAYNRAGSWSVRYRVDGLGRRVSSKSSHHLQFFFYADLTNPTKVT 2324  
Db 2263 GGDIFEYNSAGLLIKAYNRAGSWSVRYRVDGLGRRVSSKSSHHLQFFFYADLTNPTKVT 2322  
Qy 2325 HLYNHSSEITSLYYDLQGHLFAMELSSGDEFYIACDNIGTPLAVFSGTGLMIKQILLYTA 2384  
Db 2323 HLYNHSSEITSLYYDLQGHLFAMELSSGDEFYIACDNIGTPLAVFSGTGLMIKQILLYTA 2382  
Qy 2385 YGEIYMDTNPNFQIIIGYHGGLYDPLTKLVHMGRDDYDLAGRWTSPDHLMWKHLSSSNV 2444  
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Qy 2445 MPFNLYMFKNNPISNSQDIKCFMTDVNSWLLTFFGQLHNVI PGYKPKPDMAMEPSYELI 2504  
Db 2443 MPFNLYMFKNNPISNSQDIKCFMTDVNSWLLTFFGQLHNVI PGYKPKPDMAMEPSYELI 2502  
Qy 2505 HTQMKTQEWDNK-----SILGVQCEVQKQKAFVTLERFDQLYGSTITSCQQAPKT 2556  
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Qy 2557 KKFASSGSVFGKGVKFALKDGRVTTDIIISVANEDGRRVAAILNHAHYLENLHFTIDGVDT 2616  
Db 2563 KKFASSGSVFGKGVKFALKDGRVTTDIIISVANEDGRRVAAILNHAHYLENLHFTIDGVDT 2622  
Qy 2617 HYFVKPGPSEGDLAILGLSGRRRTLENGVNVTVSQINTVLNGRTRRYTDIQLQYGALCLN 2676  
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Qy 2677 TRYGTTLDEEKARVLELARQAVRQAWAREQOQLREGEGLRAWTEGEKQOVLSTGRVQG 2736  
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Qy 2737 YDGGFFVISVEQYPELSDSANNIHFMRQSEMGRR 2769  
Db 2743 YDGGFFVISVEQYPELSDSANNIHFMRQSEMGRR 2775

; Sequence 82, Application US/09808602  
; Patent No. US20020155115A1  
; GENERAL INFORMATION:  
; APPLICANT: Vernet, Corine A  
; APPLICANT: Fernandes, Elma  
; APPLICANT: Shimkets, Richard A  
; APPLICANT: Herrman, John L  
; APPLICANT: Majumder, Kumud  
; APPLICANT: Mishra, Vishnu  
; APPLICANT: Mezes, Peter S  
; APPLICANT: MacDougall, John  
; TITLE OF INVENTION: No. US20020155115a1el Proteins and Nuclec Acids Encoding Same  
; FILE REFERENCE: 15966-697 CIP  
; CURRENT APPLICATION NUMBER: US/09/808,602  
; CURRENT FILING DATE: 2001-03-14  
; PRIOR APPLICATION NUMBER: 09/800,198  
; PRIOR FILING DATE: 2001-03-05  
; PRIOR APPLICATION NUMBER: 60/186,596  
; PRIOR FILING DATE: 2000-03-03  
; NUMBER OF SEQ ID NOS: 114  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 82  
; LENGTH: 2771  
; TYPE: PRt  
; ORGANISM: Mus musculus  
US-09-808-602-82

Query Match 97.6%; Score 14529; DB 3; Length 2771;  
Best Local Similarity 97.0%; Pred. No. 0;  
Matches 2688; Conservative 40; Mismatches 41; Indels 2; Gaps 1;  
  
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Db 121 TVLSPEHPVRLWGRSTRSGRSSCLSSRANSNLTLTDTEHENTETDHPSSLQNHPRLTPP 180  
  
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Db 181 PPLPHAHTPNQHHAAASINSLNRGNFTPRSNPSPAPTDHSLSGEPPAGSAQEPTHAQDNWL 240  
  
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Db 241 LNSNIPLETRNLGKQPFGLTLQDNLIEMDILSASRHDGAYSDGHFLFKPGGTSPLFCTTS 300  
  
Qy 301 PGYPLTSSTVYSPPPRPLPRSTFARPAFNLKPSKYCNWKAALSIVISATLVILLAYF 360  
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Db 361 VAMHLFGLNWLQPMEGQMYYEITEDTASSWPVPTDVSLYPSGGTGLETPDRKKGAAE 420  
  
Qy 419 GKPSSFPEDSFIDSGEIDVGRASQKIPPGTFRWSQVFDHPVHLKFNVSLGKAALVGI 478  
Db 421 GKPSSLPEDSFIDSGEIDVGRASQKIPPGTFRWSQVFDHPVHLKFNVSLGKAALVGI 480  
  
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Db 481 YGRKGLPPSHTQDFVELLDGRRLLTQEARSLGEGTPRQSRGTVPPSSHETGFIQLDSGI 540  
  
Qy 539 WHLAFYNDGKESEVVSFLTTAIESVDNCPSNCYGNGDCISGTCFLGLGPDCCRASCP 598  
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Qy 779 PGWNGEHCTIAHYLDRVVKEGCPGLCNGNGRCTLDLNGWHVCQLGWRGAGCDTSMETAC 838  
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Qy 839 GDSKNDGDGLVDCMDPDCCLQPLCHINPLCLGSPNPLDIIQETQVPVSQQNLHSFYDRI 898  
Db 841 GDGKNDGDGLVDCMDPDCCLQPLCHVNPLCLGSPDPLDIIQETQAPVSQQNLNPFYDRI 900  
Qy 899 KFLVGRDSTHIIIPGENPFDGGHACVIRGQVMTSDGTPLVGVNISFVNNPLFGYTISRQDG 958  
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Qy 959 SFDLVTNGGISIIILRPERAPFITOEHTLWLPDRFFVMETIIMRHEENEIPSCDLSNFAR 1018  
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Qy 1079 LTHPTIPFNLKVKHLMVAVEGRLFRKWFAAAPDLSYYFIWDKTDVYNQKVFGLSEAFVS 1138  
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Qy 1259 NVTNILELRNKDPRHSHSPAHKYVYLATDPMGAVFLSDSNSRRRVFKIKSTVVVKDLVKNS 1318  
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Qy 1319 EVVAGTGDQCLPFDDTRCGDGGKATEATLTNPRGITVDKFGLIYFVDGTMIRRIDQNGII 1378  
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Db 1561 RIRFIRKNKPFNTQNMVELSSPIDQELYLFDTSKGHLTYQSLPTGDYLYNFTYTG DGDGI 1620  
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Db 1621 THITDNNGNMNVVRRDSTGMPLWLVPDQVYVWVTMTGNSALRSVTTQGHELAMMTYHGN 1680  
Qy 1679 SGLLATKSNENGWTTTFYEYDSFGRLTNVTFTPTGOVSSFRSDTSSVHVQVETSSKDDVTI 1738  
Db 1681 SGLLATKSNENGWTTTFYEYDSFGRLTNVTFTPTGOVSSFRSDTSSVHVQVETSSKDDVTI 1740







Db	601	VLCSGNGYMKGRCLCHSGWKGAECVPTNQCIDVACSSHGTCIMGTCICNPGYKGSCB	660		Db	1681	SGLLATKSNENGWTTFFYEYDSFGRLTNVTFPTGQVSSFRSDTDSVVHVQVETSSKDDVTI	1740
QY	659	EVDCMDPTCSGRGVCVRGECHCFVWGGTNCETPRATCLDQCSGHGTFLPDTGLCSCDPS	718		QY	1739	TTNLSASGAFYTLQDOVRNSYYIGADGSLRLLLANGMEVALQTEPHLLAGTVNPTVGKR	1798
Db	661	EVDCMDPTCSSRGCVCVRGECHCSVGWGTNCETPRATCLDQCSGHGTFLPDTGLCNCDPS	720		Db	1741	TTNLSASGAFYTLQDOVRNSYYIGADGSLRLLLANGMEVALQTEPHLLAGTVNPTVGKR	1800
QY	719	WTGHDCSIBICAADCGHGVCGGTCTRCEDGWMGAACDQACHPRCAEHGTCRDGKCBS	778		QY	1799	NVTLPIDNGLNLVEWRQKEQARGQVTVFGRRLRVHNRNLLSLDFDRVTRTEKIYDDHRK	1858
Db	721	WTGHDCSIBICAADCGHGVCGGTCTRCEDGWMGAACDQACHPRCAEHGTCRDGKCBS	780		Db	1801	NVTLPIDNGLNLVEWRQKEQARGQVTVFGRRLRVHNRNLLSLDFDRVTRTEKIYDDHRK	1860
QY	779	PGWNGEHCTIAHYLDRVVKEGCPGLCNGNGRCTLDLNGWHCVCOLGWRGAGCDTSMETAC	838		QY	1859	FTLRILYDQAGRPSLWSPSSRLNGVNVTVSPGGYIAGIQRGIMSERMEYDQAGRITSRIF	1918
Db	781	PGWNGEHCTIAHYLDRVVKEGCPGLCNGNGRCTLDLNGWHCVCOLGWRGTGCDTSMETGC	840		Db	1861	FTLRILYDQAGRPSLWSPSSRLNGVNVTVSPGGIAGIQRGIMSERMEYDQAGRITSRIF	1920
QY	839	GDSKDNDDGGLVDCMDPDCCLOPLCHINPLCLGSPNPLDIQETQVPVSOQNLSHFYDRI	898		QY	1919	ADGKTWSYTYLEKSMVLLHLSQRQYIFEFDKNDRLSSVTMPNVARQTLETIRSVGYRNI	1978
Db	841	GDGKDNDDGGLVDCMDPDCCLOPLCHVNPLCLGSPDPLDIQETQAPVSQONLNPFDRI	900		Db	1921	ADGKMSYTYLEKSMVLHLHSQRQYIFEFDKNDRLSSVTMPNVARQTLETIRSVGYRNI	1980
QY	899	KFLVGRDSTHIIIPGENPFDGGHACVIRGQVMTSDGTPLVGVNISFVNNPLFGYTTISRQDG	958		QY	1979	YQPEGNASVIQDFTEDGHLHLHTFYLGTGRRVIYKYGKLSKLAETLYDTTKVSFTYDETA	2038
Db	901	KFLVGRDSTHIIIPGENPFDGGHACVIRGQVMTSDGTPLVGVNISFINNPLFGYTTISRQDG	960		Db	1981	YQPEGNASVIQDFTEDGHLHLHTFYLGTGRRVIYKYGKLSKLAETLYDTTKVSFTYDETA	2040
QY	959	SFDLVNTNGISIIILRFERAPFITQBHTLWLPWDRFFVFMETIMRHEENEIPSCDLSNPAR	1018		QY	2039	GMLKTINLQNEGFTCTIRYRQIGPLIDRQIFRFTTEGVMNARFDYNDNSFRVTSMQAVI	2098
Db	961	SFDLVNTNGISIIILRFERAPFITQBHTLWLPWDRFFVFMETIMRHEENEIPSCDLSNPAR	1020		Db	2041	GMLKTVNLQNEGFTCTIRYRQIGPLIDRQIFRFTTEGVMNARFDYNDNSFRVTSMQAVI	2100
QY	1019	PNPVVSPSLTSFASSCAEKGPVPEIQALQEEISISGCKMRLSYLSSRTPGYKSVLRIS	1078		QY	2099	NETPLPIDLYRYDDVSGKTEQFGKFGVIYYDINQIITTAVMTHTKHFDAYGRMKEVQYEI	2158
Db	1021	PNPVVSPSLTSFASSCAEKGPVPEIQALQEEIIVIAGCKMRLSYLSSRTPGYKSVLRIS	1080		Db	2101	NETPLPIDLYRYDDVSGKTEQFGKFGVIYYDINQIITTAVMTHTKHFDAYGRMKEVQYEI	2160
QY	1079	LTHPTIPENLMKVHLMVAVEGRLEFRKWFAAAPDLSYYFIWDKTDVYNQKVFLSEAFVSU	1138		QY	2159	FRSLMYWMTVQYDNMGRVVVKELKVGPYANTTRYSYEYDADGQLQTVSINDKPLWRYSYD	2218
Db	1081	LTHPTIPENLMKVHLMVAVEGRLEFRKWFAAAPDLSYYFIWDKTDVYNQKVFGFSEAFVSU	1140		Db	2161	FRSLMYWMTVQYDNMGRVVVKELKVGPYANTTRYSYEYDADGQLQTVSINDKPLWRYSYD	2220
QY	1139	GYEYESCPDLILWEKRTTVLQGYEIDASKLGGWSLDKHHALNIQSILHKGNGENQFVSQ	1198		QY	2219	LNGNLHLLSPGNSARLTPLRYDIRDRITRLGDVQYKMDDEDGFLRQRGGDIFEYNSAGLLI	2278
Db	1141	GYEYESCPDLILWEKRTAVLQGYEIDASKLGGWSLDKHHALNIQSILHKGNGENQFVSQ	1200		Db	2221	LNGNLHLLSPGNSARLTPLRYDLDRDIRTRLDGVQYKMDDEDGFLRQRGGDVEYNSAGLLI	2280
QY	1199	QPPVIGSIMNGRRRSISCPSCNGLADGNKLLAPVALTCGSDGSLYVGDFNYIRRIFFPSG	1258		QY	2279	KAYNRAGWSVRVRYDGLGRRVSSKSSHHLQFFYADLTNPTKVTHLVNHSSEITSLY	2338
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QY	1259	NVTNILELRNKDFRSHSHSPAHHYYLATDPMGAVFLSDNSRRVFKIKSTVVVKDLVKNS	1318		QY	2339	YDLQGLHFAMELSSGDDEFYIACDNIGTPLAVFSGTGLMIKQILYTAYGEIYMDTNPNFQI	2398
Db	1261	NVTNILEMRNKDFRSHSHSPAHHYYLATDPMGAVFLSDTNSRRVFKVSTTVVKDLVKNS	1320		Db	2341	YDLQGLHFAMELSSGDDEFYIACDNIGTPLAVFSGTGLMIKQILYTAYGEIYMDTNPNFQI	2400
QY	1319	EVVAGTGDOCLPFDDTRCGDGGKATEATLTNPRGITVDKFGLIYFVDGTMIRRIDQNGII	1378		QY	2399	IIGYHGGLYDPLTKLVHMGRRDYDLAGRWTSPDHLELWKHLSSSNVMPFNLYMFKNNPI	2458
Db	1321	EVVAGTGDOCLPFDDTRCGDGGKATEATLTNPRGITVDKFGLIYFVDGTMIRRVQNGII	1380		Db	2401	IIGYHGGLYDPLTKLVHMGRRDYDLAGRWTSPDHLELWKHLSSSNIVPFHLYMFKNNPI	2460
QY	1379	STLLGSNDLTSARPLSCDSVMDISQVRLEWPTDLAINPMDNSLYVLDNNVVLQISENHQV	1438		QY	2459	SNSQDIKCFMTDVNSWLLTFGFQLHNVI PGYKPKDMDAMEPSYELIHTQMTQEWDSKS	2518
Db	1381	STLLGSNDLTSARPLSCDSVMEISQVRLEWPTDLAINPMDNSLYVLDNNVVLQISENHQV	1440		Db	2461	SNSQDIKCFMTDVNSWLLTFGFQLHNVI PGYKPKDMDAMEPSYELVHTQMTQEWDSKS	2520
QY	1439	RIVAGRPMHCQVPGIDHFLLSKVAIHATLESATALAVSHNGVLYIAETDEKKINRIQVU	1498		QY	2519	ILGVQCEVQKQLKAFVTLERFDQLYGSTITSCQAPKTKKFASSGSVFGKGVKPAKDGRI	2578
Db	1441	RIVAGRPMHCQVPGIDHFLLSKVAIHATLESATALAVSHNGVLYIAETDEKKINRIQVU	1500		Db	2521	ILGVQCEVQKQLKAFVTLERFDQLYGSTITSCQAPETKKFASSGSI FGKGVKPAKDGRI	2580
QY	1499	TSGEISLVAGAPSGCDCKNDANCDFSGDDGYAKDAKLNTPSSLAVCADGELYVADLGNII	1558		QY	2579	VTTDIIISVANEDGRVAAAILNHAHYLENLHFTIDGVDTHTYFVKPGPSEGLAILGLSGGR	2638
Db	1501	TSGEISLVAGAPSGCDCKNDANCDFSGDDGYAKDAKLNTPSSLAVCADGELYVADLGNII	1560		Db	2581	VTTDIIISVANEDGRRIAAILNNAHYLENLHFTIDGVDTHTYFVKPGPSEGLAILGLSGGR	2640
QY	1559	RIRFIRKNKPFNLNTQNMYYELSSPIDQELYLFDTTGKHLYTQSILPTGDLYLNFTYTGDGDI	1618		QY	2639	RTLENGVNVTVSQINTVLNGRTRRYTDIQLQYCALCLNTRYGTTLDEEKARVLELARQRA	2698
Db	1561	RIRFIRKNKPFNLNTQNMYYELSSPIDQELYLFDTSKGHLYTQSILPTGDLYLNFTYTGDGDI	1620		Db	2641	RTLENGVNVTVSQINTMLSGRTRRYTDIQLQYRALCLNTRYGTTVDEEKVRVLELARQRA	2700
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Db	1621	THITDNGNMVNVRDSTGMPLWLVPDQGVYVWTMGNTSALRSVTTQGHELAMMTYHGN	1680		Db	2701	VRQAWAREQQRLREGEEGLRAWTDGEKQQQLNTGRVQGYDGFVTVSVEQYBELSDSANNI	2760
QY	1679	SGLLATKSNENGWTTFFYEYDSFGRLTNVTFPTGQVSSFRSDTDSVVHVQVETSSKDDVTI	1738		QY	2759	HFMRQSEMGRR	2769
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RESULT 7
US-10-042-865-2
; Sequence 2, Application US/10042865
; Publication No. US20040029216A1
; GENERAL INFORMATION:
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Li, Li
; APPLICANT: Zerhusen, Bryan D
; APPLICANT: Casman, Stacie J
; APPLICANT: Shenoy, Suresh G
; APPLICANT: Spytek, Kimberly
; APPLICANT: Zhong, Mei
; APPLICANT: Gangolli, Esha A
; APPLICANT: Burgess, Catherine E
; APPLICANT: Patturajan, Meera
; APPLICANT: Vernet, Corine A.M
; APPLICANT: Taylor, Sarah
; APPLICANT: Tchernev, Velizar T
; APPLICANT: Miller, Charles E
; APPLICANT: Guo, Xiaojia
; APPLICANT: Boldog, Ference L
; APPLICANT: Grosse, William M
; APPLICANT: Alsobrook II, John P
; APPLICANT: Gerlach, Valerie L
; APPLICANT: Edinger, Shlomit R
; APPLICANT: Rothenberg, Mark E
; APPLICANT: Ellerman, Karen
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; APPLICANT: Millet, Isabelle
; APPLICANT: Peyman, John
; APPLICANT: Smithson, Glennda
; APPLICANT: Gunther, Erik
; APPLICANT: Stone, David
; TITLE OF INVENTION: Proteins, Polynucleotides Encoding Them and Methods of
; TITLE OF INVENTION: Using the Same
; FILE REFERENCE: 21402-537
; CURRENT APPLICATION NUMBER: US/10/042,865
; CURRENT FILING DATE: 2002-05-17
; PRIOR APPLICATION NUMBER: 60/260,417
; PRIOR FILING DATE: 2001-01-09
; PRIOR APPLICATION NUMBER: 60/260,831
; PRIOR FILING DATE: 2001-01-10
; PRIOR APPLICATION NUMBER: 60/272,338
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 60/274,876
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/284,704
; PRIOR FILING DATE: 2001-04-18
; NUMBER OF SEQ ID NOS: 264
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 2794
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-042-865-2

Query Match      96.8%; Score 14406.5; DB 4; Length 2794;
Best Local Similarity 96.7%; Pred. No. 0;
Matches 2704; Conservative 21; Mismatches 41; Indels 31; Gaps 11;

Qy      1 MDVKERKPYRSLTRRRDAERRYTSSSADSEEGKAPQKYSYSSSETLKAYDQDARLAYGSRV 60
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Qy      61 KDIVPQEAEEFCRTGANFTLRELGLEEVTPPHGTLTYRTDIGLPQCGYSMGAGSDADMEAD 120
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Qy      121 TVLSPEHPVRLWGRSTRSGRSSCLSSRANSNLTLTDTHEHENTETDHPGGLQNHARLRTPP 180
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      181 PPLSHAHTPNQHHAAASINSLNRGNFTPRSNPSPAPTDHSLSGEPPAGGAQEPAAHAQENWL 240
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Qy      241 LNSNIPLERNLGKQPFGLGTLODNLIEMDILGASRHDGAYS DGHFLFKPGGTSPLFCTTS 300
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Qy      361 VAMHLFGLNWLQPMEGOMYEITEDTASSWPVPTDVSLYPSGGTGLETPDRKGKGTTEGK 420
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      718 GPDCSNEICSVDCSGHGVCMGGTCRCEGWTGPACNQ RACHPRCAEHGTCRDGKCECSPG 777
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Qy      781 WNGEHCTI--AHYLD R VVK--EGCPGLCNGNGRCTL DLNGWHCVCOLGWRGAGCDTSMET 836
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Qy      897 RIKFLVGRDSTHIIIPGENPFDGGHACVIRGQVMTSDGTPLGVNISFVNPNPLFGYTISRQ 956
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      898 RIKFLVGRDSTHIIIPGENPFDGGHACVIRGQVMTSDGTPLGVNISFVNPNPLFGYTISRQ 957
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Qy      957 DGSFDLVNTGGISIIIRFERAPFITQEH TLWLPWDRFFVME TIIMRHEENEIPSCDLSNF 1016
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Qy      1137 SVGYEYESCPDLILWEKRTTVLQGYEIDASKLGWSLDKGHALNIQS -GILHKNGENQF 1195
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Qy      1196 VSQPPVIGSIMNGRRRSISCPSCNGLADGNKLLAPVALTCGSDGSLYVGDFNYIRRI F 1255
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Qy 1256 PSGNVTNILEL--RNKDFRHSHPAHKYVYLATDPMGSAVFLSDNSRRRVFKIKSTVVVKD 1313  
Db 1258 PSGNVTNILELRVRNKDFRHSHPAHKYVYLATDPMGSAVFLSDNSRRRVFKIKSTVVVKD 1317  
Qy 1314 LVKNSEVVAGTGDQCLPFDDTRCGDGGKATEATLTNPR--GIVDKFGLIYFVDGTMIR 1370  
Db 1318 LVKNSEVVAGTGDQCLPFDDTRCGDGGKATEATLTNPRGPPGIVDKFGLIYFVDGTMIR 1377  
Qy 1371 RIDQNGIISTLGSNDLTSARPLSCDSVMDISQVR--LEWPTDLAINPMDNSLYVLDDN 1427  
Db 1378 RIDQNGIISTLGSNDLTSARPLSCDSVMDISQVRQVHLEWPTDLAINPMDNSLYVLDDN 1437  
Qy 1428 VVLQISENHQVRIVAGRPMHCQVPGIDHFLLSKVAIHATLESATALAVSHNGVLYIAETD 1487  
Db 1438 VVLQISENHQVRIVAGRPMHCQVPGIDHFLLSKVAIHATLESATALAVSHNGVLYIAETD 1497  
Qy 1488 EKKINRIRQVTTSGEISLVAGAPSGCDCKNDANCDCFSGGDGYAKDAKINTPSSLAVCAD 1547  
Db 1498 EKKINRIRQVTTSGEISLVAGAPSGCDCKNDANCDCFSGGDGYAKDAKINTPSSLAVCAD 1557  
Qy 1548 GELYVADLGNIRIRFIRKNKPFNTQNMVELSSPIDQELYLFDTTGKHLYTQSLPTGDYL 1607  
Db 1558 GELYVADLGNIRIRFIRKNKPFNTQNMVELSSPIDQELYLFDTTGKHLYTQSLPTGDYL 1617  
Qy 1608 YNFTYTGDGDIITLITDNNGMVNVRRDSTGMPLWLVPDGGQVYVWMTGNTSALKSVTTQG 1667  
Db 1618 YNFTYTGDGDIITLITDNNGMVNVRRDSTGMPLWLVPDGGQVYVWMTGNTSALKSVTTQG 1677  
Qy 1668 HELAMTYHGNSGLLATKSNENGWTTFYEYDSFGRLTNVTFPTGQVSSFRSDTSSVHVQ 1727  
Db 1678 HELAMTYHGNSGLLATKSNENGWTTFYEYDSFGRLTNVTFPTGQVSSFRSDTSSVHVQ 1737  
Qy 1728 VETSSKDDVTITNLSASGAFYTLLOQVRNSYYIGADGSLRLLLLANGMEVALQTEPHLL 1787  
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Qy 1788 AGTVNPTVGKRNVTLPIDNGLNLVEWRQKEARGQVTFGRRLR--VHNRNLLSLDFD 1844  
Db 1798 AGTVNPTVGKRNVTLPIDNGLNLVEWRQKEARGQVTFGRRLRVLQVHNRNLLSLDFD 1857  
Qy 1845 RVTRTEKIYDDHRKFTLRILYDQAGRPSLWSPSSRLNGVNTYSPGGYIAGIQRGIMSER 1904  
Db 1858 RVTRTEKIYDDHRKFTLRILYDQAGRPSLWSPSSRLNGVNTYSPGGYIAGIQRGIMSER 1917  
Qy 1905 MEYDQAGRITSRIFADGKTWSYTYLEK---SMVLLLSHQRYIFEFDKNDRLLSSVTMPN 1960  
Db 1918 MEYDQAGRITSRIFADGKTWSYTYLEKAGVQSMVLLLSHQRYIFEFDKNDRLLSSVTMPN 1977  
Qy 1961 VARQTLETIRSVGYRNIYQPPEGNASVIOQFTEHGHLHFTFYLGTRRRVIYKYGKLSKL 2020  
Db 1978 VARQTLETIRSVGYRNIYQPPEGNASVIOQFTEHGHLHFTFYLGTRRRVIYKYGKLSKL 2037  
Qy 2021 AETLYDTTKVSFTYDETAGMLKTINLQNEGFTCTIRYRQIGPLIDRQIFRFTEEGMVNAR 2080  
Db 2038 AETLYDTTKVSFTYDETAGMLKTINLQNEGFTCTIRYRQIGPLIDRQIFRFTEEGMVNAR 2097  
Qy 2081 FDYNYDNSFRVTSMQAVINETPLPIDLYRDDVSGKTEQFGKFGVIYYDINQIITTAVMT 2140  
Db 2098 FDYNYDNSFRVTSMQAVINETPLPIDLYRDDVSGKTEQFGKFGVIYYDINQIITTAVMT 2157  
Qy 2141 HTKHFDAYGRMKEVQYEIFRSLMYWMTVQYDNMGRVVKELKVGPYANTTRYSEYDADG 2200  
Db 2158 HTKHFDAYGRMKEVQYEIFRSLMYWMTVQYDNMGRVVKELKVGPYANTTRYSEYDADG 2217  
Qy 2201 QLQTVSINDKPLWRYSYDLNGNLHLLSPGNSARLTPLRYDIRDRITRLGDVQYKMWDEDF 2260  
Db 2218 QLQTVSINDKPLWRYSYDLNGNLHLLSPGNSARLTPLRYDIRDRITRLGDVQYKMWDEDF 2277  
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Db 2278 LRQCGDIFEYNSAGLLIKAYNRAGSWSVRYRYDGLGRVSSKSSHHLQFFYADLTNP 2337

Qy 2321 TKVTHLYNHSSEITSLYYDLQGHLFAMELSSGDEFYIACDNIGTPLAVFSGTGLMIKQI 2380  
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Db 2398 LYTAYGEIYMDTNPNFQIIIGYHGGLYDPLTKLVHMGRRDYDVLAGRWTSPDHLELWKHLS 2457  
Qy 2441 SSNVMPFNLYMFKNNNPISNSQDIKCFMTDVNSWLLTTFGFQLHNVIPGYPKPDMDAMEPS 2500  
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Qy 2501 YELIHTQMKTQEWDNSK-----SILGVQCEVQKQLKAFVTLERFDQLYGSTITSCQQ 2552  
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Qy 2673 LCLNTRYGTTLDEKARVLELARAQRAVRQAWAREQQRLREGEGLRAWTEGKQQVLSTG 2732  
Db 2698 LCLNTRYGTTLDEKARVLELARAQRAVRQAWAREQQRLREGEGLRAWTEGKQQVLSTG 2757  
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Db 2758 RVQYDGGFFVISVEQYPELSDSANNIHFMRQSEMGRR 2794

RESULT 8

US-10-042-865-52  
; Sequence 52, Application US/10042865  
; Publication No. US20040029216A1

GENERAL INFORMATION:

; APPLICANT: Padigaru, Muralidhara  
; APPLICANT: Li, Li  
; APPLICANT: Zerhusen, Bryan D  
; APPLICANT: Casman, Stacie J  
; APPLICANT: Shenoy, Suresh G  
; APPLICANT: Spytek, Kimberly  
; APPLICANT: Zhong, Mei  
; APPLICANT: Gangolli, Esha A  
; APPLICANT: Burgess, Catherine E  
; APPLICANT: Patturajan, Meera  
; APPLICANT: Vernet, Corine A.M  
; APPLICANT: Taylor, Sarah  
; APPLICANT: Tchernev, Velizar T  
; APPLICANT: Miller, Charles E  
; APPLICANT: Guo, Xiaojia  
; APPLICANT: Boldog, Ference L  
; APPLICANT: Grosse, William M  
; APPLICANT: Alsobrook II, John P  
; APPLICANT: Gerlach, Valerie L  
; APPLICANT: Edinger, Shlomit R  
; APPLICANT: Rothenberg, Mark E  
; APPLICANT: Ellerman, Karen  
; APPLICANT: MacDougall, John  
; APPLICANT: Malyankar, Uriel M  
; APPLICANT: Millet, Isabelle  
; APPLICANT: Peyman, John  
; APPLICANT: Smithson, Glennda  
; APPLICANT: Gunther, Erik  
; APPLICANT: Stone, David

; TITLE OF INVENTION: Proteins, Polynucleotides Encoding Them and Methods of  
; TITLE OF INVENTION: Using the Same  
; FILE REFERENCE: 21402-537  
; CURRENT APPLICATION NUMBER: US/10/042,865  
; CURRENT FILING DATE: 2002-05-17  
; PRIOR APPLICATION NUMBER: 60/260,417



; PRIOR FILING DATE: 2001-01-09									
; PRIOR APPLICATION NUMBER: 60/260,831									
; PRIOR FILING DATE: 2001-01-10									
; PRIOR APPLICATION NUMBER: 60/272,338									
; PRIOR FILING DATE: 2001-02-28									
; PRIOR APPLICATION NUMBER: 60/274,876									
; PRIOR FILING DATE: 2001-03-09									
; PRIOR APPLICATION NUMBER: 60/284,704									
; PRIOR FILING DATE: 2001-04-18									
; NUMBER OF SEQ ID NOS: 264									
; SOFTWARE: PatentIn ver. 2.1									
; SEQ ID NO 52									
; LENGTH: 2715									
; TYPE: PRF									
; ORGANISM: Mus musculus									
US-10-042-865-52									
Query Match 68.7%; Score 10227; DB 4; Length 2715;									
Best Local Similarity 66.7%; Pred. No. 0;									
Matches 1864; Conservative 370; Mismatches 457; Indels 102; Gaps 19;									
Qy	1	MDVKERKPYRSLTR-RRDAERRYTTSSADSEEGKAP-QKSYSSSETLKAYDQD-ARLAYG	57						
Dd	1	MDVKERRPYCSLTKSRREKERRYTNSSADNEECRVPTQKSYSSSETLKAFDHDYRLLYG	60						
Qy	58	SRVKDIVPQEAEEFCRTGANFTLRELGLEEVTPPHGTLYRTDIGLPQCYSMGAGSDADM	117						
Dd	61	NRVKDLVHREADEYTRQGNFTLRQLGVCESATRRGVAFCAEMGLPHRGYSISAGSDADT	120						
Qy	118	EADTVLSPEHPVRLWGRSTRSGRSSCLSSRANSNLTLTDTHEHEN--TETHPGGLQNHA	174						
Dd	121	ENEAVMSPEHAMRLWGRGVKSGRSSCLSSRSNSALTLTDTHEHENRSDSESEQPSNPGQP	180						
Qy	175	RLRTPPPPLSHAHTPNQHAASINSLNRGNFTPRSNPSPAPTDHLSLGEPPAGGAQ----	230						
Dd	181	TLQPLPP--SHKQHPAQHH-PSITSLNRNSLNRNRNQSPAP-----PALPAELQTT	229						
Qy	231	-EPAHAQENWLLNSNIPLETRNLGKQPFLGTLQDNLIEMDILGASRHDGAYSDDGHFLFKP	289						
Dd	230	PESVQLQDSVWLGSNVPLESR-----HFLFKT	256						
Qy	290	G-GTSPFLCTTSPGYPLTSTSTVYSPPPRPLPRSTFARPAFNLKKPSKYNWKCAALSIV	348						
Dd	257	GTGTTPLFSTATPGYTMASSGVYSPPTRPLPRNTLSRAFKFKSSKYCSWRTCALCAVG	316						
Qy	349	ISATLVILLAYFVAMHLFGLNWLQPMEGQMYE---ITEDTASSWPVPTDVSLYPSGGTG	405						
Dd	317	VSVLLAILLSYFIAMHLFGLNWLHQQTENDTTFENGKNSDT----VPTNTVSLPSG---	368						
Qy	406	LETPDRKGKGTTEGKPSFFPEDSFIDSGEIDVGRRASQKIPPGTFWRSQVFIDHPVHLK	465						
Dd	369	-----DNGKLGGFTHENNTIDSGELDIGRRAIQEVPPGIFWRSQLFIDQPQLK	417						
Qy	466	FNVSLGKAALVGIYGRKGLPPSHTQPDFVELLDGRRLLTQEARSLGCTPRQSRGTVPSS	525						
Dd	418	FNISLQKDALIGVYGRKGLPPSHTQYDFVELLDGSRLLIAREQNLVESERAGRQARSVL	477						
Qy	526	HERGFIQYLDSGIWHLAFYNDGKESEVWSFLTTAIESVDNCPSNCYGNGDCISGTCHCFL	585						
Dd	478	HEAGFIQYLDSGIWHLAFYNDGKNPEQVSFNTIVIESVVECPRNCHGNCECVSGTCHCFP	537						
Qy	586	GFLGPDGGRASCPVLCSGNGQYMKGRCLCHSGWKGAECVDVPTNQCIDVACSNHGTCTGT	645						
Dd	538	GFLGPDCSRACPVLCSGNGQYSGRCLCFSGWKGTCECDVPTTQCIDPQCGRGICIMGS	597						
Qy	646	CICNPYKGESCEEVDGMDPTCSGRGVCVRGECHCFVWGWTNCETPRATCLDQCSGHGT	705						
Dd	598	CACNSGYKGENCEEADCLDPGCSNHGVCIHGECHCNPGWGSNCEILKTMCADQCSGHGT	657						
Qy	706	FLPDTGLCSDPSTWTHDCSIEICAADCGGHGVCVGGTCRCEDGWMGAACDQACHPRCA	765						
Dd	658	YLQESGSCTCDPNWTGPDCSNEICSVDCSHGVCMGGSCRCEEGWTGPACNQACHPRCA	717						

Qy	766	EHGTCRDCKCECSPGWNGEHCTIAHYLDRVVVKEGCPGLCNGNGRCTLDLNGWHCVCOLGW	825
Dd	718	EHGTCCKDGKCECSQGWNGEHCTIAHYLDKIVKEGCPGLCNSNGRCTLDQNGWHCVCPGW	777
Qy	826	RGAGCDTSMETACGDSKONDGDLVDCWDPDCCLOPLCHINPLCLGSPNPLDIIQETQVP	885
Dd	778	RGAGCDVAMETLCTDSKONEGDGLDCMDPDCCLOSSCONQPYCRGLPDPQDIISQSLQT	837
Qy	886	VSQONLHSFYDRIKFLVGRDSTHIIIPGENPFDGGHACVIRGQVMTSDGTPLVGVNISFVN	945
Dd	838	PSQQAAKSFYDRISFLIGSDSTHVLPGESPENKSLASVIRGQVLTADGTPPLIGVNVSFLH	897
Qy	946	NPLFGYTISRQDGSFDLVNNGGISIILRPERAPFITQEHTLWLPWDRFFVFMETIIMRHEE	1005
Dd	898	YSEYGYTITRQDGMFDLVANGGASLTLVFPERSPFLTQYHTVWIPWNVYVMDTLVMKKEE	957
Qy	1006	NEIPSCDLSNFAFPNPVSPSPLTSFASSCAEKGPIVPEIQALQEEISISGCKMRLSYLS	1065
Dd	958	NDIPSCDLSGCVRPSPPIIVSSPLSTFFRSPSPEDSPIIPETQVLHEETIPGTDLKL SYLS	1017
Qy	1066	SRTPGYKSVLRISLTHPTIPFNLMKVHLMVAVEGRLLFRKWFAAAPDLSYFIWDKTDVYN	1125
Dd	1018	SRAAGYKSVLKITMTQAVIPFNLMKVHLMVAVVGRLLFQKWFPPASPNLAYTFIWDKTDAYN	1077
Qy	1126	QKVFGLSEAFVSVGYEYESCPDLILWEKRTTVLQGYEIDASKLGGWLDLKHHLNIQSGI	1185
Dd	1078	QKVYGLSEAVVSVGYEYESCLDLTLWEKRTAVLQGYELDASNMGWTLDKHHVLDVQNGI	1137
Qy	1186	LHKGNGENQFVSQQPPVIGSIMGNRRRSISCPSCNGLADGNKLLAPVALTCGSDGSLYV	1245
Dd	1138	LYKGNGENQFISQQPPVSVSSIMGNRRRSISCPSCNGQADGNKLLAPVALACGIDGSLYV	1197
Qy	1246	GDFNYIRRIFFSGNVNTNILELRNKDFRHSHPAHKYYLATDPMSGAVFLSDSNSRRVFKI	1305
Dd	1198	GDFNYVRRIRFFSGNVTSVLELRNKDFRHSNPAHYYLATDPVTGDLVVSNTTRRIYRP	1257
Qy	1306	KSTVVVKDLVNSEVVAGTGDQCLPFDDTRCGDGGKATEATLTNPRGITVDKFGLIYFVD	1365
Dd	1258	KSLTGAKDLTKNAEVVAGTGEQCLPFDEARCGDGGKAVEATLMSPKGMAIDKNGLIYFVD	1317
Qy	1366	GTMRIRIDQNGIISTLLGSNDLTSARPLSCDSVMDISQVRLEWPTDLAINPMDNSLYVLD	1425
Dd	1318	GTMRKVDQNGIISTLLGSNDLTSARPLTCDTSMHISQVRLEWPTDLAINPMDNSIYVLD	1377
Qy	1426	NNVLQISENHQVRIVAGRPMHCQVPGIDHPELLSKVAIHATLESATALAVSHNGVLYIAE	1485
Dd	1378	NNVLQITENQVRIAAGRPMHCQVPGVE-YPVGKHAVQTTLESATAIAVSYSGLVYTE	1436
Qy	1486	TDEKKINRIRQVTTSGEISLVAGAPSGCDCXNDANCDCFSGDDGYAKDAKLNTPSSLAVC	1545
Dd	1437	TDEKKINRIRQVTTDGEISLVAGIPSECDCKNDANCDCYQSGDGYAKDAKLNAPSSLAAS	1496
Qy	1546	ADGELYVADLGNIRIRFIRKNKPFLLNTQNMVELSSPIDQELYLFDTTGKHLYTQSLPTGD	1605
Dd	1497	PDGTLYIADLGNIRIRAVSKNKPLLNSMNFYEVASPTDQELYIFDINGTHQYTVSLVTGD	1556
Qy	1606	YLYNFTYTGDDITLITDNNGNMNVNRRDSTGMPLWLAVPDQVYVVTMTGNSALKSVTT	1665
Dd	1557	YLYNFSYNDNDVTAVTDNGNTLRIRRDPNRPVVRVWSPDNQVWLITIGTNGCLKSMTA	1616
Qy	1666	QGHELAMMTYHGNSGLLATKSNENGWTTTFEYDVSFGLRTNVTFTPTQVSSFRSDTSSVH	1725
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Qy	1726	VQVETSSK-DDVTITNLSASGAFYTLTLDQDVNSYVIGADGSLRLLLLANGMEVALQTEP	1784
Dd	1677	VDIESSSREEDVSITSNLSSIDSFYTMVQDQLRNSYQIGYDGLRIFYASGLDSHYQTEP	1736
Qy	1785	HLLAGTVNPTVGKRNVTLPIDNGLNLVEWRQRKEQARGQVTVFGRRLRVHNRNLLSLDFD	1844
Dd	1737	HVLAGTANPTVAKRNMTLPGENGQNLVEWRFRKEQAQGVNFGKRLRVNGRNLSSVDFD	1796
Qy	1845	RVTRTEKIYDDHRKFTLRILYDQAGRPSLWSPSSRLNGVNVVTVSPGGYIAGIQRGIMSER	1904

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Db 1857 VDYDSQGRIVSRVFADGKTWSYTYLEKSMVLLHSQRQYIFEYDMWDRLSAITMPSVARH 1916  
QY 1965 TLETIRSVGYRNIYQPPEGNASVIOQFTEDGHLLHTFYLGTGRRRVYKYGKLSKLAETL 2024  
Db 1917 TMQTIRSIGYRNIYNPPESNASIITDYNEEGLLQTAFLGTSRRVLPFKYRQTRLSEIL 1976  
QY 2025 YDTTKVSFTYDETAGMLKTINLQNEGFTCTIRYRQIGPLIDRQIFRTEEGMVNARFDYN 2084  
Db 1977 YDSTRVSFTYDETAGVLKTVNLQSDGFCITIRYRQIGPLIDRQIFRSEDGMVNARFDYS 2036  
QY 2085 YDNSFRVTSMAVINETPLPIDLYRYDDVSGKTEQFGKFGVIYYDINQIITAVMTHTKH 2144  
Db 2037 YDNSFRVTSMQVINETPLPIDLYQFDDISGKVEQFGKFGVIYYDINQIISTAVMTYTKH 2096  
QY 2145 FDAYGRMKEVQYEIERSLMMYMTVOYDNMGRVVKELKVGPIYANTRYSYEYDADGQLQT 2204  
Db 2097 FDAHGRIKEIQYEIERSLMMYWITIYQDNMGRVTKREIKIGPFANTKYAYEYDVGQLQT 2156  
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Db 2456 ----KSQQWEDVPPIFGVQQQVARQAKAFSLGKMAEV-----QVSRRKAGAEQSW 2502  
QY 2559 --FASSGSVFGKGVKFALKDGRVTITDIISVANEDGRRVAAILNHAHYLENLHFTIDGVD 2616  
Db 2503 LWFATVKSILGKGM LAVSQGRVQTVNLNIANEDCIKVAALNNAFYLENLHFTIEGKDT 2562  
QY 2617 HYFVKPGSEGD LAILGLSGRRITLENGVNVTVSQINTVLNGRTRRYTDIQLQYGALCLN 2676  
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Db 2623 VRYGMTLDEEKARILEQARQALARAWAREQQRVRDGEGARLWTEGEKQRLSAGKVQG 2682  
QY 2737 YDGFFVISVEQYPELSDSANNIHFMRQSEMGR 2769  
Db 2683 YDGYVVLVSVEQYPELADSANNIQFLRQSEIGKR 2715

RESULT 9  
US-10-029-020-51  
; Sequence 51, Application US/10029020  
; Publication No. US20040033971A1  
; GENERAL INFORMATION:  
; APPLICANT: Gangolli et al.  
; TITLE OF INVENTION: Polypeptides and Nucleic Acids Encoding Same  
; FILE REFERENCE: 21402-225  
; CURRENT APPLICATION NUMBER: US/10/029,020

; CURRENT FILING DATE: 2001-12-19  
; PRIOR APPLICATION NUMBER: 60/256,704  
; PRIOR FILING DATE: 2000-12-19  
; PRIOR APPLICATION NUMBER: 60/311,590  
; PRIOR FILING DATE: 2001-08-10  
; PRIOR APPLICATION NUMBER: 60/257,314  
; PRIOR FILING DATE: 2000-12-20  
; PRIOR APPLICATION NUMBER: 60/311,613  
; PRIOR FILING DATE: 2001-08-10  
; PRIOR APPLICATION NUMBER: 60/315,617  
; PRIOR FILING DATE: 2001-08-29  
; PRIOR APPLICATION NUMBER: 60/307,506  
; PRIOR FILING DATE: 2001-07-24  
; PRIOR APPLICATION NUMBER: 60/322,358  
; PRIOR FILING DATE: 2001-09-14  
; PRIOR APPLICATION NUMBER: 60/294,075  
; PRIOR FILING DATE: 2001-05-29  
; PRIOR APPLICATION NUMBER: 60/288,153  
; PRIOR FILING DATE: 2001-05-02  
; NUMBER OF SEQ ID NOS: 190  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 51  
; LENGTH: 2715  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-10-029-020-51

Query Match 68.7%; Score 10227; DB 4; Length 2715;  
Best Local Similarity 66.7%; Pred. No. 0;  
Matches 1864; Conservative 370; Mismatches 457; Indels 102; Gaps 19;

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QY 58 SRVKDIVPQEAEEFCRTGANFTLRELGLEEVTPPHGTLYRTDIGLPQCGYSMGAGSDADM 117  
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QY 231 -EPAHAQENWLLNSNIPLETRNLGKQPFGLTQDNLIEMDILGASRHDGAYS DGHFLFKP 289  
Db 230 PESVOLQDSWVLGSNVPLESR-----HFLFKT 256  
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Db 317 VSVLLAILLSYFIAMHLFGLNWHLQQTENDTFENGKVNSDT-----VPTNTVSLPSG--- 368  
QY 406 LETPDRKKGTTGKPPSSFFPEDSFIDSGEIDVGRRASQKIPPGTFWRSQVFIDHPVHLK 465  
Db 369 -----DNGKLGGFTHENNTIDS GELDIGRRAIQIEVPPGIFWRSOLFIDQPQFLK 417  
QY 466 FNVSLGKAAALVGIYGRKGLPPSHTQDFVELLDGRRLLTQEARSLGEGTQRSGRTVPPSS 525  
Db 418 FNIQLKDALIGVYGRKGLPPSHTQYDFVELLDGSRLLIAREQNLVSEERAGRARSVSL 477  
QY 526 HETGFTQYLDSDGIWHLAFYNDGKESEVVSFLTTAIESVDNCPNSCYNGDCISGTCHCFL 585  
Db 478 HEAGFTQYLDSDGIWHLAFYNDGNKPQEVSFNTIVIESVVECPRNCHNGECVSGTCHCFP 537  
QY 586 GFLGPCGRASCVPVLCSGNGOYMKGRCLCHSGWKGAECDVPTNQCIDVACSNHGTCITGT 645



Db 538 GFLGPDCSRACPVLCSGNGQVSKGRCLCFSGWKGTEDVPTTQCIDPQCGRGICIMGS 597

QY 646 C1CNPYKGESCEEVDCMDPTCSGRGVCVRGECHECFVWGGTNCETPRATCLDQCSGHGT 705

Db 598 CACNSGYKGENCEEADCLDPGCSNHGVCIHGECHCNPGWGSNCEILKTMCADQCSGHGT 657

QY 706 FLPDITGLSCDPSWTGHDCSIIEICAADCGGHGVCVGGTCRCEDGWMGAACDORACHPRCA 765

Db 658 YLOESGSCDTPNWTGPDCSNEICSVDCSGHGVCMGSGRCEEGWTPACNQORACHPRCA 717

QY 766 EHGTCRDGKCECSPGWNGEHCTIAHYLDRVVKEGCPGLCNGNGRCTLDLNGWHCVQCQLGW 825

Db 718 EHGTCRDGKCECSQGWNGEHCTIAHYLDKIVKEGCPGLCNSNGRCTLDQNGWHCVCPQGW 777

QY 826 RGAGCDTSMETACGDSKNDGDGLVDCMDPDCCLOPLCHINPLCLGSPNPLDI1QETQVP 885

Db 778 RGAGCDVAMETLCTDSKDNEGDGLIDCMDPDCCLOQSSCONQPYCRGLPDPQDI1SQSLQT 837

QY 886 VSQQNLHSFYDRIKFLVGRDSTHIIPIGENPFDGGHACVIRGQWMTSDGTPLVGVNISFVN 945

Db 838 PSQQAAKSFYDRISFLIGSDSTHVLPGESPFNKSLASVIRGQVLTADGTPLIGNVVSFLH 897

QY 946 NPLFGYIISRODGSFDLVTNGGIIILRFERAPFITQEH7LWLPWDRFFV7METIIMRHEE 1005

Db 898 YSEYGTITRODGMFDLVANGGASLTLVFERSPFLTQYHTWIPWNVFVMDTLVMKKEE 957

QY 1006 NEIPSCDLSNFARPNPVVSPSPLTSFASSCAEKGP1VPE1QALQEEISISGCKMRLSYLS 1065

Db 958 NDIPSCDLSGFRVPSPIIVSSPLSTFFRRSPEDSPIIPETQV7LHEET7TIPGTDLKLSYLS 1017

QY 1066 SRTPGYKSVLRISLTHPTIPFNLMKVHLMVAVEGRLFRKWFAPAAAPDLSYFIWDKTDVYN 1125

Db 1018 SRAAGYKSVLKITMTQAVIPFNLMKVHLMVAVVGRLFQXWFPASP7LAYTFIWDKTDAYN 1077

QY 1126 QKVFGLSBAFVSVGYEYESCPDLJLWEKRTTVLQGYEIDASKLGWSLDKXHALNIOSGI 1185

Db 1078 QKVYGLSEAVVSVGYEYESCLDLTLWEKRTAVLQGYELDASNMGGWTLDKXHVLDVQNGI 1137

QY 1186 LHKNGENQFVSQOPPVIGSIMGNRRRSISCPSCNGLADGNKLLAPVALTCGSDGSLYV 1245

Db 1138 LYKNGENQFISIQOPPVSSIMGNRRRSISCPSCNGQADGNKLLAPVALACGIDGSLYV 1197

QY 1246 GDFNYIRRI1PPSGNV7NILELRNKDFRHSHPAKHY1LATDPMSCGAVFLSDSNSRRVFKI 1305

Db 1198 GDFNYVRRIPPSGNV7SVLELRNKDFRHSNPAHRY1LATDPVTGDLYVSDTNTRR1YRP 1257

QY 1306 KSTVVVKDLVKNSEWAGTGDOQLPFDPTRCGDDGKGATEATL7NPRGITVDKFGLIYFVD 1365

Db 1258 KSLTGAKDLTKNAEWVAGTGEQCLPFDEARCGDGGKAVEATLSPKGMAIDKXGLIYFVD 1317

QY 1366 GTMIRRIDQNGIISTLLGSNDLTSARPLSCDSVMDISQVRLEWPTDLAINPMDNSLYVLD 1425

Db 1318 GTMIRKVDQNGIISTLLGSNDLTSARPLTCDTSMHISQVRLEWPTDLAINPMDNSIYVLD 1377

QY 1426 NNVLQISENHQVRIVAGRPMHCQVPGIDHFLLSKVAIHATLESATALAVSHNGVL7YIAE 1485

Db 1378 NNVLQITENRQVRIAAGRPMHCQVPGVE-YPVGKHAVQTTLESATAIAVSYSGVL7YITE 1436

QY 1486 TDEKKINRIRQV7TSGEISLVAGAPSGCDCKNDANCDCFSGDDGVAKDAK7LNPSSLAVC 1545

Db 1437 TDEKKINRIRQV7T7DGEISLVAGIPSECDCKNDANCD7CQSGDGYAKDAK7LNPSSLAAS 1496

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Db 1497 PDG7LYIADLGNIRIRAVSKNKP7LLNSMNFYEVASPTDQEL7YIFDINGTHQ7YTVSLV7GD 1556

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Db 1557 YLYNFSYSNDNDV7TAV7DSNGNTLIRRRDPNMPVRV7VSPDNQV7IWL7TIG7NGLKSM7TA 1616

QY 1666 QGHELAM7TYHGNSGLLATKSNENGW7TTFEYDSFGRL7TNV7P7TQGVSSFRSD7TSSVH 1725

Db 1617 QGLELV7FTYHGNSGLLATKSDETGT7TFFDYDSEGR7L7TNV7P7TGV7V7TNLHGDMDKAIT 1676

QY 1726 VQVETSSK-DDVTITTNLSASGAFY7LLQDQVRNSYYIGADGSLR7LLLANGMEVALQ7EP 1784

Db 1677 VDIESSSREEDV7SITNSLSSIDSFY7TMVQDQLRNSYQIGYDGLRIPFASGLDSHYQ7EP 1736

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Db 1737 HVLAGTANPTVAKRNMTLP7GENGQNLV7WRFRKEQAQGVN7VFG7RKL7RVNGR7LLSVDFD 1796

QY 1845 RV7RTEKIYDDHRKFTLR7ILYDQAGRPSLWS7PSSRLNGVN7V7SPGGYIAGIQRGIMSER 1904

Db 1797 RT7KTEKIYDDHRKELLRIAYD7TSGHPTLW7PSSK7LMAVN7V7S7TQ7IASIQRGT7SEK 1856

QY 1905 MEYDQAGRITSRIPADGKTWSY7TYLEKSMV7LL7LH7SORQYIFEFDKNDRLSSV7TMPNVARQ 1964

Db 1857 VDYDSQGRIVSRVFADGKTWSY7TYLEKSMV7LL7LH7SORQYIFEYDMWDR7LSAITMPSVARH 1916

QY 1965 TLETIRSVGYRNIYQPPEGNASV7IQDFTEDGH7LLHTF7YLG7RRRV7YKYGKLSKLAETL 2024

Db 1917 TMQ7IRSIGYRNIYPPESNASIITDYN7EGL7LQ7TAF7LGT7RRV7LFKYRRQ7TRLSEIL 1976

QY 2025 YDTTKVSFTYDE7TAGMLKTINLQNEGFTCTIRYQIGPLIDRQIFR7FTEEGMVNARFDYN 2084

Db 1977 YDSTRVSFTYDE7TAGVLK7TNV7LQSDGFICTIRYQIGPLIDRQIFR7FSEDGMVNARFDYS 2036

QY 2085 YDNSFRV7TSMQAVINETPLPIDLYR7YDDVSGKTEQFQK7FV7YYDINQIIT7TAVM7TTHKH 2144

Db 2037 YDNSFRV7TSMQGVINETPLPIDLYQ7FDDISGKVEQFQK7FV7YYDINQIISTAVM7TYTKH 2096

QY 2145 FDAYGRMKEVQYEIFRSLMYWMTVQYDNMGRV7VKELKVGPYANT7TRYSEYEDADQ7LO7T 2204

Db 2097 FDAHGRIKEIQYEIFRSLMYWITIYQYDNMGRV7TKREIKIGPFANT7TKYAYEYDV7DQ7LO7T 2156

QY 2205 VSINDKPLW7YSYDLNGLN7LHLLSPGNSARLTPLRYD7IRD7RITRLGDVQYKMD7EDGFLRQR 2264

Db 2157 VYLNEKIMW7RYNYDLNGLN7LHLLNPSSARLTPLRYD7LRD7RITRLGDVQYRL7DEDGFLRQR 2216

QY 2265 GGDIFEYNSAGLLIKAYNRAGSWSVRYR7YDGLGRRVSSKSSH7HLQFFYADLTNP7TKVT 2324

Db 2217 GTEIFEYSSKGLLT7RVYSKSGWTVIYR7YDGLGRRVSSK7TSLG7HLQFFYADLTYP7TRIT 2276

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Db 2277 HVYNHSSEITSLYYDLQ7HLFAMEISSGDEFYIASDNTGT7PLAVFSSNGL7MLKQ7QYTA 2336

QY 2385 YGEIYMD7NPNFQIIIGYHGGLYDPLTKLVHMGR7RDYDLAGRWTSPD7HELWK7LSSNV 2444

Db 2337 YGEIYFDSNVDFQ7LVIGFHGGLYDPLTKLIHFGERDYDILAGRWT7TDIEIWKRI-GKDP 2395

QY 2445 MPFNLYMFKN7NPISNQDIKCFMTDVNSWLL7TFG7QLHN7VPGYPK7PMDMAMEPSYELI 2504

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Db 2456 ----KSQQWEDVPPIFGVQOQV7ARQAKAFLSLGKMAEV-----QV7RRKAGAEQSW 2502

QY 2559 --PASSGSVFGKGVK7FALKDGRV7T7DIIISVANEDGRRVAAILNHAHYLEN7LHFTIDGVD7T 2616

Db 2503 LWFATVKS7LIGKVM7LAVSQGRVQ7TNV7LNIANEDCIKVA7V7LNNAFYLEN7LHFTIEGKDT 2562

QY 2617 HYFVK7PGP7SEGDLAILGLSGGR7TLENGVN7V7SQINTV7LNGR7TRRYTDIOLQY7GALCLN 2676

Db 2563 HYFIK7TTPESDLG7TLR7LTSR7KALENGIN7V7V7SQSTTVV7NGR7TRRFADVEMQ7F7GALAH 2622

QY 2677 TRYGT7LDEEKARV7LELARQ7RAVRQAWAREQQ7RLREGE7GLRAWTEGEKQQ7VLSTGRVQ7 2736

Db 2623 VRYGMTLDEEKARILEQARQ7RALARAWAREQQ7VRDGE7GARLWTEGEK7RQLLSAGK7VQ7 2682

QY 2737 YDGF7FV7ISVEQ7PELSDSANNI7HFM7RQSEMGR 2769

Db 2683 YDGYV7LV7SVEQ7PELAD7SANNIQ7FLRQSEIGKR 2715



Qy	58	SRVKDIVPQEAEEFCRTGANFTLRELGLBEVTPPHGTLTYRTDIGNLPCQCGYSMGAGSDADM	1117
Db	61	NRVKDLVHREADDEFTRQGNFTLRQLGVCEPATRRGLAFCFAEMGLPHRGYSISAGSDADT	120
Qy	118	EADTVLSPEHPVRLWGRSTRSGRSSCLSSRANSNLTLTDEHEN---TETDHPGGLQNH	174
Db	121	ENEAVMSPEHAMRLWGRGVKSGRSSCLSSRSNSALTLTDEHENKSDSENEQPASNQGS	180
Qy	175	RLRTPPPPLSHAHTPNQHHAAASINSLNRGNFTPRSNPSPAPT D H S L S G E P P A G G A Q	230
Db	181	TLQPLPP--SHKQSAQHH-PSITSLNRNSLTNRNRNQSPAP-----PAALPAELQTT	229
Qy	231	-EPAHAQENWLLNSNIPLETRNLGKQPFGLGTIQDNLNLIEMDILGASRHDGAYS D G H F L F K P	289
Db	230	PESVOLQDSWILGSNVPLESR-----HFLFKT	256
Qy	290	G-GTSPLFCITTSFGYPLTSSTVYSPPPRPLPRSTFARPAFNLKKPSKYCNWKCAALSAIV	348
Db	257	GTGTTPLFSTATPGYTMASGSVYSPTRPLPRNTLSRSAFKFKKSSKYCSWKCTALCAVG	316
Qy	349	ISATLVILLAYFVAMHLFGLNWHLQPMEGQMYE---ITEDTASSWPVPTDVSLYPSGGTG	405
Db	317	VSVLLAILLSYFIAMHLFGLNWLQLOQTENDTFENGKVNSDT-----MPTNTVSLPSG---	368
Qy	406	LETPDRKKGTTTEGKPSFFPEDSFIDSGEIDVGRRASQKIPPGTFWRSQVFEIDHPVHLK	465
Db	369	-----DNKGLGGFTQENNTIDSGELDIGRRAIQEIPPGIFWRSQLFIDQPQFLK	417
Qy	466	FNVSLGKAALVGIYGRKGLPPSHTQDFVBEILLDGRRLLTQEARSLLEGTPRQSRGTVPSS	525
Db	418	FNISLQKDALIGYGRKGLPPSHTQYDFVBEILLDGRRLIAREQSRSLLETERAGRQARSVL	477
Qy	526	HETGFIQYLDSGIWHLAFYNDGKESEVVSFLTITAEISVDNCPSCNYGNGDCISGTCHCFL	585
Db	478	HEAGFIQYLDSGIWHLAFYNDGKNAEQVSFNTIVIESVVECPRNCHNGECVSGTCHCFP	537
Qy	586	GFLGPDCCGRASCPVLCSGNGQYMKGRCLCHSGWKGAECDVPTNQCIDVACSNHGTCTGT	645
Db	538	GFLGPDCSRAACPVLCSGNGQYSKGRCLCFSGWKGTEDVPTTQCIDPQCGRGICIMGS	597
Qy	646	CICNPGYKGESCEEVD CMDPTCSGRGVCVRGECHECFVGWGTNCETPRATCLDQC SGHGT	705
Db	598	CACSSGYKGESCEEADCIDPGCSNHGVCIHGECHCSPGWGGSNCEILKTMCPDQC SGHGT	657
Qy	706	FLPDTGLCSDPSWTGHDCSI E I C A A D C G G H G V C V G G T C R C E D G M W G A A C D Q R A C H P R C A	765
Db	658	YLQESGSC TCDPNWTGPDCSNEICSVDCSGHGVCMGGTCRCEEGTGPACNQ RACHPRCA	717
Qy	766	EHGTCRDGKCECSPGWNGEHCTIAHYLDRVV-----KEGCPGLCNGNGRCTLDLNGWHC	819
Db	718	EHGTCRDGKCECSPGWNGEHCTIAHYLDKIVKDKIGYKEGCPGLCNSNGRCTLDQNGGHC	777
Qy	820	VCQLGWRGAGCDTSMETACGDSKONDGDLVDCMDPDCCLOPLCHINPLCLGSPNPLDII	879
Db	778	VCQPGWRGAGCDVAMETLCTDSKDNEGDLIDCMDPDCCLOQSSCQNPQCYRGLPDPQDII	837
Qy	880	QETQVPVSQQNLHSFYDRIKFLVGRDSTHIIIPGENPFDGGHACVIRGQVMTSDGTPLGV	939
Db	838	SQSLQSPSQQAASFYDRISFLIGSDSTHVIPGESPFNKSLASVIRGQVLTADGTPLIGV	897
Qy	940	NISFVNNPLFGYTISRQDGSFDLVNNGGISIILRFERAPFITQEHTLWLPWDRFFVMETI	999
Db	898	NVSFFHYPEYGYTITRQDGMFDLVANGGASLTLVFERSPFLTQYHTVWIPWNVFYVMDTL	957
Qy	1000	IMRHEENEIPSCDLSNFARPNPVVSPSPLTSPASSCAEKGPVPEIQALQBEISISGCKM	1059
Db	958	VMEKEENDIPSCDLSGFRPNPIIVSSPLSTFFRSPEDSPIIPETQVLHBEETIPGTDL	1017
Qy	1060	RLSYLSSRTPGKYSVLRISLTHPTIPFNLMKVHLMVAVEGRLFRKWFAAABDLSYFFIWD	1119
Db	1018	KL SYLSSRAAGKYSVLKITMTQSIIPFNLMKVHLMVAVVGRLFQKWFPPASNLAYTFIWD	1077

Qy 1120 KTDVYNQKVFGLSEAFVSGVEYYESCPDLILWEKRTTVLQGYEIDASKLGWSLDKHHAL 1179  
Db 1078 KTDAYNQKVYGLSEAVVSGVEYYESCLDLTLWEKRTAILQGYELDASNMGWTLDKHHVL 1137  
Qy 1180 NIQSGILHKGNGENQFVSQQPPVIGSIMGNRRRSICPSCNGLADGNKLLAPVALTCGS 1239  
Db 1138 DVQNGILYKNGENQFISQQPPVSSIMGNRRRSICPSCNGQADGNKLLAPVALACGI 1197  
Qy 1240 DGSLYVGDFENYIRIFPSPGNVTNILELRNKDFRHSHPAHKYYLATDPMGAVFLSDSNS 1299  
Db 1198 DGSLYVGDFENYVRRIFPSPGNVTSVLELRNKDFRHSNPAHRYYLATDPVTGLYVSDTNT 1257  
Qy 1300 RRVEFKIKSTVVVKDLVKNSEVVAGTGDQCLPFDDTRCGDGGKATEATLTNPRGITVDKFG 1359  
Db 1258 RRIYRPKSLTGAKDLTKNAEVVAGTGEQCLPFDEARCGDGGKAVEATLMSPKMAVDKNG 1317  
Qy 1360 LIYFVDGTMIRRIDQNGIISTLLGSNDLTSARPLSCDSVMDISQVRLEWPTDLAINPMDN 1419  
Db 1318 LIYFVDGTMIRKVDQNGIISTLLGSNDLTSARPLTCDTSMHISQVRLEWPTDLAINPMDN 1377  
Qy 1420 SLYVLDDNNVVLQISENHQVRIVAGRPMHCQVPGIDHFLLSKVAIHATLESATALAVSHNG 1479  
Db 1378 SIYVLDDNNVVLQITENRQVRIAAAGRPMHCQVPGVE-YPVGKHAVQTTLESATAIAVSYSG 1436  
Qy 1480 VLYIAETDEKKINRIQVTTSGEISLVAGAPSGCDCKNDANCDGSGDDGYAKDAKLNTP 1539  
Db 1437 VLYITETDEKKINRIQVTTDGEISLVAGIPSECDCKNDANCDYQSGDGYAKDAKLSAP 1496  
Qy 1540 SSLAVCADGELYVADLGNIRIRFIRKNKPFNLNTQNMVELSSPIDQELYLFDTTCKHLYTQ 1599  
Db 1497 SSLAASPDGTLYIADLGNIRIRAVSKNKPLLNSMNFIEVASPTDQELYIFDINGTHQYTV 1556  
Qy 1600 SLPTGDYLYNFTYTGDDITLITDNNGMNVNRRDSTGMPLWLVPDGOVYVWMTGTNSA 1659  
Db 1557 SLVTGDYLYNFSYNDNDITAVTDSNGNTLRIRRDPNRMPVRVWSPDNQVIMLTIGTNGC 1616  
Qy 1720 TDSSVHVQVETSSK-DDVTITTNLSASGAFYTLQDQVRNSYVIGADGSLRLLLANGMEV 1778  
Db 1677 MDKAITVDIESSSREEDVSTISNLSSIDSFYTMVQDQLRNSYQIGYDGSRLRIYASGLDS 1736  
Qy 1779 ALQTEPHLLAGTVNPTVGKRNVTLPIDNGLNLVEWRORKEQARGQVTVFGRRLRVHNRNL 1838  
Db 1737 HYQTEPHVLAGTANPTVAKRNMTPGENGQNLVEWFRKEQAQKVNFGKRLRVNGRNL 1796  
Qy 1839 LSLDFDRVTRTEKIYDDHRKFTLRILYDQAGRPSLWSPSSRLNGVNVTVSPGVIAGIQR 1898  
Db 1797 LSVDFDRTTKTEKIYDDHRKFLRLIAYDTSGHPTLWLPSSKLMVNVTVYSTGQIASIQR 1856  
Qy 1899 GIMSERMEYDQAGRITSRIFADGKTWSYTYLEKSMVLLHSQRQYIFEFDKNDRLSVMTM 1958  
Db 1857 GTTSEKVDYDGGRIVSRVFADGKTWSYTYLEKSMVLLHSQRQYIFEYDMWDRLSAITM 1916  
Qy 1959 PNVARQTLTIRSVGYRNIYQOPPEGNASVIOQDFTEDGHLLHTFYLGTGRRVIYKYGKLS 2018  
Db 1917 PSVARHTMQTIRSIGYRNIYNPPESNASIITDYNEEGULLQTAFLGTSRRRVLFKYRQT 1976  
Qy 2019 KLAETLYDTTKVSFTYDETAGMLKTINLQNEGFTCTIRYRQIGPLIDRQIFRFTBEGMVN 2078  
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Qy 2079 ARFDYNDNSFRVTSMQAVINETPLPIDLYRYDDVSGKTEQFGKFGVIYYDINQIITAV 2138  
Db 2037 ARFDYSYDNSFRVTSMQGVINETPLPIDLYQFDDISGKVEQFGKFGVIYYDINQIISTAV 2096  
Qy 2139 MTHTKHFDAYGRMKEVQYEIFRSLMYWMTVQYDNMGRVVVKELKVGPYANTTRYSEYDA 2198  
Db 2097 MTYTKHFDAHGRIKEIQYEIFRSLMYWITIQYDNMGRVTKREIKIGPFANTTKVAYEYDV 2156  
Qy 2199 DGQLQTVSINDKPLWRYSYDLNGLNLHLSPGNSARLTPLRYDIRDRITRLGDVQYKMDDED 2258

Db 2157 DGQLQTVYLNBEKIMWRYNYDLNGLNLHLLNPSNSARLTPLRYDLRDRITRLGDVQYRLDED 2216  
Qy 2259 GFLRQRGDIFEYNSAGLLIKAYNRAGSVRYRYDGLGRRVSSKSSHHLQFFYADLT 2318  
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Qy 2379 QILYTAYGEIYMDTNPNFQIIIGYHGGLYDPLTKLVHMGRRDYDVLAGRWTSPDHELWKH 2438  
Db 2337 QIQYTAYGEIYFDSNIDFQLVIGFHHGGLYDPLTKLIHFGERDYDILAGRWTTPDIEIWK 2396  
Qy 2439 LSSSNVMPFNLYMFKNNNPISNSQDIKCFMTDVNSWLLTFGFQLHNVIPGYPKPDMNAME 2498  
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Qy 2499 PSYELIHTQMKTBWDNSKSIILGVQCEVQKQKAFVTLERFDQLYGSTITSCQQAPKTKK 2558  
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Db 2508 WLWFATVKSLLIGKVMNAVSGRVQTNVLNIANEDCIKVAAVLNNAFYLENLHFTIEGKD 2567  
Qy 2616 THYFVKPGPSEGDLAAILGLSGRRRTLENGVNVTVSQINTVLNGRTRRYTDIQLQYGALCL 2675  
Db 2568 THYFIKTTTPESDLGTLRLTSGRKALENGINVTVSQSTTVNGRTRRFADVEMQFGALAL 2627  
Qy 2676 NTRYGTTLDEEKARVLELARQAVRQAWAREQORLREGEGLRAWTEGEKQQVLSTGRVQ 2735  
Db 2628 HVRYGMTLDEEKARILEQARQARALARAWAREQORVRDGEGARLWTEGEKQQLLSAGKVQ 2687  
Qy 2736 GYDGFVVISVEQYPELSDSANNIHFMRQSEMGR 2769  
Db 2688 GYDGYVLSVEQYPELADSANNIQFLRQSEIGRR 2721

RESULT 11

US-10-038-854-36  
; Sequence 36, Application US/10038854  
; Publication No. US20040022781A1  
; GENERAL INFORMATION:  
; APPLICANT: Spytek, Kimberly A  
; APPLICANT: Li, Li  
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; APPLICANT: Spaderna, Steven K  
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; APPLICANT: Kekuda, Ramesh  
; APPLICANT: Patturajan, Meera  
; APPLICANT: Gusev, Vladimir Y  
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; APPLICANT: Guo, Xiaojia S  
; APPLICANT: Shenoy, Suresh G  
; APPLICANT: Rastelli, Luca  
; APPLICANT: Casman, Stacie J  
; APPLICANT: Boldog, Ferenc  
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; APPLICANT: Ellerman, Karen  
; APPLICANT: Gunther, Erik  
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; APPLICANT: Millet, Isabelle  
; APPLICANT: MacDougall, John R  
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same

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; FILE REFERENCE: 21402-230
; CURRENT APPLICATION NUMBER: US/10/038,854
; CURRENT FILING DATE: 2003-01-22
; PRIOR APPLICATION NUMBER: 60/258,928
; PRIOR FILING DATE: 2000-12-29
; PRIOR APPLICATION NUMBER: 60/259,415
; PRIOR FILING DATE: 2001-01-02
; PRIOR APPLICATION NUMBER: 60/259,785
; PRIOR FILING DATE: 2001-01-04
; PRIOR APPLICATION NUMBER: 60/269,814
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: 60/279,832
; PRIOR FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/279,833
; PRIOR FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/279,863
; PRIOR FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/283,889
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/284,447
; PRIOR FILING DATE: 2001-04-18
; PRIOR APPLICATION NUMBER: 60/286,683
; PRIOR FILING DATE: 2001-04-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 411
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 36
; LENGTH: 2725
; TYPE: PRF
; ORGANISM: Homo sapiens
US-10-038-854-36
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Query Match      68.5%; Score 10201; DB 4; Length 2725;
Best Local Similarity 66.9%; Pred. No. 0;
Matches 1872; Conservative 362; Mismatches 462; Indels 102; Gaps 21;

QY      1 MDVKERPYSLTR-RRDAERRYTSSADSEEGKAP-QKSYSSETLKAYDQD-ARLAYG 57
      |||||: || |||: |||: |||||: |||: |||: |||||: |||: |||: |||||: |||: |||: ||
Db      1 MDVKERRPYCSLTKSRRREKERRYTNSSADNEECRVPTQKSYSSETLKAFDHDSSRLLYG 60

QY      58 SRVKDIVPOBAEEFCRTGANFTLRELGLEEVTPPHGTLYRTDGLPQCYSMGAGSDADM 117
      :|||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||
Db      61 NRVKDLVHREADEFTROQNFTLRQLGCEPATRRGLAFCAEMGLPHRGYISAGSDADT 120

QY      118 EADTVLSPHPVRLWGRSTRSGRSSCLSSRANSNLTLTDTHEH---TETDHPGGLQNH 174
      | :|||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||:
Db      121 ENEAVMSPHAMRLWGRGVKSGRSSCLSSRSNSALTTLTDTHEHKSDSENEQPASNQGS 180

QY      175 RLRTPPPLSHAHTPNQHAAASINSLNRGNFTPRSNPSPAPTDHLSGEPAGGAQ----- 230
      | : || || || || || || || || || || || || || || || || || || || || ||
Db      181 TLQPLPP--SHKQHSAQHH-PSITSLNRNSLTNRRNQSPAP-----PAALPAELQTT 229

QY      231 -EPAHAQENWLLNSNIPLETRNLGKQDFLGTLDQNLNLIEMDILGASRHDGAYS DGHFLFKP 289
      | |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||:
Db      230 PESVQLQDSWVLGSNVPLESR-----HFLFKT 256

QY      290 G-GTSPFCTTSPGYPLTSSTVYSPPPRPLPRSTFARPAFNLUKPKSKYCNWKCAALSIV 348
      | |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||:
Db      257 GTGTTPLFSTATPGYTMASGSVYSPPTRPPLRNTLSRSAFKKSKSKYCSWKTCALCAVG 316

QY      349 ISATLVILLAYFVAMHLFGLNWHLQPMEGQMYE---ITEDTASSWPVPTDVSLYPSGGTG 405
      : |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||:
Db      317 VSVLLAILLSYFIAMHLFGLNWQLQQTENDTFENGKVNSDT-----MPTNTVSLPSG--- 368

QY      406 LETPDRKKGKTEGKPSFFPEDSFIDSGEIDVGRRASQKIPGTFWRSQVFIDHPVHLK 465
      || || || || || || || || || || || || || || || || || || || || ||
Db      369 -----DNGKLGFTQENNTIDSGELDIGRRAIQEIIPPFIWRSQLFIDQPQLK 417

QY      466 FNVSLGKAALVGIYGRKGLPPSHT---QDFVELLDGRRLLTQEARSLGEGTPRQSGRTV 521
      ||: || || || || || || || || || || || || || || || || || || || ||
Db      418 FNIQLQDALIGVYGRKKLPPSHTQSSPQYDFVELLDGSRLLIAREQSRSLLETERAGQAR 477

QY      522 PPSSHETGFIQYLDSGIWHLAFYNDGKESEVWSFLTTAIESVDNCPNSCYGNCGDCISGTC 581
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Db      478 SVSLHEAGFIQYLDSGIWHLAFYNDGKNAEQVSNFTIVIESVVECPRNCHNGGECVSGTC 537

QY      582 HCFLGLFLPDCCGRASCPVLCSGNGQYMKGRCLCHSGWKGAECDVPTNQCIDVACSNHGTC 641
      ||| ||||| |||: ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||| |||
Db      538 HCFPGFLGPDCSRACPVLCSGNGQYSKGRCLCFSGWKGTEDVPTTQCIDPQCGRGIC 597

QY      642 ITGTICINPGYKGESCEEVDCMDPTCSGRGVVVRGECHCFVWGVTNCETPRATCLDQCS 701
      | : || || || || || || || || || || || || || || || || || || || ||
Db      598 IMGSCACSSGYKGESCEADCIDPGCSNHGVCIHGECHCSPGWGGSNCEILKTMCPDQCS 657

QY      702 GHGTFLPDTGLCSDPSWTGHDCSIEICAAACGCGHGVVCGGTCTCRCEDEGMMGAACDQRACH 761
      ||||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||
Db      658 GHGTYLQESGCTCDPNWTGPDSCNEICSVDGSHGVCMGGTCRCEEGWTPACNQACH 717

QY      762 PRCAEHGTCRDGKCECSPGWNGEHCTIAHYLDRVV-----KEGCPGLCNGNGRCTLDLN 815
      |||||: |||||: |||||: |||||: |||||: |||||: |||||: |||||: |||||: |||||
Db      718 PRCAEHGTCCKDGKCECSPGWNGEHCTIAHYLDKIVDKIGYKEGCPGLCNSNGRCTLQDN 777

QY      816 GWHCVCOLGWRGAGCDTSMETACGDSKDNDDGDLVDCMDPDCCLOPLCHINPLCLGSPNP 875
      |||||: |||||: |||||: |||||: |||||: |||||: |||||: |||||: |||||: |||||
Db      778 GGHCVCQPGWRGAGCDVAMETLCTDSKDNEGDGLDCMDPDCCLOSSCQNPYCRGLPDP 837

QY      876 LDIIQETQVPVSQQNLHSPYDRIKFLVGRDSTHIIIPGENPFDGGHACVIRGQVMTSDGTP 935
      ||||: ||| |||||: |||||: |||||: |||||: |||||: |||||: |||||: |||||
Db      838 QDIISQSLQSPSQAAKSFYDRISFLIGSDSTHVIPGESPFNKSLASVIRGQVLTADGTP 897

QY      936 LVGVNISFVNNPLFGYTISRQDGSFDLVNTNGISIIILRFERAPFITQEHTLWLPWDRFFV 995
      | :|||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||
Db      898 LIGVNVSFHYPEYGYTITRQDGMFDLVANGASLTLVFERSPFLTQYHTVMIPWNVYV 957

QY      996 METIIMRHEENIPSCDLSNFARPNPVVSPSLTSFASSCAEKGPVIVPEIQALQEEISIS 1055
      | :||: |||||: |||||: |||||: |||||: |||||: |||||: |||||: |||||: |||
Db      958 MDTLVMEKEENDIPSCDLSGFVRPNPIIVSSPLSTFFRSSPEDSPIIPETQVLHEETTIP 1017

QY      1056 GCKMRLSYLSRTPGYKSVLRISLTHPTIPENLMKVHLMVAVEGRLFRKWFAAAPDLSY 1115
      | :||| |||||: |||||: |||||: |||||: |||||: |||||: |||||: |||||: |||
Db      1018 GTDLKLSYLSSRAAGYKSVLKITMTQSIIPENLMKVHLMVAVVGRLLFQKWFEPASNLAYT 1077

QY      1116 FIWKTDVYNQKVFLSEAFVSUGVEYESCPDLILWEKRTTVLQYEIDASKLGWSLDK 1175
      |||||: |||||: |||||: |||||: |||||: |||||: |||||: |||||: |||||: |||||
Db      1078 FIWKTDAYNQKVYGLSEAVSVUGVEYESCLDLTLWEKRTAILQGYELDASNMGWTLDX 1137

QY      1176 HHAALNIQSGILHKNGENQFVSQQPPVIGSIMGNRRRRSISCPSCNGLADGNKLLAPVAL 1235
      || :||: |||||: |||||: |||||: |||||: |||||: |||||: |||||: |||||
Db      1138 HHVLDVQNGILYKNGENQFISQQPPVSVSSIMGNRRRRSISCPSCNQADGNKLLAPVAL 1197

QY      1236 TCGSDGSLYVGDFNYIRRIFFPSGNVTNILELRNKDFRSHSHSPAHKYIYLATDMSGAVFLS 1295
      || :||| |||||: |||||: |||||: |||||: |||||: |||||: |||||: |||||
Db      1198 ACGIDGSLYVGDFNYIRRIFFPSGNVTSVLELRNKDFRHSNPAHRYIYLATDPVTGDLVVS 1257

QY      1296 DSNRRRVFKIKSTVVVKDLVKNSEVAGTGQCLPFDDTRCGDGGKATEATLTNPRGITV 1355
      | :||: ||| |||||: |||||: |||||: |||||: |||||: |||||: |||||: |||||
Db      1258 DNTNRIYRPKSLTGAKDLTKNAEVVAGTGEQCLPFDEARCGDGGKAVEATLMSPKGMV 1317

QY      1356 DKFGLIYFVDGTMIRRIDQNGIISTLLGSNDLTSARPLSCDSVMDISQVRLEWPTDLAIN 1415
      || |||||: |||||: |||||: |||||: |||||: |||||: |||||: |||||: |||||
Db      1318 DKNGLIYFVDGTMIRKVDQNGIISTLLGSNDLTSARPLTCDTSMHISQVRLEWPTDLAIN 1377

QY      1416 PMDNSLYVLDNNVVLQISENHQVRIVAGRPMHCQVPGIDHFLLSKVAIHATLESATALAV 1475
      ||||: |||||: |||||: |||||: |||||: |||||: |||||: |||||: |||||: |||||
Db      1378 PMDNSIYVLDNNVVLQITENRQVRIAAGRPMHCQVPGVE-YPVGKHAVQTTLESATAIAV 1436

QY      1476 SHNGVLYIAETDEKKNIRIQVTTSGEISLVAGAPSGCDCKNDANCDFCGDDGYAKDAK 1535
      | :||| |||||: |||||: |||||: |||||: |||||: |||||: |||||: |||||
Db      1437 SYSGVLYITETDEKKNIRIQVTTDGEISLVAGIPSECDCKNDANCDCYQSGDGYAKDAK 1496

QY      1536 LNTPSSLAVCADGELYVADLGNIRIRFIRKNKPFPLNTQNMYELSSPIDQELYLFDTTGKH 1595
      | :||| || |||||: |||||: |||||: |||||: |||||: |||||: |||||: |||||
Db      1497 LSAPSSLAASPDGTYIADLGNIRIRAVSKNPKLLNSMNFYEVASPTDQELYIFDINGTH 1556

QY      1596 LYTQSLPTGDYLYNFTYTGDDGITLITDNNGNMNVRRDSTGMPLWLVPDGVVYVWTMG 1655
      || || |||||: ||| |||: |||||: |||||: |||||: |||||: |||||: |||||: |||
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Db 1557 QYTVSLVTGDYLYNFYSNDNDITAVTDSNGNTLRIIRDPNRPVRVVSPPDNQVILWTIG 1616

Qy 1656 TNSALKSVTTQGHELAMWYTHGNSGLLATKSNENGWTFYEYDSFGRLTNVTFPTQOVSS 1715

Db 1617 TNGCLKGMTAQGLELVLFYTHGNSGLLATKSDETGWTFFDYDSEGRLLTNVTFPTGVVTN 1676

Qy 1716 FRSDTSSVHVQVETSSK-DDVTITTNLSASGAFYTLQDQVRNSYYIGADGSLRLLLAN 1774

Db 1677 LHGDMDKAITVDIESSREEDVSITSNLSSIDSFTYMWQDLRNSYQIGYDGSRLRIYAS 1736

Qy 1775 GMEVALQTEPHLLAGTVNPTVGKRNVTLPIDNGLNLVWRQRKEAQRGQVTVFGRRLRVH 1834

Db 1737 GLDSHYQTEPHVLAGTANPTVAKRNMTLPGENGQNLVWRFRKEQAQGVNFGKRLVN 1796

Qy 1835 NRNLLSLDFDRVTRTEKIYDDHRKFTLRILYDQAGRPSPSLWSPSSRLNGVNVYSPGGYIA 1894

Db 1797 GRNLLSVDFDRTTKIEKIYDDHRKFLRLRIAYDTSGHPTLWLPSSKLMVNVYSSTGQIA 1856

Qy 1895 GIORGIMSERMEYDQAGRITSRIFADGKTWSYTVLEKSMVLLLSHSQRQYIFEFDKNDRLS 1954

Db 1857 SIQGGTTSEKVDYDGGRIVSRVFADGKTWSYTVLEKSMVLLLSHSQRQYIFEYDMWDRLS 1916

Qy 1955 SVTMPNVARQTLETIRSVGYRNIYQPPEGNASVIOQFETEDGHLHTFYLGTGRRVIYKY 2014

Db 1917 AITMPSVARHTMQTIRSIGYRNIYNPPESNASIITDYNEEGLLQTAFLGTSRRVLFKY 1976

Qy 2015 GKLSKLAETLYDTTKVSFTYDETAGMLKTINLQNEGTCTIRYQIGPLIDROIIFRFTEE 2074

Db 1977 RRQTRLSEILYDSTRVSFYDETAGVLKTVNLQSDGFICTIRYQIGPLIDROIIFRSED 2036

Qy 2075 GMVNARFDYNDNSFRVTSMQAVINETPLPIDLYRDDVSGKTEQFGKFGVIYYDINQII 2134

Db 2037 GMVNARFDYSYDNSFRVTSMQGVINETPLPIDLYQFDDISGKVEQFGKFGVIYYDINQII 2096

Qy 2135 TTAVMTHTKHFDAYGRMKEVQYEIFRSLMYMTVQYDNMGRVVKELKVGVPYANTTRYSY 2194

Db 2097 STAVMTYTKHFDAGHRIKEIQYEIFRSLMYWITIQYDNMGRVTKREIKIGPEANTTKYAY 2156

Qy 2195 EYDADGLOQTVSINDKPLWYSYDLNGLNHLSPGNSARLTPLRYDIRDRIIRLGDVQYK 2254

Db 2157 EYDVGLOQTVLYLNEKIMWRNYDNLGNLHLLNPSNSARLTPLRYDLRDRITRLGDVQYR 2216

Qy 2255 MDEGFLRQGGDIFEVNSAGLLIKAYNRAGSWSVRYDGLGRRVSSKSSHHLQFFY 2314

Db 2217 LDEGFLRQRGTEIFEYSSKGLLTRVYSGSGWTVIYRYDGLGRRVSSKTSLGHLQFFY 2276

Qy 2315 ADLTNPTKVTHLYNHSSEISLTYDLOGLHFLAMELSSGDEFYIACDNIGTPLAVFSGTG 2374

Db 2277 ADLTYPTRITHVYNHSSSEISLTYDLOGLHFLAMEISSGDEFYIASDNTGTPLAVFSSNG 2336

Qy 2375 LMIKQILYATYGEIYMDTNPNFQIIIGYHGGLYDPLTKLVHMGRRDYDLVLAGRWTSPPDHE 2434

Db 2337 LMLKQIQYTAYGEIYFDSNIDFQLVIGFHGGLYDPLTKLIHFGERDYDILAGRWTTPDIE 2396

Qy 2435 LWKHLSSSNVMPFNLYMFKNPNPISNSQDIKCFMTDVNSWLLTFGFQLHNVIPGYPKPDM 2494

Db 2397 IWKRI-GKDPAPFNLYMFRNNPNPASKIHDVKDYITDVNSWLVTFGFHLHNAIPGFPVPKF 2455

Qy 2495 DAMEPSYELIHTQMKTOEWDNSKSLGVQCEVQKQLKAFVTLERFDQLYGSTITSCQAP 2554

Db 2456 DLTEPSYELV---KSQQWDDIPPIFGVQQQVARQAKAFSLGKMAEVQ----VSRRRAG 2507

Qy 2555 KTKK---FASSGSVFGKGVKFAKDKGRVTTDIIISVANEDGRRVAAILNHAHYLENLHFTI 2611

Db 2508 GAQSWLWFATVKSLIGKGMVLAVSQGRVQTNVLNIANEDCIKVAAVLNNAFYLENLHFTI 2567

Qy 2612 DGVDTHYFVKPGPSEGDIALGLSGGRRRTLENGVNVTVSQINTVLNGRTRRRYTDIQLQYG 2671

Db 2568 EGDTHYFIKTTTPESDLGLRLTSGRKALENGINVTVSQSTTVVNGRTRRRFADVEMQFG 2627

Qy 2672 ALCINTRYGTTLDEEKARVLELARQAVRQAWAREQQRLREGEEGLRAWTEGEKQOVLST 2731

Db 2628 ALALHVRYGMTLDEEKARILEQARALARAWAREQQRVRDGEGARLWTEGEKRQLLSA 2687

Qy 2732 GRVQYDGFFFVISVEQYPELSDSANNIHFMRQSEMGRR 2769

Db 2688 GKVQYDGYVVLVSVEQYPELADSANNIQFLRQSEIGRR 2725

RESULT 12

US-10-038-854-40

; Sequence 40, Application US/10038854

; Publication No. US20040022781A1

; GENERAL INFORMATION:

; APPLICANT: Spytek, Kimberly A

; APPLICANT: Li, Li

; APPLICANT: Wolenc, Adam R

; APPLICANT: Vernet, Corine

; APPLICANT: Eisen, Andrew J

; APPLICANT: Liu, Xiaohong

; APPLICANT: Malyankar, Uriel M

; APPLICANT: Shimkets, Richard A

; APPLICANT: Tchernev, Velizar

; APPLICANT: Spaderna, Steven K

; APPLICANT: Gorman, Linda

; APPLICANT: Kekuda, Ramesh

; APPLICANT: Patturajan, Meera

; APPLICANT: Gusev, Vladimir Y

; APPLICANT: Gangolli, Esha A

; APPLICANT: Guo, Xiaojia S

; APPLICANT: Shenoy, Suresh G

; APPLICANT: Rastelli, Luca

; APPLICANT: Casman, Stacie J

; APPLICANT: Boldog, Ferenc

; APPLICANT: Burgess, Catherine E

; APPLICANT: Edinger, Shlomit R

; APPLICANT: Ellerman, Karen

; APPLICANT: Gunther, Erik

; APPLICANT: Smithson, Glennda

; APPLICANT: Millet, Isabelle

; APPLICANT: MacDougall, John R

; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same

; FILE REFERENCE: 21402-230

; CURRENT APPLICATION NUMBER: US/10/038,854

; CURRENT FILING DATE: 2003-01-22

; PRIOR APPLICATION NUMBER: 60/258,928

; PRIOR FILING DATE: 2000-12-29

; PRIOR APPLICATION NUMBER: 60/259,415

; PRIOR FILING DATE: 2001-01-02

; PRIOR APPLICATION NUMBER: 60/259,785

; PRIOR FILING DATE: 2001-01-04

; PRIOR APPLICATION NUMBER: 60/269,814

; PRIOR FILING DATE: 2001-02-20

; PRIOR APPLICATION NUMBER: 60/279,832

; PRIOR FILING DATE: 2001-03-29

; PRIOR APPLICATION NUMBER: 60/279,833

; PRIOR FILING DATE: 2001-03-29

; PRIOR APPLICATION NUMBER: 60/279,863

; PRIOR FILING DATE: 2001-03-29

; PRIOR APPLICATION NUMBER: 60/283,889

; PRIOR FILING DATE: 2001-04-13

; PRIOR APPLICATION NUMBER: 60/284,447

; PRIOR FILING DATE: 2001-04-18

; PRIOR APPLICATION NUMBER: 60/286,683

; PRIOR FILING DATE: 2001-04-25

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 411

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 40

; LENGTH: 2628

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-038-854-40

Query Match 66.4%; Score 9888.5; DB 4; Length 2628;

Best Local Similarity 65.2%; Pred. No. 0;



Qy	2142	TKHFDAYGRMKEVQYEI	FRSLMYMTVQYDNNGRVVKELKVGPYANTTRYSEYDADGQ	2201
Db	2007	TKHFDAGRIKBEIQYEI	FRSLMYWITIQYDNNGRVTKEIKIGPFANTTKYAYEYDVGQ	2066
Qy	2202	LQTVSINDKPLWRYSYD	LNGNLHLLSPGNSARLTP	2261
Db	2067	LQTVYLNKIMRWYND	LNGNLHLLNPSNSARLTP	2126
Qy	2262	RQGGDI	FEYNSAGLLIKAYNRAGSWSVR	2321
Db	2127	RQRGTEI	FEYSSKGLLTRVYSKSGWT	2186
Qy	2322	KVTHLYNHSSEIT	SLYYDLOGHLFAMELSSGDEFY	2381
Db	2187	RI	THVYNHSSEITSLYYDLOGHLFAMEISSGDEFY	2246
Qy	2382	YTAYGEI	YMDTNPNFQIIIGYHGGLYDPLTKLVHMGRRDYDVLAGRWTSPDHELWKHLSS	2441
Db	2247	YTAYGEI	YFDSNIDFQLVIGFHGGLYDPLTKLIHFGERDYDILAGRWTTPDIEIWKRI-G	2305
Qy	2442	SNVMPFNLYMFKNNPI	SNSDQIKCFMTDVNSWLLTFFGQLHNVI	2501
Db	2306	KDPAPFNLYMERNNP	PASKIHVDKDYITDVNSWLVTFFGHLHNAIPGFPVPKFDLTPSY	2365
Qy	2502	ELIHTQMTQEWDN	SKSILGVQCEVQKQKAFVTLERFDQLYGSTITSCQQAPTKK---	2558
Db	2366	ELV----	XSQQWDDIPPIFGVQQQVARQAKAFSLGLKQMAEVQ----	2417
Qy	2559	FASSGSVFGKGVKPA	KDGRVTTDIIISVANEDGRRVAAILNHAHYLENLHFTDGVDTHY	2618
Db	2418	FATVKS	LIGKGYMLAVSQGRVQTNVLNIANEDCIKVAAVLNNAFYLENLHFTTEGKDTHY	2477
Qy	2619	FVKPGPSEGLAILGL	SGGRRRTLENGVNVTVSQINTVLNGRTRRYTDIQLQYGALCLNTR	2678
Db	2478	FIKTTTPESDLG	TLRLTSGRKALENGINVTVSQSTTVVNGRTRRFADVEMQFGALALHVR	2537
Qy	2679	YGTTLDEEKARVLE	LARQAVRQAWAREQQRLREGEGLRAWTEGEKQQVLSTGRVQGYD	2738
Db	2538	YGMTLDEEKARILE	QARQARALARAWAREQQRVRDGEGARLWTEGEKQRLLSAGKVQGYD	2597
Qy	2739	GFFVISVEQYPEL	SDSANNIHFMRQSEMGR	2769
Db	2598	GYYVLSVEQYPEL	ADSANNIQFLRQSEIGRR	2628

RESULT 13  
US-10-038-854-42

GENERAL INFORMATION:

APPLICANT: Li, Li

APPLICANT: wolenc, Adam R

APPLICANT: Vernet, Corine

; APPLICANT: Eisen, Andrew J

APPLICANT: Liu, Xiaohong

APPLICANT: Malyankar, Uriel M  
APPLICANT: Shimbets, Richard A

APPLICANT: SHUMKEL, RICHARD A  
APPLICANT: Tchernev Velizar

APPLICANT: ICHENIEV, STEVEN K  
APPLICANT: Spaderna, Steven K

APPLICANT: Gorman, Linda

**APPLICANT:** Kekuda, Ramesh

; APPLICANT: Patturajan, Me

; APPLICANT: Gusev, Vladimir Y

APPLICANT: Gangoli, Esha A

APPLICANT: GUO, Xiaojia S  
APPLICANT: Eshonov, Gursbek C

APPLICANT: SURENOY, SURESH S  
APPLICANT: RAGTELLI, LUCA

APPLICANT: Casman, Stacie J

APPLICANT: Boldog, Ferenc

APPLICANT: Burgess, Catherine

; APPLICANT: Edinger, Shlomo

; APPLICANT: Ellerman, Karen

```

; APPLICANT: Gunther, Erik
; APPLICANT: Smithson, Glenda
; APPLICANT: Millet, Isabelle
; APPLICANT: MacDougall, John R
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-230

```

;; CURRENT APPLICATION NUMBER: US/10/038,854

; CURRENT FILING DATE: 200

;  
;  
PRIOR APPLICATION NUMBER: 6

PRIDE

1. PRIOR APPLICATION

PRIOR APPLICATION NUMBER

PRIOR FILING DATE: 2001

PRIOR APPLICATIONS:

Query Match 66.2%; Score 9856; DB 4; Length 2613;

QY		1	MDVKRKPYSRLTR-RRDAERYTTSSSADSEEGKAP-QKSYSSTETLKAYDQD-ARLAYG	57
			:     :     :     :     :     :     :     :	
			:     :     :     :     :     :     :     :	
nb		1	MDVKRRPYCSITKSBRERKERRYNTSSADNEECRVPTOKSYSSSETLKAFDHDSRLLYG	60

QY	58	SRVKDIVPQEAEEFCRTGANFTLRELGLLEEVTPPHGTLVYRTDIGLPQCGYSMGAGSDADM	117
		:   : : : :	
ph	61	NRVKQIVVPEAEEFTP	76

QY 118 EADTVLSPEHPVRLWGRSTRGRSSCLSSRANSNLTLTDEHENTETDHPGGLQNHLR 177  
 ||| ||| ||| |||  
 77 -----CEFAIRAGNOCST-----10-----90

QY	178	T P P P P L S H A H T N Q H A A S I N S L N R G N F T P R S N P S P A P T D H S L S C E P P A G G A Q -----EP 232
st	21	<div style="display: flex; justify-content: space-between;"> <span>         </span> <span>          :          </span> <span>         </span> </div> <div style="display: flex; justify-content: space-between;"> <span>O I P P C H V A U S A U Y</span> <span>D E I T S I N S C I N S I T A B O N C O S A B</span> <span>- - - - - D A A I P A E I O T T P B S</span> </div>

QY 233 AHAEQWLLNSNTPLETRNLGKQPFGLTQDNLNLIEMDILGASRHDGAYS DGHFLFKPG-G 291

QY 292 TSPLFCTTSPGYPLTSSWVSPPPRPLPRSTFARPAFNLKKPSKYCNWKAALSAIVISA 351

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QY      352 TLVILLAYFVAMHIFGLNWHLQPMEGQMYE---ITEDTASSWPVPTDVSLYPSGGTGLET 408
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QY 409 PDRKKGTTGKPSFFPEDSFIDSGEIDVGRRASQKIPGTFWRSQVFI DHPVHLKFN V 468





Db 2469 PESDLGTLRLTSGRKALENGINVTVSQSTTVVNGRTRRFADVEMQFGALALHVRYGMTLD 2528

Qy 2685 EEKARVLELARQRAVRAWAREQOQLREGEGLRAWTEGEKQOVLSTGRVQGYDGFVIS 2744

Db 2529 EEKARILEQARQALARAWAREQQRVRDGEGARLWTEGEKRLQLLSAGKVQGYDGYVLS 2588

Qy 2745 VEQYPELSDSANNIHFMRQSEMGR 2769

Db 2589 VEQYPELADSANNIQLRQSEIGRR 2613

RESULT 14

US-09-808-602-81

; Sequence 81, Application US/09808602

; Patent No. US20020155115A1

; GENERAL INFORMATION:

; APPLICANT: Vernet, Corine A

; APPLICANT: Fernandes, Elma

; APPLICANT: Shimkets, Richard A

; APPLICANT: Herrman, John L

; APPLICANT: Majumder, Kumud

; APPLICANT: Mishra, Vishnu

; APPLICANT: Mezes, Peter S

; APPLICANT: MacDougall, John

; TITLE OF INVENTION: No. US20020155115A1el Proteins and Nuclec Acids Encoding Same

; FILE REFERENCE: 15966-697 CIP

; CURRENT APPLICATION NUMBER: US/09/808,602

; CURRENT FILING DATE: 2001-03-14

; PRIOR APPLICATION NUMBER: 09/800,198

; PRIOR FILING DATE: 2001-03-05

; PRIOR APPLICATION NUMBER: 60/186,596

; PRIOR FILING DATE: 2000-03-03

; NUMBER OF SEQ ID NOS: 114

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 81

; LENGTH: 2802

; TYPE: PRT

; ORGANISM: Gallus gallus

US-09-808-602-81

Query Match 64.6%; Score 9616.5; DB 3; Length 2802;

Best Local Similarity 61.3%; Pred. No. 0;

Matches 1775; Conservative 411; Mismatches 491; Indels 217; Gaps 27;

Qy 1 MDVKERKPYRSLTRRR-DAERRYTSSSADSEEGKAP-QKSYSSSETLKAYDQADARLAYGS 58

Db 1 MDIKDOR-HRSLTRGRCKECRYTSSSLDSEDCRVPKQKSYSSSETLKAYGHDTRMHYGN 59

Qy 59 RVKDIVPQEAEEFCRTGANFTLRELGLEEVTPPHGTLYRTDIGLPQCQGYSMGAGSDADME 118

Db 60 RVSDLVHRESDEFPRQGTNFTLAELGICEPS-PHRSGYCSDIGILHQYSLSTGSDADSD 118

Qy 119 ADTVLSPEHPVRLWGRSTRSGRSSCLSSRANSNLTLTDTTEHEN----- 161

Db 119 TEGGMSPEHAIRLWGRGIKSSRSSGLSSRENSALTLTDSDNENKSDDEENDFHTLSEKLK 178

Qy 162 -----TETDH--- 166

Db 179 DRQTSWQQLAETKNSLIRPIPTSSSSLLPSAQLPSSHNPVPPVSCQMPLLDSNTSHQIM 238

Qy 167 -----PGGLQNH---ARLRTP-PPPLSHAHTPNQHHASI 197

Db 239 DTNPDEEFPNSYLLRACSGPQQAASSGSPSNHHSQSLRPPPLPPPHNHSLs----HHHSSA 295

Qy 198 NSLNRGNFTPRSN---PSPAPTDHLSGEPAGGAQBAHAQENWLLNSNIPLETRNLG 253

Db 296 NSLNRNSLTNRRNQIHAPAPAPND--LATTP-----ESVQLQDSVVLNSNVPLETR--- 344

Qy 254 KQPFGLGLQDNLIEMDILGASRHDGAYS DGHFLFK-PGQTSPLFCTTSPGYPLTSTSVYS 312

Db 345 -----HFLFKTSSCTPLFSSSSPGYPLTSGTVYT 374

Qy 313 PPRPLRSTFARPAFNLLKPKSKYCNWKCAALSIAIVISATLIVILLAYFVAMHLFGLNWHL 372

Db 375 PPRLLPRTFTSRNAFKLKKPSKYCSWKCAALSIAAAVLLAILLAYFIAMHLLGLNWQL 434

Qy 373 QPMEGQMYEI-----TEDTASSWPVPTDVSLYPSGGTGLETPDRKGKGTTEGKPSSF 424

Db 435 QPADGHTFSNGLRPGAAGAEAGAAAPPA-----GRG-----PW 467

Qy 425 FPEDSFIDSFEIDVGRRASOKIPPGTFWRSQVFIDHPVHLKENVSLGKAALVGIYGRKGL 484

Db 468 VTRNSSIDSGETEVGRKVTOEVPVPGVFWFSQIHISQPQFLKENISLGKDALFGVYIRRL 527

Qy 485 PPSHTQDFVELLDGRRLLLTQEARSLGCTPRQSRGTVPSSSHETGFIQYLDGSIWHLAFY 544

Db 528 PPSHAQYDFMERLDGK----EKWSVVESPRRRRSIQTLVQNEAVFVQYLDVGLWHLAFY 582

Qy 545 NDGKESEVVVSFLTTAIESVDNCPNSCYNGDCISGTCFLGLGFLGPDGCRASCPVLCSGN 604

Db 583 NDGKOKEVVVSFTVILDSVQDCPRNCHGNGECVSGVCHCFPGFHGADCAKAAACPVLCSGN 642

Qy 605 GOYMKGRCLCHSGWKGAECDVPTNQCIDVACSNHGTCTGTCTICNPGYKGESCEEVDCMD 664

Db 643 GQYSKGTCLCYSGWKGPEDVPISQCIDPSCGGHSGCIEGNCVCSIGYKGENCEEVDCLD 702

Qy 665 PTCSGRGVCVRGECHCFVGGWGTNCETPRATCLDQCDSGHGTFLPDTGLCSCDPSWTGHDC 724

Db 703 PTCSNHGVCVNGECLCSPGWWGINCELPRAQCPCQCSGHGTYSLDTGLCSCDNWMPDC 762

Qy 725 SIEICAADCGGHGVCVGGTCRCEDGWMGAACDQACHPRCAEHGTCRDGKCECSPGWNGE 784

Db 763 SVEVCSVDCGTHGVCIGGACRCEBGTGVACDQRVCHPRCTEHGTCCKDGKCECREGNGE 822

Qy 785 HCTIAHYLDRVVKEGCPGLCNGNGRCTLDLNGMHCVCQLGWRGAGCDTSMETACGDSKDN 844

Db 823 HCTIGRQTGTETDGCPCDLCNGNGRCTLGQNSWQCVCQCTGWRGPGCNVAMETSCADNKN 882

Qy 845 DGDGLVDCMDPCCLQPLCHINPLCLGSPNPLDIQETQVPVSQQNLHLSFYDRIKFLVGR 904

Db 883 EGDGLVDCLVPDCCLQSTCQNSLLCRGSRDPLDIQQSH--SGSPA VKSFYDRIKLLVGK 940

Qy 905 DSTHIIPGENPFDGGHACVIRGOVMTSDGTPLVGWNISFVNNPFLFYTISRQDSFDLVT 964

Db 941 DSTHIIPGENPFNSLSLIRGOVTTDGTPLGVNVSVFKYPKGYTITRQDGMFDLVA 1000

Qy 965 NGGISIILRFERAPFITQEHTLWLPWDRFFVMETIIMRHEENEIPSCDLSNFARNPVVS 1024

Db 1001 NGSSSLTLHFERAPFMSQERTVWLPWNSFYAMDTLVMKTEENSIPSCDLSGFVRDPVII 1060

Qy 1025 PSPLTSFASSCAEGPIVPEIQALQEEISISGCKWRLSYLSRTPGYKSVLRISLTHPTI 1084

Db 1061 SSPLSTFFSDAPGRNPVPEPQTVLHEEIEVPGSSIKLIYLSRRTAGYKSLKIIIMTQSLV 1120

Qy 1085 PFNLMKVHLMVAVEGRILFRKWFAAAPDLSYYFIWKTVDVYNQKVFGLSEAFVSUGVEYES 1144

Db 1121 PLNLIKVHLMVAVEGHLFQKSFSLASPNLAYTFIWDKTDAYGQKVGLSDAVSVSGPEYET 1180

Qy 1145 CPDLILWEKRTTVLQGYEIDASKLGGWSLDKHHALNIQSILHKNGENQFVSQQPPVIG 1204

Db 1181 CPSLILWEKRTALLOGFELDPNSLGGWSLDKHHVLNVKSGILHKNGENQFLTQOPAVIT 1240

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Db 1241 SIMGNRRRSISPCSCNGLAEGNKLLAPVALAVGIDGSLFVGDFNYIRRIFFPSRNVTSIL 1300

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Db 1301 ELRNKEFKHSNNPAHKYIYLAVDPVSGSLYVSDTNSRRRIYKVKSLTGTKOLAGNSEVVAGT 1360

Qy 1325 GDQCLPFDDTRCGDGGKATEATLTNPRGITVDKFGLIYFVDGTMIRRIDQNGIISTLLGS 1384

Db 1361 GEQCLPFDEARCGDGGKAVDATLMSPRGIAVDKYGLMYFVDATMIRKVDQNGIISTLLGS 1420

Qy 1385 NDLTSARPLSCDSVMDISQVRLEWPTDLAINPMDNSLYVLDNNVVLQISENHQVRIVAGR 1444

Db 1421 NDLTAVRPLSCDSSMDVSOVRLEWPTDLAVDPMDNSLYVLNNVILRITENHQVSIAGR 1480

Qy 1445 PMHCQVPGIDHELLSKVAIHATLESATALAVSHNGVLYIAETDEKKINRIRQVTTSGEIS 1504

Db 1481 PMHCQVPGID-YLSKLAHSALESASAIAISHTGVLYISETDEKKINRLRQVTTNGEIC 1539

Qy 1505 LVAGAPSGCDCKNDANCDFCSGDDGYAKDAKLNTPSSLAVCADGELYVADLGNIRIRFIR 1564

Db 1540 LLAGAASDCCKNDVNCNCYSGDDGYATDAILNSPSSLAVAPDGTIYIADLGNIRIRAVS 1599

Qy 1565 KMKPFLNTQNMVELSSPIDQELYLFDTGKHLYTQSLPTGDLYNFTYTGDGITLITDN 1624

Db 1600 KMRPILNSFNQYEAASPGEQELYVFNADGIHQYTLSLVTGEYLYNFTYSSDNDVTEVMS 1659

Qy 1625 NGNMVNVRDSTGMPLWLVPDGVVWVTMGNTSALKSVTTQGHELAMMTYHGNSGLLAT 1684

Db 1660 NGNSLKVRRDASGMPRHLLMPDNQIVTLAVGTNGGLKLVSTQTLDELGLMTYNGNSGLLAT 1719

Qy 1685 KSNENGWTTFYEYDSFGRLLTNVTFPTGQVSSFRSDTSSVHVQVETSSK-DDVTITTNLS 1743

Db 1720 KSDETGWTTFDYDHEGRLTNVTRPTGVVTSLHREMEKSITIDIENSNRDDDDVTITNLS 1779

Qy 1744 ASGAFYTLLOQVRNSYYIGADGSLRLLLLANGMEVALQTEPHLLAGTVNPTVGKRVNLTLP 1803

Db 1780 SVEASYTVVQDQVRNSYQLCNGNGLRVMYANGMSISFHSPEHVLAGTVTPTIGRCNLSLP 1839

Qy 1804 IDNGLNLVEWRQKEQARGQVTVFGRRLRVHNRNLLSLDFDVRTRTEKIYDDHRKFTLRI 1863

Db 1840 MENGLNSIEWRLRKEQIKGKTVVFGKRLRVHGRNLLSIDYDRNIRTEKIYDDHRKFTLRI 1899

Qy 1864 LYDQAGRPSLWSPSSRLNGVNVTYSPGGYIAGIORGIMSERMEYDQAGRITSRIFADGKT 1923

Db 1900 IYDQGRPELWLPSSGLAAVNVSYFFNGRLAGLQRGAMSERDIDKQGRIIISRMFADGKV 1959

Qy 1924 WSYTYLEKSMVLLLSQRQYIFEFDKNDRLLSSVTMPNVARQJLETIRSVGYRNIYQPPPE 1983

Db 1960 WSYTYLEKSMVLLLSQRQYIFEYDSSDRLLHAVTMPSVARHSMSTHTSVGYIRNIYNPPE 2019

Qy 1984 GNASVIOFTEDGHLLHTFYLGTGRRVYIKYGLSKLAETLYDTTKVSFTYDETAGMLKT 2043

Db 2020 SNASVIFYDSDGRILKTSFLGTGRQVFKYKGLSKLSEIYVDSYAVTFGYDETTGVLMK 2079

Qy 2044 INLQNEGFTCTIRYRQIGPLIDRQIFRFTTEEGMVNARFDVNY-DNSFRVTSMQAVINETP 2102

Db 2080 VNLSQGGFSTIRYKIGPLVDKQIYRFSEEGMVNARFDYTHDNSFRIASIKPIISETP 2139

Qy 2103 LPIDLRYDDVSGKTEQFGFVYVDINQIITAVMTHPKHFDAYGRMKEVOYEIERSL 2162

Db 2140 LPVDLYRYDEISGKVEHFGKFGVYVDINQIITAVMTLSKHFDTHGRIKEVOYEMFRSL 2199

Qy 2163 MYWMTVQYDNMGRVVKKELKVGPYANTTRYSYEYDADGQLQTVSINDKPLWRYSYDLNGN 2222

Db 2200 MYWMTVQYDSMGRVTKRELKLGPYANTTKYTYDYDGGQLQSVAVNDRPTWRYSYDLNGN 2259

Qy 2223 LHLLSPGNSARLTPLRYDIRDRITRLGDVQYKMDDEGFLRQRGDIFEYNSAGLLIKAYN 2282

Db 2260 LHLLNPGNSVRLMPLRYDLRDIRLGDIPYKIDDDGFLCQRGSDVFEYNSKGLLTRAYN 2319

Qy 2283 RAGWSVRYRYDGLGRRVSSKSSHHLQFFYADLTNPTKVTHLYNHSSEITSLYYDLQ 2342

Db 2320 KANGWNVQYRYDGLGRRASCKTNLGHHLQYFYADLHNPTRVTHVYNSNSEITSLYYDLQ 2379

Qy 2343 GHLPAMELSSGDEFYIACDNIGTPLAVFSGTGLMIKQILYTAYGEIYMDTNPNFQIIGY 2402

Db 2380 GHLPAMESSSGEEYYVASDNTGTPLAVFSINGLMIKQLQYAYGEIYYDSNPDPQLVIGF 2439

Qy 2403 HGGLYDPLTKLVHMGRRDYDVLAGRWTSPDHELWKHLSSSNVMPFNLYMFKNNPISNSQ 2462

Db 2440 HGGLYDPLTKLVHFTQRDYDVLAGRWTSPDYTMWKNIGREPA-PFNLYMFKSNNPISNEL 2498

Qy 2463 DIKCFMTDVNSWLLTTFGFQLHNVIPGYPKPDMADAMEPSYELIHTQMKTQEWDNKSILGV 2522

Db 2499 DLKQNVTDVKSWLVMFGFQLSNIIIPGFPRAKMYFVSPPYEL----TESQACENGQLITGV 2554

Qy 2523 QCEVQQLKAFVTLERFDQLYGSTITSCQQAPKTKK-----PASSGSVFGKGVKPFALKDGR 2578

Db 2555 QOTTERHNQAFMALE-----GQVISKRLHASIREKAGHWFATSTPIIGKIMFAVKKGR 2608

Qy 2579 VTTDIISVANEDGRRVAAILNHAHYLENLHFTIDGVDTHYFVKPGPSEGLAIIGLSGGR 2638

Db 2609 VTTGISSIATDDSRKIASVLNSAHYLEMKHYSIEBKDTHYFVKIGSADSDLVTLAMTSGR 2668

Qy 2639 RTLENGVNVTVSQINTVLNGRTRRYTDIQLQYGALCLNTRYG---TTLDEEKARVLELAR 2695

Db 2669 KVLDSGVNVTVSQPTLLINGRTRRFTNIEFQYSTLLINIRYGLTADTLDEEKARVLDQAR 2728

Qy 2696 QRAVRQAWAREQQRLREGEGLRAWTEGEKQQVLSTGRVQGYDGFVVISVEQYPELSDSA 2755

Db 2729 QRALGSAWAKEQQKARDGREGSRVWTDGKQQLLNTGRVQGYEGYVYVLPVEQYPELADSS 2788

Qy 2756 NNHFMRQSEMGR 2769

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RESULT 15

US-09-800-198-69

; Sequence 69, Application US/09800198

; Publication No. US20030087816A1

; GENERAL INFORMATION:

; APPLICANT: Vernet, Cornie AM

; APPLICANT: Fernandes, Elma

; APPLICANT: Shimkets, Richard A

; APPLICANT: Herrmann, John L

; APPLICANT: Majumder, Kumud

; APPLICANT: Mishra, Vishna

; APPLICANT: Mezes, Peter S

; APPLICANT: Rastelli, Luca

; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME

; FILE REFERENCE: 15966-697

; CURRENT APPLICATION NUMBER: US/09/800,198

; CURRENT FILING DATE: 2001-03-05

; PRIOR APPLICATION NUMBER: 60/186,596

; PRIOR FILING DATE: 2000-03-03

; NUMBER OF SEQ ID NOS: 98

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 69

; LENGTH: 2802

; TYPE: PRT

; ORGANISM: Gallus gallus

US-09-800-198-69

Query Match 64.6%; Score 9616.5; DB 3; Length 2802;

Best Local Similarity 61.3%; Pred. No. 0;

Matches 1775; Conservative 411; Mismatches 491; Indels 217; Gaps 27;

Qy 1 MDVKERKPYRSILTRRR-DAERRYTSSSADSEEGKAP-QKSYSSSETLKAYDQDARLAYGS 58

Db 1 MDIKDRR-HRSLTRGRCGKECRYTSSSLDSEDCRVPAQKSYSSSETLKAYGHDTRMHYGN 59

Qy 59 RVKDIVPQEAEEFCRTGANFTLRELGLEEVTPPHGTLYRTDIGLPQCGYSMGAGSDADME 118

Db 60 RVSDLVHRESDEFPRQGTNFTLAEELGICEPS-PHRSGYCSDIGILHQYSLSTGSDADSD 118

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Db 119 TEGGMSPEHAIRLWGRGIKSSRSSGLSSRENSALTLTDSNENKSDENDFHTHLSSEKLK 178

Qy 162 -----TETDH--- 166

Db 179 DRQTSWQQLAETKNSLIRRPPIPTSSSSLLPSAQLPSSHNPVPVSCOMPLLDSENTSHQIM 238

Qy 167 -----PGGLQNH-----ARLRTP-PPPLSHAHTPNQHHAAASI 197

Db 239 DTNPDEEFPNSYLLLRACSGPQQAASSSGPSNHHHSQSTLRPPLPPPHNHSLS---HHHSSA 295



QY 198 NSLNRGNFTPRSN-----PSPAPTDHSLSGEPPAGGAQEPAHAQENWLLNSNIPLETRNLG 253  
| | | | : | | | | | | | | : | | | | | | | | : | | | | | | | | : | | | | | | | |  
Db 296 NSLNRNSLTNRNQIHAPAPAPND--LATT-----ESVQLQDSWVLNSNPLETR--- 344  
QY 254 KQPFLGTLQDNLIEMDILGASRHDGAYS DGHFLFK- PGGTSP LCTTSPGYPLTSSTVYS 312  
| | | | : | | | | | | | | : | | | | | | | | : | | | | | | | | : | | | | | | | |  
Db 345 -----HFLFKTSSGTTPLFSSSSPGYPLTSGTVYT 374  
QY 313 PPRPLPRSTFARPAFNLLKPKSKYCNWKCAALSIAVISATLVILLAYFVAMHLFGLNWHL 372  
| | | | : | | | | | | | | : | | | | | | | | : | | | | | | | | : | | | | | | | |  
Db 375 PPRLLPRNTFSRPAFNLLKPKSKYCSWKCAALSIAAAVLLAILLAYFIAMHLLGLNWQL 434  
QY 373 QPMEGQMYEI-----TEDTASSWPVPVPTDVS LYPSSGGTGLETPDRKGKGTTGPKPSSF 424  
| | | | : | | | | | | | | : | | | | | | | | : | | | | | | | | : | | | | | | | |  
Db 435 QPADGHTFSNGLRPGAAGEDGAAAPPA-----GRG-----PW 467  
QY 425 FPEDSFIDSGEIDVGRRASQKIPPGTFWRSQVFI DHPVHLKFNVS LKGAALGYGRKGL 484  
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Db 468 VTRNSSIDSGETEVEGRKVTVQEVPPGVFWRSQIHISQBPFLKFNISLGKDALFGVYIRRLG 527  
QY 485 PPSHTQFDFVELLDGRRLLTQEARSLGTPRQSRGTVPPSSHETGFIQYLDSGIWHLAFY 544  
Db 528 PPSHAQYDFMERLDGK-----EKWSVVESPRRERSIQTLVQNEAVFVQYLDVGLWHLAFY 582  
QY 545 NDGKESEVVSFLTITAIESVDNCPNSCYNGDCISGTC HCFGLFGLPDCGRASC PVLCSGN 604  
| | | | : | | | | | | | | : | | | | | | | | : | | | | | | | | : | | | | | | | |  
Db 583 NDGKDKEVVSFSTVILDSVQDCPRNCHNGGECVSGVCHCFPGF HGAADCAKAACPVLCSGN 642  
QY 605 GOYMKGRCLCHSGWKGAECVPTNQCIDVACSNHGTICITGTCI CNPGYKGESCEEVD CMD 664  
| | | | : | | | | | | | | : | | | | | | | | : | | | | | | | | : | | | | | | | |  
Db 643 GOYSKGTCLCYSGWKGPCECDVPISQCIDPSCGGHGSIEGNCVC SIGYKGENCEEVDCLD 702  
QY 665 PTCSGRGVCVRGECHCFVWGNGTNCETPRATCLDQCSGHGTFLPD TGLCSDPSWTHDC 724  
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Db 703 PTCSNHGVCVNGECLCSPGWGINCELPRACPDQC SGHGTYSLDTGLCSDPNMWPDC 762  
QY 725 SIEICAADCGGHGVCVGGTCRCE DGMGAACDQACHPRCAEHGT CRDGKCECSPGWNGE 784  
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Db 763 SVEVCSDVCGTHGVCIGGACRCEEGWTVACDQRVCHPRCTE HGTCKDGKCECREGWNGE 822  
QY 785 HCTIAHYLDRVVKEGCPGLCNGNGRCTL DLNGWHCVCOLGWRGAGCDTSMETACD SKDN 844  
| | | | : | | | | | | | | : | | | | | | | | : | | | | | | | | : | | | | | | | |  
Db 823 HCTIGRQTTGTETDGC PDL CNGNGRCTLGQNSWQCVCQCGWRGPGC NVAMETSCADNKDN 882  
QY 845 DGDGLVDCMDPDCCLOPLCHINPLCLGSPNPLDIIQETQVPVSQQNLH SFYDRIKFLVGR 904  
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Db 883 EGDGLVDCLVPDCCLOSTCQNSLLCRGSRDPLDIIQOSH--SGSPA VKSFYDRIKLLVGK 940  
QY 905 DSHIIPGENPFDGGHACVIRGQVMTSDGTPLGVNI SFVNNPLFGYTI SRQDGSFDLVT 964  
| | | | : | | | | | | | | : | | | | | | | | : | | | | | | | | : | | | | | | | |  
Db 941 DSHIIPGENPNFSSVLIRGQVTTDGTPLGVNVVSFKYPKYGTITIRQDGMFDLVA 1000  
QY 965 NGGTSIILRFERAPFITQEH TLWLPWDRFFVME TIIMRHEENEIPSCDLSNFARPNPVVS 1024  
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Db 1001 NGSSLT LHFERAPFMSQERTVWLPWNSFYAMD TLVMKTEENSIPSCDLSGFVRDPVII 1060  
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Db 1061 SSPLSTFFSDAPGRNP IVPETQVLHEEIEVPGSSIKLIYLSRRTAGYKSLLLKIIMTQSLV 1120  
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Db 1121 PLNLIKVHLMVAVEGHLFQKSF LASNLAYTFIWDKTDAYGQKVYGLSDAVSVSGFEYET 1180  
QY 1145 CPDLILWEKRTTVLQGYEIDASKLGWWSLDKXHALNIOSGILHKNGENQFVSQQPPVIG 1204  
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Db 1181 CPSLILWEKRTALLQGFELDP SNLGGWSLDKXHVNLNVKSGILHKNGENQFLTQQPAVIT 1240  
QY 1205 SIMGNRRRSISCPSCNGLADGNKLLAPVALTCGSDGSLYVGDFNYIRRIFFPSGNVTNIL 1264  
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Db 1241 SIMGNRRRSISCPSCNGLAEGNKLLAPVALAVGIDGSLFVGDFNYIRRIFFPSRNVTSIL 1300  
QY 1265 ELRNKDFRHSHPAHKYYLATDPM SGAVFLSDSNSRRRVFKISTVWVKDLVKNSEVVAGT 1324

Db 1301 ELRNKEFKHSNNPAHKYYLAVDPVSGSLYSDVTNSRR IYKVKSLTGTKDLAGNSEVVAGT 1360  
QY 1325 GDQCLPFDDTECGDGGKATEATLTNPRGITVDK FGLIYFVDGTMIRRIDONGIISTLLGS 1384  
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Db 1361 GEQCLPFDEARGDGGKAVDATLMSPRGTA VDKYGLMYFVDATMIRKVDQNGIISTLLGS 1420  
QY 1385 NDLTSARPLSCDSVMDISOVRLEWPTDLA INPMDNSLYVL DNNVVLQISENHQVRIVAGR 1444  
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Db 1421 NDLTAVRPLSCDS SMDVSQVRLEWPTDLA VDPMDNSLYVLENNVILRITENHQVSI IAGR 1480  
QY 1445 PMHCQVPGIDHFLLSKVAIHATLESATA LAVSHNGVLYIAETDEKKINRIROVTTSGEIS 1504  
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Db 1481 PMHCQVPGID-YSLSKLAHSALESASAIASH TGVLYISETDEKKINRLRQVTTNGEIC 1539  
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Db 1540 LLAGAASDCDCCKNDVNCNCYSGDDGYATDA ILSNPSSSLAVAPDGTIYIADLGNIRIRAVS 1599  
QY 1565 KNKPFLNTQNMVELSSPIDQELYLFDTTGK HLYTQSLPTGDYLYNFYTGDDITLITDN 1624  
| | | | : | | | | | | | | : | | | | | | | | : | | | | | | | | : | | | | | | | |  
Db 1600 KNRPIILNSFNQYEAASPGEQELYVFNADGH QYTL SVTGEYLYNFYSSDNDVTEVMS 1659  
QY 1625 NGNMVNRDSTGMP LVLVVPDGOVYVWVTMG TNSALKSVTTQGHELAMMTYHGNSGLLAT 1684  
| | | | : | | | | | | | | : | | | | | | | | : | | | | | | | | : | | | | | | | |  
Db 1660 NGNSLKVRRDASGMPRHLLMPDNQIVTLA VGTNGGLKLVSTQTLEGLMTYNGNSGLLAT 1719  
QY 1685 KSNENGWTTFFEYDVSFGRLTNVTPPTGQ VSSFRSDTSSVHVQVETSSK-DDVTITTNLS 1743  
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Db 1720 KSDETGWTTFYDHEGRLTNVTRPTGVVTS LHRMEKSI TIDIENSNRDDDVTVITNLS 1779  
QY 1744 ASGAFYTL LQDQVRNSYYIGADGSLRL LLANGMEVALQTEPHLLAGTVNPTVGKRNVTLP 1803  
: | | | | : | | | | | | | | : | | | | | | | | : | | | | | | | | : | | | | | | | |  
Db 1780 SVEASYTVVQDQVRNSYQLCNNGTLRVMYANG MSISFHSEPHVLAGTVPTIGRCNISLP 1839  
QY 1804 IDNGLNLVEWORKEQARGQVTVFGRRLRV HNRNLLSLDFDRVTRTEKIYDDHRKFTLRI 1863  
: | | | | : | | | | | | | | : | | | | | | | | : | | | | | | | | : | | | | | | | |  
Db 1840 MENGLNSIEWRLKEQIKGKVTVFGRKL RVHGRNLLSIDYDRNIRTEKIYDDHRKFTLRI 1899  
QY 1864 LYDQAGRPSLWSPSSRLNGVNVTYSPGGY IAGIQGIMSERMEYDQAGRITSRIFADGKT 1923  
: | | | | : | | | | | | | | : | | | | | | | | : | | | | | | | | : | | | | | | | |  
Db 1900 IYDQLGRPFLLPSSGLAANVS YFFNGRLAGLQRGAMSE RTDIDKQGR IISRMFADGKV 1959  
QY 1924 WSYTYLEKSMVLLLHHSQRQYIFEFDKNDR LSSVTMPNVARQTL ETIRSVGVYRNIYQPPE 1983  
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Db 1960 WSYTYLEKSMVLL LQSQRQYIFEYDSSDR LHAVTMPSVARHSMSTHTSVGVYRNIYNPPE 2019  
QY 1984 GNASVIQDFTEDGHLLHTFYLGTGRRVIY KYGKLSKLAETLYDTTKVSFTYDETAGMLKT 2043  
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Db 2020 SNASVIFDYSDDGRILKTSFLGTGRQV FYKYGKLSKLSEI VYDSTAVTFGYDETTGV LKM 2079  
QY 2044 INLQNEGFTCTIRYRQIGPLIDRQIFRFE TEEGMVNARFDYNY -DNSFRVTSMQAVINETP 2102  
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QY 2103 LPIDLRYRDDVSGKTEQFGKFGVIYYDINQ IITTAVMTHTKHEDAYGRMKEVOYEI FRSL 2162  
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Db 2140 LPVDLYRYDEISGKVEHFGKFGVIYYDINQ IITTAVMTL SKHFDTHGRIKEVQYEMFRSL 2199  
QY 2163 MYWMTVOYDNMGRVVKKELKVGPYANTTRY SYEYDADGQLQTVSINDKPLWRYSYDLNGN 2222  
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Db 2200 MYWMTVOYDSMGRVTRKRELKLGPYANTT KYTYDYDGDGQLQSVAVNDRPPTWRYSYDLNGN 2259  
QY 2223 LHLLSPGNSARLTPLRYDIRDRITRLGDVQY KMDGDFLQRGGDI FEYNSAGLLIKAYN 2282  
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Db 2260 LHLLNPGNSVRLMPLRYDLRDRITRLGDI PYKIDDDGFLCORGSDVFEYNSKGLL TRAYN 2319  
QY 2283 RAGSWSVRYRYDGLGRRVSSKSSHHLQFF YADLTNPTKVTHLYNHSSEITSLY YDLQ 2342  
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QY 2343 GHLFAMELSSGDEFIACDNIGTPLAVFSG TGLMIKQILYTA YGEIYMDTNPNFQIIGY 2402  
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Db	2380	GHLFAMESSGEEYYVASDNTGTPLAVFSINGLMIKQLQYTAYGEIYYDSNPDPQLVIGF	2439
Qy	2403	HGGLYDPLTKLVHMGRRDYDVLAGRWTSPDHELWKHLSSSNVMPFNLMPKNNNPISNSQ	2462
Db	2440	HGGLYDPLTKLVHFTQRDYDVLAGRWTSPDYTMWKNIGREPA-PFNLMPKSNNPLSNEL	2498
Qy	2463	DIKCFMTDVNSWLLTFGQQLHNVIPGYPKPDMAMEPSYELIHTQMKTQEWDNKSILGV	2522
Db	2499	DLKNYVTDVKSWLMFGQLSNIIPGFPRAKMYFVSPPYEL----TESQACENGQLITGV	2554
Qy	2523	QCEVQKQLKAFVTLERFDQLYGSTITSCQQAPKTKK----FSSGSVFGKGVKFALKDGR	2578
Db	2555	QOTTERHNQAFMALE-----GQVISKRLHASIREKAGHWFATSTPIIGKIMFAVKGR	2608
Qy	2579	VTDDIISVANEDGRRVAAILNHAHYLENLHFTIDGVDTHYFVKPGPSEGDLAAILGLSGGR	2638
Db	2609	VTGISSIATDDSRKIASVLNSAHYLEKMHYSIEGKDTHYFVKIGSADSDLVTLAMTSGR	2668
Qy	2639	RTLENGVNVTVSQINTVLNGRTRRYTDIQLQYGALCLNTRYG---TTLDEEKARVLELAR	2695
Db	2669	KVLDSGVNVTVSQPTLLINGRTRRFTNIEFOYSTLLINIRYGLTADTLDEEKARVLDQAR	2728
Qy	2696	QRAVRQAWAREQQRLREGEGLRAWTEGEKQOVLSTGRVQGYDGFFVISVEQYPELSDSA	2755
Db	2729	QRALGSAWAKEQQKARDGREGSRVWTDGKQQLLNTGRVQGYGYVYLPVEQYPELADSS	2788
Qy	2756	NNIHFMRQSEMGRR	2769
Db	2789	SNIQFLRQNE MGKR	2802

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 11, 2005, 04:48:57 ; Search time 11 Seconds  
(without alignments)  
1405.752 Million cell updates/sec

Title: US-10-029-020-14  
Perfect score: 14887  
Sequence: 1 MDVKERKPYRSLRRRDAER.....ELSDSANNIHFMRQSEMGR 2769

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 32527 seqs, 5584426 residues

Total number of hits satisfying chosen parameters: 32527

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA New:\*  
1: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep:\*  
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8: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES				
Result No.	Score	Query Match	Length DB	ID Description
1	14887	100.0	2769	7 US-11-113-424-14 Sequence 14, Appl
2	10258	68.9	2715	7 US-11-096-051-2 Sequence 2, Appli
3	10227	68.7	2715	7 US-11-113-424-51 Sequence 51, Appl
4	10221	68.7	2721	7 US-11-096-051-10 Sequence 10, Appl
5	10201	68.5	2725	7 US-11-096-051-8 Sequence 8, Appli
6	9584	64.4	2725	7 US-11-113-424-52 Sequence 52, Appl
7	9296	62.4	2376	7 US-11-096-051-4 Sequence 4, Appli
8	4175.5	28.0	1094	6 US-10-821-234-1097 Sequence 1097, Ap
9	3979.5	26.7	1045	7 US-11-113-424-54 Sequence 54, Appl
10	3854	25.9	730	7 US-11-113-424-50 Sequence 50, Appl
11	3804.5	25.6	2515	7 US-11-113-424-53 Sequence 53, Appl
12	3276	22.0	862	7 US-11-096-051-20 Sequence 20, Appl
13	3270	22.0	821	7 US-11-096-051-6 Sequence 6, Appli
14	2418.5	16.2	607	7 US-11-096-051-14 Sequence 14, Appl
15	1268.5	8.5	257	7 US-11-096-051-12 Sequence 12, Appl
16	1268.5	8.5	296	7 US-11-096-051-18 Sequence 18, Appl
17	546	3.7	214	7 US-11-096-051-16 Sequence 16, Appl
18	411.5	2.8	1218	7 US-11-078-735-20 Sequence 20, Appl
19	404.5	2.7	1238	7 US-11-078-735-21 Sequence 21, Appl
20	342	2.3	723	7 US-11-078-735-17 Sequence 17, Appl
21	334.5	2.2	379	6 US-10-131-826A-308 Sequence 308, App
22	334	2.2	723	6 US-10-131-826A-346 Sequence 346, App
23	323.5	2.2	685	6 US-10-131-826A-88 Sequence 88, Appl
24	323.5	2.2	685	7 US-11-078-735-19 Sequence 19, Appl
25	316	2.1	484	7 US-11-078-735-43 Sequence 43, Appl

26	293	2.0	618	7	US-11-078-735-18	Sequence 18, Appl
27	291.5	2.0	3717	6	US-10-821-234-1076	Sequence 1076, Ap
28	279.5	1.9	3002	6	US-10-821-234-916	Sequence 916, App
29	278	1.9	383	7	US-11-147-047-38	Sequence 38, Appl
30	275	1.8	1400	6	US-10-821-234-1045	Sequence 1045, Ap
31	264	1.8	369	7	US-11-078-735-38	Sequence 38, Appl
32	261.5	1.8	3500	7	US-11-085-775-2	Sequence 2, Appli
33	243.5	1.6	504	6	US-10-999-782-2	Sequence 2, Appli
34	227	1.5	816	7	US-11-090-439-48	Sequence 48, Appl
35	222	1.5	336	6	US-10-478-345-4	Sequence 4, Appli
36	216	1.5	965	7	US-11-113-424-2	Sequence 2, Appli
37	213	1.4	357	6	US-10-478-345-6	Sequence 6, Appli
38	212	1.4	331	7	US-11-078-735-33	Sequence 33, Appl
39	212	1.4	332	7	US-11-078-735-51	Sequence 51, Appl
40	209.5	1.4	897	7	US-11-137-465-35	Sequence 35, Appl
41	208	1.4	964	7	US-11-137-465-58	Sequence 58, Appl
42	208	1.4	965	7	US-11-147-047-51	Sequence 51, Appl
43	205.5	1.4	961	7	US-11-113-424-35	Sequence 35, Appl
44	204.5	1.4	652	6	US-10-821-234-1016	Sequence 1016, Ap
45	199.5	1.3	321	6	US-10-478-345-8	Sequence 8, Appli

ALIGNMENTS

RESULT 1

US-11-113-424-14  
; Sequence 14, Application US/11113424  
; Publication No. US20050260713A1  
; GENERAL INFORMATION:  
; APPLICANT: Gangolli et al.  
; TITLE OF INVENTION: Polypeptides and Nucleic Acids Encoding Same  
; FILE REFERENCE: 21402-225  
; CURRENT APPLICATION NUMBER: US/11/113,424  
; CURRENT FILING DATE: 2005-04-21  
; PRIOR APPLICATION NUMBER: 60/256,704  
; PRIOR FILING DATE: 2000-12-19  
; PRIOR APPLICATION NUMBER: 60/311,590  
; PRIOR FILING DATE: 2001-08-10  
; PRIOR APPLICATION NUMBER: 60/257,314  
; PRIOR FILING DATE: 2000-12-20  
; PRIOR APPLICATION NUMBER: 60/311,613  
; PRIOR FILING DATE: 2001-08-10  
; PRIOR APPLICATION NUMBER: 60/315,617  
; PRIOR FILING DATE: 2001-08-29  
; PRIOR APPLICATION NUMBER: 60/307,506  
; PRIOR FILING DATE: 2001-07-24  
; PRIOR APPLICATION NUMBER: 60/322,358  
; PRIOR FILING DATE: 2001-09-14  
; PRIOR APPLICATION NUMBER: 60/294,075  
; PRIOR FILING DATE: 2001-05-29  
; PRIOR APPLICATION NUMBER: 60/288,153  
; PRIOR FILING DATE: 2001-05-02  
; NUMBER OF SEQ ID NOS: 190  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 14  
; LENGTH: 2769  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-113-424-14

Query Match 100.0%; Score 14887; DB 7; Length 2769;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2769; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db	1	MDVKERKPYRSLRRRDAERRYTTSSSADSEEGKAPQKSYSSSETLKAYDQDARLAYGSRV	60
QY	61	KDIVPQEAEEFCRTGANFTLRELGLEEVTPPHGTLYRTDIGLPQCGYSMGAGSDADMEAD	120
Db	61	KDIVPQEAEEFCRTGANFTLRELGLEEVTPPHGTLYRTDIGLPQCGYSMGAGSDADMEAD	120



QY 121 TVLSPEHPVRLWGRSTRSGRSSCLSSRANSNLTLTDTHEHENTETDHPGGLQNHARLRTPP 180  
Db 121 TVLSPEHPVRLWGRSTRSGRSSCLSSRANSNLTLTDTHEHENTETDHPGGLQNHARLRTPP 180  
QY 181 PPLSHAHTPNQHHAASINSLNRGNFTPRSNPSPAPTDHSLSGEPAGGAQEPAHAQENWL 240  
Db 181 PPLSHAHTPNQHHAASINSLNRGNFTPRSNPSPAPTDHSLSGEPAGGAQEPAHAQENWL 240  
QY 241 LNSNIPLERNLGKQPFGLGTLQDNLIEMDILGASRHDGAYS DGHFLEFKPGGTSPLFCCTS 300  
Db 241 LNSNIPLERNLGKQPFGLGTLQDNLIEMDILGASRHDGAYS DGHFLEFKPGGTSPLFCCTS 300  
QY 301 PGYPLTSSTVYSPPPRPLPRSTFARPAFNLKKPSKYCNWKCAALSAIVISATLVILLAYF 360  
Db 301 PGYPLTSSTVYSPPPRPLPRSTFARPAFNLKKPSKYCNWKCAALSAIVISATLVILLAYF 360  
QY 361 VAMHLFGLNWLQPMEGQMYEITEDTASSWPVPTDVSLYPSGGTGLETPDRKGKGTTEGK 420  
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QY 421 PSSFFPEDSFIDSGEIDVGRRASQKIPPGTFWRISOVFIDHPVHLKFNVSLGKAALVGIYG 480  
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QY 481 RKGLPPSHQTQDFVELLDGRRLLTQEARSLEGTPRQSRGTVPPSSHETGFIQYLDSDGIWH 540  
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QY 541 LAFYNDGKESEVVSFLLTTAIESVDNCPSNICYNGDCTPRATCLDQCSHGHTFLPDTGLCSCDPSWT 600  
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QY 601 CSGNGQYMKGRCLCHSGWKGAECDVPTNQCIDVACSNHGTCITGTICINPGYKGESCEBV 660  
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Db 661 DCMDDPTCSGRGVCVRGECHCFVGWGTNCETPRATCLDQCSHGHTFLPDTGLCSCDPSWT 720  
QY 721 GHDCSIEICAADCGHGVCGGTCTCEDGWMGAACDQACHPRCAEHGTCRDGKCECSPG 780  
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QY 781 WNGEHCTIAHYLDRVVKEGCPGLCNGNGRCTLDLNGWHVCVOLGWRGAGCDTSMETACGD 840  
Db 781 WNGEHCTIAHYLDRVVKEGCPGLCNGNGRCTLDLNGWHVCVOLGWRGAGCDTSMETACGD 840  
QY 841 SKONDGGLVDCMDPDCCLQPLCHINPLCLGSPNPLDIIQETQVPVVSQQNLHSFYDRIKF 900  
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Db 901 LVGRDSTHIIPGENPFDGGHACVIRGQVMTSDGTPLVGVNISFVNNPLFGYTTISRQDGSF 960  
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QY 1141 EYESCPDLILWEKRTTVLQGYEIDASKLGWSLDKHHALNTQSGILHKNGENQFVSQQP 1200  
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Db 1201 PVIGSIMGNRRRSISCPSCNGLADGNKLLAPVALTCGSDGSLYVGDFNYIRRIFFPSGNV 1260  
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QY 1381 LIGSNDLTSARPLSCDSVMDISQVRLEWPTDLAINPMDNSLYVLDNNVVLQISENHQVRI 1440  
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QY 1561 RFIRKNKPFLLNTQNMVELSSPIDQELYLFDTFGKHLYTQSLPTGDLYNFYTGDDITL 1620  
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QY 1861 LRILYDQAGRPSLWSPSSRLNGVNVITYSPGYIAGIQRGIMSERMEYDQAGRITSRIFAD 1920  
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QY 1921 GKTWSYTYLEKSMVLLLSHSQRQYIFEFDKNDRLSSVTMPNVARQTLETIRSVGYRNIYQ 1980  
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QY 1981 PPEGNASVIQDFTEDGHLLHTFYLGTGRRVIYKYGKLSKLAETLYDTTKVSFTYDETAGM 2040  
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QY 2041 LKTINLQNEGFTCTIRYRQIGPLIDRQIFRFTTEEGMVNARFDYNDNSFRVTSMQAVINE 2100  
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QY 2101 TPLPIDLYRYDDVSGKTEQFGKFGVIYYDINQIITAVMTHTKHFDAYGRMKEVQYEIFR 2160  
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QY 2161 SLMYWMTVQYDNMGRVVKELKVGPYANTTRYSEYDADGQLQTVSINDKPLWRYSYDLN 2220  
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QY 2221 GNLHLLSPGNSARLTPLRYDIRDRIITRLGDVQYKMEDEGFLRQGGDIFEYNSAGLLIKA 2280  
Db 2221 GNLHLLSPGNSARLTPLRYDIRDRIITRLGDVQYKMEDEGFLRQGGDIFEYNSAGLLIKA 2280  
QY 2281 YNRAGSWSVRYRVDGLGRRVSSKSSHILQFFYADLTNPTKVTHLYNHSSEITSLYYD 2340  
Db 2281 YNRAGSWSVRYRVDGLGRRVSSKSSHILQFFYADLTNPTKVTHLYNHSSEITSLYYD 2340



Qy 1186 LHKNGENQFVSQQPPVIGSIMGNRRRSISCPSCNGLADGNKLLAPVALTCGSDGSLYV 1245  
Db 1138 LYKNGENQFISQQPPVSSIMGNRRRSISCPSCNGQADGNKLLAPVALACGIDGSLYV 1197  
Qy 1246 GDFNYIRRIFFSGNVNTNILELRNKDFRHSHPAHKYIYLATDPMGSAFVLSDSNSRRVFKI 1305  
Db 1198 GDFNYVRRIFPSGNVTSVLELRNKDFRHSNPAHRYIYLATDPVTGDLYVSDTNTRRIYRP 1257  
Qy 1306 KSTVVVKDLVKNSEVVAGTGDQCCLPDDTRCGDGGKATEATLTNPRGITVDKFLGIYFVD 1365  
Db 1258 KSLTGAKDLTKNAEVAAGTGEQCLPFDEARCGDGGKAVEATLMSPKGMAVDKNGLIYFVD 1317  
Qy 1366 GTMIRRIDQNGIISTLLGSNDLTSARPLSCDSVMDISQVRLEWPTDLAINPMDNSLYVLD 1425  
Db 1318 GTMIRKVDQNGIISTLLGSNDLTSARPLTCDTSMHISQVRLEWPTDLAINPMDNSIYVLD 1377  
Qy 1426 NNVLQISENHQVRIIVAGRPMHCQVPGIDHFLLSKVAIHATLESATALAVSHNGVLXIAE 1485  
Db 1378 NNVLQITENRQVRIAAGRPMHCQVPGVE-YPVGKHAVQTTLESATAIAVSYSGLYITE 1436  
Qy 1486 TDEKKINIRQVTTSGEISLVAGAPSCDCCKNDANCDFCSGDGYAKDAKLNTPSSLAVC 1545  
Db 1437 TDEKKINIRQVTTDGEISLVAGIPSECDCKNDANCDYQSGDGYAKDAKLSAPSSLAAS 1496  
Qy 1546 ADGELYVADLGNIRIRFIRKKNKPFNTQNMYYELSSPIDQELYLFDTTGKXLYTQSLPTGD 1605  
Db 1497 PDGTLYIADLGNIRIRAVSKNKPLLNSMNFYEVASPTDQELYIFDINGTHQYTVSLVTGD 1556  
Qy 1606 YLYNFTYTGDGITLITDNNGNMNVNRDSTGMPLWLVPDQGVYVWMTGMTNSALKSVTT 1665  
Db 1557 YLYNFSYNDNDITAVTDSNGNTLIRRDNPVRVSPDNQVILWTIGTNGCLKSMTA 1616  
Qy 1666 QGHELAMTYHGNSGLLATKSNENGWTTFFEYDSFGRLTNVTFPTQGVSSFRSDTDSVH 1725  
Db 1617 QGLELVFTYHGNSGLLATKSDETGWTTFFDYDSEGRLTNVTFPTGVVTNLHGDMDKAIT 1676  
Qy 1726 VQVETSSK-DDVTITNLSASGAFYTLQDQVRNSYYIGADGSLRLLLLANGMEVALQTEP 1784  
Db 1677 VDIESSSREEDVSITSNLSSIDSFYTMVQDQLRNSYQIGYDGLRIIYASGLDSHYQTEP 1736  
Qy 1785 HLLAGTVNPTVGKRNVTLPIDNGLNLVWVRQKEAQGVTVFGRRLRVHNRNLLSLDFD 1844  
Db 1737 HVLAGTANPTVAKRNMTLPGENGQNLVWVRFRKEQAQGVNFGKRLRVNGRNLLSVDFD 1796  
Qy 1845 RVTRTEKIYDDHRKFTLRILYDQACRPSSLWSPSSRLNGVNTYSPGGYIAGIQRGIMSER 1904  
Db 1797 RTTKTEKIYDDHRKFLRLRIAYDTSGHPTLWLPSSKLMVNVYSSSTGQIASIQRGTTSEK 1856  
Qy 1905 MEYDQAGRITSRIFADGKTWSYTYLEKSMVLLLSHSQRQYIPEFDKNDRLSSVTMPNVARQ 1964  
Db 1857 VDYDQGRIVSRVFADGKTWSYTYLEKSMVLLLSHSQRQYIFEYDMWDRLSAITMPSVARH 1916  
Qy 1965 TLETIRSVGYRNIYQPPEGNASVIQDFTEDGHLLHTFYLGTGRRVYKYGKLSKLAETL 2024  
Db 1917 TMQTIRSIGYRNIYNPPESNASITDYNEEGLLQTAFLGTSRRVLFKYRQTRLSEIL 1976  
Qy 2025 YDTTKVSFTYDETAGMLKTINLQNEGFTCTIRYRQIGPLIDRQIFRFTTEEGMVNARFDYN 2084  
Db 1977 YDSTRVSFTYDETAGVLKTVNLQSDGFICTIRYRQIGPLIDRQIFRFSDEGGMVNAFSDYS 2036  
Qy 2085 YDNSFRVTSMQAVINETPLPIDLYRYDDVSGKTEQFGKFGVIYYDINOIITTAVMTHTKH 2144  
Db 2037 YDNSFRVTSMQGVINETPLPIDLYQFDDISGKVEQFGKFGVIYYDINOIISTAVMTYTKH 2096  
Qy 2145 FDAYGRMKEVQYEIFRSLMYMWTVQYDNMGRVVKKELKVGPPYANTTRYSEYEDADGQLQT 2204  
Db 2097 FDAHGRIKEIQYEIFRSLMYWITIQYDNMGRVTKREIKGPFANTTKYAYEYDQQLQT 2156  
Qy 2205 VSINDKPLWRYSYDLNGLNHLSPGNSARLTPLRYDIRDRITRLGDVQYKMWDEDFLRQR 2264  
Db 2157 VYLNEXIMWRYNYDLNGLNHLNPSNSARLTPLRYDLDRITRLGDVQYRLDEDEGFLRQR 2216

Qy 2265 GGDIFEYNSAGLLIKAYNRAGSWSVRYRYDGLGRRVSSKSSSHHLLQFFYADLTNPTKVT 2324  
Db 2217 GTEIFEYSSKGLLTRVYSGSGWTVIYRYDGLGRRVSSKTSLGHLQLOFFYADLTYPTRIT 2276  
Qy 2325 HLYNHSSEITSLYDLQGHLFAMELSSGDEFYIACDNIGTPLAVFSGTGLMIKQILYTA 2384  
Db 2277 HVYNHSSEITSLYDLQGHLFAMEISSGDEFYIASDNTGTPLAVSSNGMLKQIQYTA 2336  
Qy 2385 YGEIYMDTNPNFQIIGYVHGGLYDPLTKLVHMGRRDYDVLAGRWTSPDHFWKHLSSSNV 2444  
Db 2337 YGEIYFDSNIDFQVIGFHGGLYDPLTKLIHFGERDYDILAGRWTTPDIEIWKRI-GKDP 2395  
Qy 2445 MPFNLYMFKNNPNISQDIKCFMTDVNSWLLTFGFQLHNVIPGYPKPMDMAMEPSYELI 2504  
Db 2396 APFNLYMFRNPNPASKIHDVKDYITDVNSWLVTFGFHLHNAIPGFPVPKFDLTPEPSYELV 2455  
Qy 2505 HTQMKTQEWDNKSILGVQCEVQKQKAFVTLERFDQLYGSTITSCQQAPKTKK---FAS 2561  
Db 2456 ----KSQQWDDIPPIFGVQQQVARQAKAFLSLQKMAEVQ----VSRRRAGGAQSWLWFAT 2507  
Qy 2562 SGSVFGKGVKFAKDGRTVTDIISVANEDGRRVAAILNHAHYLENLHFTIDGVVDTHYFVK 2621  
Db 2508 VKSLIGKVMLAVSQGRVQTNVLNIANEDCIKVAAVLNNAFYLENLHFTIEGKDTHYFIK 2567  
Qy 2622 PGPSEGDLAILGLSGRRRTLENGVNVTVSQINTVLNGRTRRYTDIQLQYGALCLNTRYGT 2681  
Db 2568 TTPESDLGTLRLTSGRKALENGINVTVSQSTTVVNGRTRRFADVEMQFGALAHVRYGM 2627  
Qy 2682 TLDEEKARVLELARQAVRQAWAREQQRLRFEGEGLRAWTEGEKQQVLSTGRVQGYDGF 2741  
Db 2628 TLDEEKARILEQARALARAWAREQQRVDRGEGARLWTEGEKROLLSAGKVQGYDGY 2687  
Qy 2742 VISVEQYPELSDSANNIHFMRQSEMGR 2769  
Db 2688 VLSVEQYPELADSANNIQFLRQSEIGRR 2715

RESULT 3

US-11-113-424-51  
; Sequence 51, Application US/11113424  
; Publication No. US20050260713A1  
; GENERAL INFORMATION:  
; APPLICANT: Gangolli et al.  
; TITLE OF INVENTION: Polypeptides and Nucleic Acids Encoding Same  
; FILE REFERENCE: 21402-225  
; CURRENT APPLICATION NUMBER: US/11/113,424  
; CURRENT FILING DATE: 2005-04-21  
; PRIOR APPLICATION NUMBER: 60/256,704  
; PRIOR FILING DATE: 2000-12-19  
; PRIOR APPLICATION NUMBER: 60/311,590  
; PRIOR FILING DATE: 2001-08-10  
; PRIOR APPLICATION NUMBER: 60/257,314  
; PRIOR FILING DATE: 2000-12-20  
; PRIOR APPLICATION NUMBER: 60/311,613  
; PRIOR FILING DATE: 2001-08-10  
; PRIOR APPLICATION NUMBER: 60/315,617  
; PRIOR FILING DATE: 2001-08-29  
; PRIOR APPLICATION NUMBER: 60/307,506  
; PRIOR FILING DATE: 2001-07-24  
; PRIOR APPLICATION NUMBER: 60/322,358  
; PRIOR FILING DATE: 2001-09-14  
; PRIOR APPLICATION NUMBER: 60/294,075  
; PRIOR FILING DATE: 2001-05-29  
; PRIOR APPLICATION NUMBER: 60/288,153  
; PRIOR FILING DATE: 2001-05-02  
; NUMBER OF SEQ ID NOS: 190  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 51  
; LENGTH: 2715  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-11-113-424-51



Query Match		68.7%;	Score 10227;	DB 7;	Length 2715;		
Best Local Similarity		66.7%;	Pred. No. 0;				
Matches 1864;		Conservative 370;	Mismatches 457;	Indels 102;	Gaps 19;		
Qy	1	MDVKERKPYRSLTR-RRDAERRYTSSSADSEEGKAP-QKSYSSSETLKAYDQD-ARLAYG	57				
Ddb	1	MDVKERRPYCSLTKSRREKERRYTNSSADNEECRVPTQKSYSSSETLKAFDHYSRLLYG	60				
Qy	58	SRVKDIVPQEAEEFCRTGANFTLRELGLBEVTPPHGTLRYRTDIGLPQCQYSMGAGSDADM	117				
Ddb	61	NRVKDLVHREADEYTRQGNFTLRQLGVCESATRGRGVAFAEAMGLPHRGYSISAGSDADT	120				
Qy	118	EADTVLSPHEHPVRLWGRSTRSGRSSCLSSRANSNLTLTDTEHEN--TETDHPGGLQNH	174				
Ddb	121	ENEAVMSPEHAMRLWGRGVKSGRSSCLSSRSNSALTTLTDTEHENRSDSESEQPSNPGQP	180				
Qy	175	RLRTPPPPLSHAHTPNQHHAAASINSLNRGNFTPRSNPSPAPTDSLSGEPAGGAQ----	230				
Ddb	181	TLQPLPP--SHKQHPAQHH-PSITSLNRNSLTNRNQSPAP-----PAALPAELQTT	229				
Qy	231	-EPAHAQENWLLNSNIPLETRNLGKQPLGTLQDNLIEMDILGASRHDGAYSDBGHFLFKP	289				
Ddb	230	PESVQLQDSWVLGSNVPLESR-----HFLFKT	256				
Qy	290	G-GTSPLECTTSPGYPLTSSTVYSPPRPLRSTFARPAFNLKKPSKYCNWKCAALSAIV	348				
Ddb	257	GTGTTPLFSTATPGYTMASGSVYSPTRPLPRNTLSRSFAFKFKSSKYCWRCTALCAVG	316				
Qy	349	ISATLVILLAYFAVMHLFGLNWHLQPMEGQMYE---ITEDTASSWPVPTDVSLYPSGGTG	405				
Ddb	317	VSVLLAILLSYFIAMHLFGLNWHLQQTENDTFENGKVNST-----VPTNTVSLPSG---	368				
Qy	406	LETPDRKKGTTTEGKPSFFPEDSFIDSGEIDVGRRASQKIPPGTFWRSQVFIIDHPVHLK	465				
Ddb	369	-----DNGKLGFTHENNTIDSGELDIGRRAIQEVPPGIFWRSQVFIIDHPVHLK	417				
Qy	466	FNVSIGKAALVGIYGRKGLPPSHTQDFVELLDGRLLLTQEARSLEGTPRQSRGTVPVPS	525				
Ddb	418	FNISLQKDALIGVYGRKGLPPSHTQYDFVELLDGSRLLIAREQNLVESERAGQARSVSL	477				
Qy	526	HETGFIQYLDSGIWHLAFYNDGKESEVSWFLTTAIESVDNCPSCNYGNGDCISGTCHCFL	585				
Ddb	478	HEAGFIQYLDSGIWHLAFYNDGKNPEQVSFNTIVIESVVECPRNCHNGEGECVSTCHCFP	537				
Qy	586	GFLGPDCCRASCPLVCSNGQYMKGRCLCHSGWKGAECDDVPTNQCIDVACSNHGTICITGT	645				
Ddb	538	GFLGPDCSRACAPVLCSNGQYSGRCLCFSGWKWGTEDCVPTTQCIDPQCGGRGICIMGS	597				
Qy	646	CICNPGYKGESCEEVD CMDPTCSGRGVCVRGECCHFCVWGGTNCETPRATCLDQCSGHGT	705				
Ddb	598	CACNSGYKGENCEEADCLDPGCSNHGVCIHGECHCNPNMGWGSNCEILKTMCAEQCSGHGT	657				
Qy	706	FLPDTGLCSCDPSSWTGDCSIEICAADCGGHGVCVGGTCRCEDEGWMGAACDQACHPRCA	765				
Ddb	658	YLQESGSCTCDPNWTGPDCSNEICSVDCSGHGVCMGSGRCREEGWTGPACNORACHPRCA	717				
Qy	766	EHGTCRDGKCECSPGWNGEHCTIAHYLDRVVKEGCPGLCNGNGRCTLDLNGWHCVQCQLGW	825				
Ddb	718	EHGTCKDGKCECSQGWNGEHCTIAHYLDKIVKEGCPGLCNSNGRCTLDQNGWHCVQCQGW	777				
Qy	826	RGAGCDTSMETACGDSKDNDDGLVDCMDPDCCLOPLCHINPLCLGSPNPLDIIQETQVP	885				
Ddb	778	RGAGCDVAMETLCTDSKDNEGDGLIDCMDPDCCLOSSCQNPYCRGLPDPDQDIISQSLQT	837				
Qy	886	VSQNLHSFYDRIKFLVGRDSTHIIIPGENPFDGGHACVIRGQVMTSDGTPLVGVNISFVN	945				
Ddb	838	PSQAAKSFYDRISFLIGSDSTHVLPGESPFNKSLASVIRGQVLTADGTPLIGVNVSFLH	897				
Qy	946	NPLFGYTI SRQDGSFDLVNNGGISII LRFERAPFITQEHTLWLPWDRFFVFMETIIMRHEE	1005				
Ddb	898	YSEYGYTITRQDGMFDLVANGGASLTLVFERSPFLTQYHTVWIPWNVFYVMDTLVMKKEE	957				
Qy	1006	NEIPSCDLSNFARNPNVWSPSPLTSFASSCAEKGPVPEIQALQEEISISGCKMRLSYLS	1065				

Db	958	NDIPSCDLSGFVRPSPPIIVSSPLSTFFRSSPEDSPIIPETQVLHEETTPGTDLKLSYLS	1017				
Qy	1066	SRTPGYKSVLRISLTHPTIPFNLMKVHLMVAVEGRLFRKWFAAAPDLSYFIWDKTDVYN	1125				
Db	1018	SRAAGYKSVLKITMTQAVIPFNLMKVHLMVAVVGRLFQKWFPASPNNLAYTFIWDKTDAYN	1077				
Qy	1126	QKVFLGLSEAFVSUGYEYESCPDLILWEKRTVLQGYEIDASKLGGWSLDKHHALNIQSGI	1185				
Db	1078	QKVYGLSEAVVUGYEYESCLDLTLWEKRTAVLQGYELDASNMGWTLDKHHVLDVQNGI	1137				
Qy	1186	LHKGNGENQFVSQQPPVIGSIMGNRRRSISCPSCNGLADGNKLLAPVALTCGSDGSLYV	1245				
Db	1138	LYKGNGENQFISQQPPVVSIMGNRRRSISCPSCNQADGNKLLAPVALACGIDGSLYV	1197				
Qy	1246	GDFNYIRRIFFPSGNVTNILELRNKDFRHSHPAHKYIYLATDPMMSGAVFLSDNSRRRVFKI	1305				
Db	1198	GDFNYVRRIRFPNGNVTSVLELRNKDFRHSNPAHRYIYLATDPVTGDLVSDTNRRIYRP	1257				
Qy	1306	KSTVVVKDLVKNSEWVAGTGDQCLPFDDTRCGDGGKATEATLTNPRGITVDKFGLIYFVD	1365				
Db	1258	KSLTGAKDLTKNAEVVAGTGEQCLPFDEARCGDGGKAVEATLMSPKGMAIDKNGLIYFVD	1317				
Qy	1366	GTMIRRIDQNGIISTLLGSNDLTSARPLSCDSVMDISQVRLEWPTDLAINPMDNSLYVLD	1425				
Db	1318	GTMIRKVDQNGIISTLLGSNDLTSARPLTCDTSMHISQVRLEWPTDLAINPMDNSIYVLD	1377				
Qy	1426	NNVLQISENHQVRIVAGRPMHCQVPGIDHFLLSKVAIHATLESATALAVSHNGVLYIAE	1485				
Db	1378	NNVLQITENRQVRIAAGRPMHCQVPGVE-YPVGKHAVQTTLESATAIAVSYSGVLYITE	1436				
Qy	1486	TDEKKINRIRQVTTSGEISLVAGAPSGCDCKNDANCDCFSGDDGYAKDAKLNTPSSLAVC	1545				
Db	1437	TDEKKINRIRQVTTDGEISLVAGIPSECDCKNDANCDCYQSGDGYAKDAKLNAPSSLAAS	1496				
Qy	1546	ADGELYVADLGNIRIRFIRKNKPFNTQNMVELSSPIDQELYLFDTTGKHLYTQSLPTGD	1605				
Db	1497	PDGTLYIADLGNIRIRAVSKNPKLLNSMNFYEVASPTDQELYIFDINGTHQYTVSLVTGD	1556				
Qy	1606	LYNFTYTGDDITLITDNNGNMNVRRDSTGMPMLWLVPDQGVVYVVTMGTSALKSVTT	1665				
Db	1557	LYNFSYSNNDVTAVTDNGNTLRIRRDNRMPVRVVSFDPNQVILWTIGTNGCLKSMTA	1616				
Qy	1666	QGHELAMMTYHGNSGLLATKSNENGWTTTFEYDSFGRLTNVTFTPTGOVSSFRSDTSSVH	1725				
Db	1617	QGLELVFTYHGNSGLLATKSDETGWTTFEYDSEGRLTNTVTFTGVVTVNLHGDMDKAIT	1676				
Qy	1726	VQVETSSK-DDVTITTNLSASGAFYTLQDQVRNSYIIGADGSLRLLLANGMEVALQTEP	1784				
Db	1677	VDIESSSREEDVSITSNLSSIDSFYTMVQDQLRNSYQIGYDGLSRIFYASGLDSHYQTEP	1736				
Qy	1785	HLLAGTVNPTVGRKNVTLPIDNGLNLVEWQRKEQARGQVTVFGRRLRVHNRNLLSLDFD	1844				
Db	1737	HVLAGTANPTVAKRNMTLPGENGQNLVEWRFRKEQAQGVNVFGRKLRVNGRNLSSVDFD	1796				
Qy	1845	RVTRTEKIYDDHRKFTLRILYDQAGRPSLWSPSSRLNGVNVITYSPGGYIAGIQRGIMSER	1904				
Db	1797	RTTKTEKIYDDHRKFLLRRIAYDTSGHPTLWLPSSKLMANVTYSSTGQIASIQRTTSEK	1856				
Qy	1905	MEYDQAGRITSRIFADGKTWSYTYLEKSMVLLLHHSQRQYIFEFDKNDRLSSVTMPNVARQ	1964				
Db	1857	VDYDSQGRIVSRVFADGKTWSYTYLEKSMVLLLHHSQRQYIFEYDMWDRLSAITMPSVARH	1916				
Qy	1965	TLETIRSVGYRYNIYQPPPEGNASVIQDFTEDGHLLHTFYLGTGRRRVYKYGKLSKLAETL	2024				
Db	1917	TMQTIRSIGYRYNIYPPESPESNASIITDYNEEGLLQTAFLGTSRRRVLFKYRRQTRLSEIL	1976				
Qy	2025	YDTTKVSFTYDETAGMLKKTINLQNEGFTCTIRYRQIGPLIDRQIRFRFTEEGMVNARFDYN	2084				
Db	1977	YDSTRVSFTYDETAGVLKTVNLQSDGFICTIRYRQIGPLIDRQIRFRFSEDGMVNARFDYS	2036				
Qy	2085	YDNSFRVTSMQAVINETPLPIDLYRYDDVSGKTEQFGKFGVIYVDINQIITTAVMTHTKH	2144				





QY 1000 IMRHEENEIPSCDLSNFARPNPVWSPSPLTSFASSCAEKGPIVPEIQALQBEISISGCKM 1059  
Db :| |||:||||| |||: |||:| | |||:| | |||:| | :  
QY 958 VMEKEENDIPSCDLSGCFVRPNPIIVSSPLSTFFRSPPEDSPIIPETQVLHEETIPGTDL 1017  
Db :| |||:||||| |||: |||:| | |||:| | |||:| | :  
QY 1060 RLSYLSRTPGYKSVLRISLTHPTIPFNLKMKVHLMAVEGRLEFRKWFFAAAPDLSYFIWD 1119  
Db :| |||:||||| |||: |||:| | |||:| | |||:| | |||:| | :  
QY 1018 KLSYLSRAAGYKSVLKITMTQSIIPFNLKMKVHLMAVVGRLEFQKWFPPASPNLAYTFIWD 1077  
Db :| |||:||||| |||: |||:| | |||:| | |||:| | |||:| | :  
QY 1120 KTDVYNQKVFGLSEAFVSGYEYESCPDLILWEKRTTVLQGYEIDAASKLGSWLDKHHAL 1179  
Db :| |||:||||| |||: |||:| | |||:| | |||:| | |||:| | |||:| | :  
QY 1180 NIQSGILHKGNGENQFVSQOPPVIIGSIMGNRRRSISPCSCNGLADGNKLLAPVALTCGS 1239  
Db :| |||:||||| |||: |||:| | |||:| | |||:| | |||:| | |||:| | :  
QY 1138 DVQNGILYKNGENQFISQOPPPVWSSIMGNRRRSISPCSCNGQADGNKLLAPVALACGI 1197  
QY 1240 DGSLYVGDFNYIRRIFFPSGNVTNILELRNKDFRHSHPAHKYXLATDPMGAVFLSDSNS 1299  
Db :| |||:||||| |||: |||:| | |||:| | |||:| | |||:| | |||:| | :  
QY 1198 DGSLYVGDFNYVRRRIFFPSGNVTSVLELRNKDFRHSNPAHYXLATDPVTGLVYSDTNT 1257  
QY 1300 RRVFYKIKSTVVVKDLVKNSEVVAGTGDQCLPFDDTRCGDGKATEATLTNPRGTVTDKFG 1359  
Db :| |||: ||| |||:||||| |||: |||:| | |||:| | |||:| | |||:| | :  
QY 1258 RRIYRPKSLTGAKDLTKNAEVVAGTGEQCLPFDEARCGDGKKAVEATLMSPKGNAVDKNG 1317  
QY 1360 LIYFVDGTMIRRIDQNGIISTLLGSNDLTSARPLSCDSVMDISQVRLEWPTDLAINPMDN 1419  
Db :| |||:||||| |||: |||:| | |||:| | |||:| | |||:| | |||:| | :  
QY 1318 LIYFVDGTMIRKVDQNGIISTLLGSNDLTSARPLTCDTSMHISQVRLEWPTDLAINPMDN 1377  
QY 1420 SLYVLDDNNVLOISENHQVRIVAGRPMHCQVPGIDHFLLSKVAIHATLESATALAVSHNG 1479  
Db :| |||:||||| |||: |||:| | |||:| | |||:| | |||:| | |||:| | :  
QY 1378 SIYVLDDNNVLOITENQVRIAAGRPMHCQVPGVE-YPVGKHAVQTTLESATALAVSYSG 1436  
QY 1480 VLYIAETDEKKINRIQVTTSGEISLVAGAPSGCDCKNDANCDGSGDDGYAKDAKLNTP 1539  
Db :| |||:||||| |||: |||:| | |||:| | |||:| | |||:| | |||:| | :  
QY 1437 VLYITETDEKKINRIQVTTDGEISLVAGIPSECDCKNDANCDYQSGDGYAKDAKLSAP 1496  
QY 1540 SSLAVCADGELYVADLGNIRIRFIRKNKPFNTQNMVELSSPIDQELYLFDDTTGKHLTYQ 1599  
Db :| |||: ||| |||:||||| |||: |||:| | |||:| | |||:| | |||:| | :  
QY 1497 SSLAASPDGTLXIADLGNIRIRAVSKNKPLLNSMNFYEVASPTDQELYIFDINGTHQYTV 1556  
QY 1600 SLEPTGDYLYNFTYTGDDITLITDNNGNMNVNRRDSTGMPLWLVPDGOVYVWTMGNTSA 1659  
Db :| |||:||||| |||: |||:| | |||:| | |||:| | |||:| | |||:| | :  
QY 1557 SLVTGDYLYNFSYNDNDITAVTDSNGNTLRIRRDPNRMPVRVWSPDNQVIMWLTIGTNGC 1616  
QY 1660 LKSVTTQGHELAMTYHGNSGLLATKSNENGWTTFYEYDSFGRLTNVTFPTQVSSFRSD 1719  
Db :| |||: ||| |||:||||| |||: |||:| | |||:| | |||:| | |||:| | :  
QY 1617 LKGMTAQGLELVLFTHGNSGLLATKSDEGTWTTFFDYDSEGRLTNVTFPTGVVTNLHGD 1676  
QY 1720 TDSSVHVQVETSSK-DDVTITTNLSASGAFYTLLOQDVRSYVIGADGSLRLLLLANGMEV 1778  
Db :| |||: ||| |||:||||| |||: |||:| | |||:| | |||:| | |||:| | :  
QY 1677 MDKAITVDIESSSREEDVSITNSLSSIDSFYTMVQDQLRNSYQIGYDGSRLRIIVASGLDS 1736  
QY 1779 ALQTEPHLLAGTVNPTVGRKNVTLPIDNGLNLVEWRQRKEQARGQVTVFGRRLRVHNRNL 1838  
Db :| |||:||||| |||: |||:| | |||:| | |||:| | |||:| | |||:| | :  
QY 1737 HYQTEPHVLAGTANPTVAKRNMVTLPGENGQNLVEWRFERKEQAQGVNVEGRKLRVNGRNL 1796  
QY 1839 LSLDFRVTRETEKIYDDHRKFTRLILYDQAGRPSLWSPSRLNGVNVVYSPGGYIAGIQR 1898  
Db :| |||:||||| |||: |||:| | |||:| | |||:| | |||:| | |||:| | :  
QY 1797 LSVDFDRTTKTEKIYDDHRKFLRLIAYDTSGHPTLWLPSSKLMAVNVVYSSSTGQIASIQR 1856  
QY 1899 GIMSERMEYDQAGRITSRIFADGKTWSYTYLEKSMVLLHLSQRQYIFEFDKNDRLSVVTM 1958  
Db :| |||: ||| |||:||||| |||: |||:| | |||:| | |||:| | |||:| | :  
QY 1857 GTTSEKVDYDGGRIVSRVFADGKTWSYTYLEKSMVLLHLSQRQYIFEYDMWDRLSAITM 1916  
QY 1959 PNVARQTLETIRSVGYRNIYQPPEGNASVIQDFTEDGHLLHTFYLGTGRRVIYKYGKLS 2018  
Db :| |||: ||| |||:||||| |||: |||:| | |||:| | |||:| | |||:| | :  
QY 1917 PSVARHTMQTIRSIGYRNIYNPPESNASIITDYNEEGLLQTAFLGTSRRRVLFKVRQT 1976  
QY 2019 KLAETLYDTTKVSFTYDETAGMLKTINLQNEGFTCTIRYRQIGPLIDRQIFRFTEEGMVN 2078  
Db :| |||: ||| |||:||||| |||: |||:| | |||:| | |||:| | |||:| | :  
QY 1977 RLSEILYDSTRVSFTYDETAGVLKTVNLQSDGFICTIRYRQIGPLIDRQIFRSESDGMVN 2036

QY 2079 ARFDYNDNSFRVTSMQAVINETPLPIDLYRYDDVSGKTEQFGKFGVIYDINQIITAV 2138  
Db :| |||:||||| |||: |||:| | |||:| | |||:| | |||:| | |||:| | :  
QY 2037 ARFDYSYDNSFRVTSMQGVINETPLPIDLYQFDDISGKVEQFGKFGVIYDINQIISTAV 2096  
Db :| |||:||||| |||: |||:| | |||:| | |||:| | |||:| | |||:| | :  
QY 2139 MTHTKHFDAYGRMKEVQYEIFRSLMYMTVQYDNMGRVVKKELKVGPYANTTRYSYEYDA 2198  
Db :| |||:||||| |||: |||:| | |||:| | |||:| | |||:| | |||:| | :  
QY 2097 MTYTKHFDAGHRIKEIQYEIFRSLMYWITIYQDNMGRVTYKREIKIGPFANTTKYAYEYDV 2156  
QY 2199 DGQLQTVSINDKPLWRYSYDLNGLNLHLSPGNSARLTPLRYDIRDRITRLGDVQYKMD 2258  
Db :| |||:||||| |||: |||:| | |||:| | |||:| | |||:| | |||:| | :  
QY 2157 DGQLQTVYLNKIMWRNYDLNGLNLHLLNPSNSARLTPLRYDLRDRITRLGDVQYRLDE 2216  
QY 2259 GFLRQRGDIFEYNSAGLLIKAYNRAGSVRYRYDGLGRRVSSKSSHHLQFFYADLT 2318  
Db :| |||:||||| |||: |||:| | |||:| | |||:| | |||:| | |||:| | :  
QY 2217 GFLRQRGTEIFEYSSKGLLTRVYKSGSWTVIYRYDGLGRRVSSKSLGQHLQFFYADLT 2276  
QY 2319 NPTKVTHLYNHSSEITSLYYDLQHLFAMELSSGDEFYIACDNIGTPLAVFSGTGLMIK 2378  
Db :| |||:||||| |||: |||:| | |||:| | |||:| | |||:| | |||:| | :  
QY 2277 YPTRITHVYNNHSSEITSLYYDLQHLFAMEISSGDEFYIASDNTGTPLAVFSSNGMLMK 2336  
QY 2379 QILYTAYGEIYNDTNPNFQIIIGYHGGLYDPLTKLVHMGRRDYDVLAGRWTSPDH 2438  
Db :| |||:||||| |||: |||:| | |||:| | |||:| | |||:| | |||:| | :  
QY 2337 QIQYTAYGEIYFDSNIDFQLVIGFHGGLYDPLTKLIHFGERDYDILAGRWTTFDIEIWK 2396  
QY 2439 LSSSNVMPFNLYMPKNNNPISNQDIKCFMTDVNSWLLTFGFLHNVIPGYPKPDM 2498  
Db :| |||:||||| |||: |||:| | |||:| | |||:| | |||:| | |||:| | :  
QY 2397 I-GKDPAPFNLYMFRNNNPASKIHVDKDYITDVNSWLVTFGFHLHNAIPGPPVPKFDL 2455  
QY 2499 PSYELIHTQMKTEBWDNSKSILGVQCEVQKQKAFVTLERFDQLYGSTITSCQQA 2558  
Db :| |||: ||| |||:||||| |||: |||:| | |||:| | |||:| | |||:| | :  
QY 2456 PSYELV----KSQWDDIPPIFGVQQQVARQAKAFSLGKMAEVQ----VSR 2507  
QY 2559 ---FASSGSVFGKVKFALKDGRVTTDIISVANEDGRRVAAILNHAHYLENLHFTID 2615  
Db :| |||: ||| |||:||||| |||: |||:| | |||:| | |||:| | |||:| | :  
QY 2508 WLWFATVKSLLIGKGMVLAVSQGRVQTNVLNATANEDCIKVAAVLNNAFYLENLHFTIE 2567  
QY 2616 THYFVKPGPSEGLAILGLSGRRRTLENGVNVTVSQINTVLNGRTRRYTDIQLQY 2675  
Db :| |||: ||| |||:||||| |||: |||:| | |||:| | |||:| | |||:| | :  
QY 2568 THYFIKTTTPESDLGTLRLTSGRKALENGINVTVSQSTTVNGRTRRREADVEMQF 2627  
QY 2676 NTRYGTTLDEEKARVLELARQAVRQAWAREQORLREGEGLRAWTEGEKQQLSTGR 2735  
Db :| |||: ||| |||:||||| |||: |||:| | |||:| | |||:| | |||:| | :  
QY 2628 HVRYGMTLDEEKARILEQARALARAWAREQORVRDGEGARLWTEGEKRLLSAGKV 2687  
QY 2736 GYDGFVVISVEQYPELSDSANNIHFMRQSEMGR 2769  
Db :| |||: ||| |||:||||| |||: |||:| | |||:| | |||:| | |||:| | :  
QY 2688 GYDGYVVLVVEQYPELADSANNIQFLRQSEIGR 2721

RESULT 5

US-11-096-051-8  
; Sequence 8, Application US/11096051  
; Publication No. US20050244868A1  
; GENERAL INFORMATION:  
; APPLICANT: Kekuda, Ramesh  
; APPLICANT: MacLachlan, Timothy K  
; APPLICANT: Rastelli, Luca  
; APPLICANT: Vernet, Corine  
; APPLICANT: Ettenberg, Seth  
; TITLE OF INVENTION: Ten-M3 Polypeptides and Polynucleotides and their Methods of Use  
; FILE REFERENCE: Attorney Docket No. Cura 967  
; CURRENT APPLICATION NUMBER: US/11/096,051  
; PRIOR APPLICATION NUMBER: 2005-03-30  
; PRIOR FILING DATE: 2005-03-30  
; PRIOR FILING DATE: 2001-12-31  
; PRIOR APPLICATION NUMBER: 10/455,772  
; PRIOR FILING DATE: 2003-06-04  
; PRIOR APPLICATION NUMBER: 60/557,978  
; PRIOR FILING DATE: 2004-03-30  
; NUMBER OF SEQ ID NOS: 38  
; SOFTWARE: CuraSeqList version 0.1  
; SEQ ID NO 8  
; LENGTH: 2725



; TYPE: PRT									
; ORGANISM: Homo sapiens									
US-11-096-051-8									
Query Match 68.5%; Score 10201; DB 7; Length 2725;									
Best Local Similarity 66.9%; Pred. No. 0;									
Matches 1872; Conservative 362; Mismatches 462; Indels 102; Gaps 21;									
QY	1	MDVKERKPYRSLTR-RRDARRYTSSADSEEGKAP-QKSYSSSETLKAYDQD-ARLAYG	57						
Db	1	MDVKERRPYCSLTKSRREKERRYTNSSADNEECRVPTQKSYSSSETLKAFDHDSSRLLYG	60						
QY	58	SRVKDIVPQEAEEFCRTGANFTLRELGLEEVTTPHGTLYRTDIGLPQCGYSMGAGSDAD	117						
Db	61	NRVKDLVHREADEFTTQQNQFTLRQLGVCPEPATRRGLAFCAEMGLPHRGYSISAGSDAD	120						
QY	118	EADTVLSPHPVRLWGRSTRSGRSSCLSSRANSNLTLTDTHEHEN---TETDHPGGLQNH	174						
Db	121	ENEAVMSPEHAMRLWGRGVKSGRSSCLSSRSNSALTTLTDTHEHKNKSDSENEQPASNQ	180						
QY	175	RLRTPPPPLSHAHTPNQHHAASINSLNRGNFTPRSNPSPAPTTHSLSGEPPAGGAQ---	230						
Db	181	TLQPLPP--SHKQHSAQHH-PSITSLNRNSLTNRNRNQSPAP-----PAALPAELQTT	229						
QY	231	-EPAHAQENWLLNSNIPTLETRNLGKQPFLGTLQDNLIEMDILGASRHDGAYS	289						
Db	230	PESVOLQDSVWLGSNVPLESR-----HFLPKT	256						
QY	290	G-GTSPFLCTTSPGYPLTSSTVSPPPRPLPRSTFARPAENLKKPSKYCNWKCAALS	348						
Db	257	GTGTTPLFSTATPGYTMASGSVSPPTPLPRNTLSRSAFKFKSKSKYCSWKCTALCAVG	316						
QY	349	ISATLVILLAYFVAMHLFGLNWHLQPMEGQMYE---ITEDTASSWPVPTDVS	405						
Db	317	VSVLLAILLSYFIAMHLFGLNWQLQQTENTDFENGKVNSDT-----MPTNTVSLPSG---	368						
QY	406	LETPDRKGGTTEGKPSFFPEDSFIDSGHIDVGRRASQKIPPGTFWRSQVFI	465						
Db	369	-----DNGKLGGFTQENNTIDSGELDIGRRAIQEIPIPGIFWRSQLFIDQP	417						
QY	466	FNVSLGKAALVGIYGRKGLPPSHT-----QPDFVELLDGRRLLTQEARSL	521						
Db	418	FNISLOKDALIGYGRKCLPPSHTQSSPQYDFVELLDGSRLLIAREQRSLL	477						
QY	522	PPSSHETGFIQYLDSGIWHLAFYNDGKESEVVVSFLTTAIESVDNCPSN	581						
Db	478	SVSLHEAGFIQYLDSGIWHLAFYNDGKNAEQVSFNTIVIESVVECP	537						
QY	582	HCFLGLGPDGCRASCVPVLCSGNGQYMKGRCLCHSGWKGBACDVP	641						
Db	538	HCFPGLGPDCSRACVPVLCSGNGQYSKGRCLCFSGWKGTGEDVPTT	597						
QY	642	ITGTCICNPGYKGESCEEVDCTSGRGVCVRGECHCFVGWGTNCET	701						
Db	598	IMGSCACSGYKGESCEEADCIDPGCSNHGVCIHGECHCSPGWGGSN	657						
QY	702	GHGTFLPDTGLCSDPSSWTGHDCSIEICAADCGHGVCVGGTCRC	761						
Db	658	GHGTYLQESGSCDTPNWTGPDCSNEICSVDCSGHGVCMGGTCRC	717						
QY	762	PRCAEHGTCRDGKCECSPGWNGEHTIAHYLDRVV-----KEGCPGL	815						
Db	718	PRCAEHGTCRDGKCECSPGWNGEHTIAHYLDKIVKDKIGYKEGCP	777						
QY	816	GWHCVCQLGWRGAGCDTSMETACGDSKDNDDGLVDCMDPDCCLO	875						
Db	778	GGHCVCQPGWRGAGCDVAMEITLCTDSKDNEDGLLDCMDPDCCLO	837						
QY	876	LDIIQETQVPVVSQONLHSFYDRIKFLVGRDSTHIIIGENPFDGGH	935						
Db	838	QDIISQLSQSPSQAAKSFYDRISFLIGSDSTHVIPEGSFNFKSLAS	897						
QY	936	LUGVNISFVNNPLFGYTTISRQDSFDLVTNGGISILRPERAPFITQ	995						

Db	898	LIGVNVSFFHYPEGYTTITRQDGMFDLVANGGASLTLVFERSPFLTQYHTV	957						
QY	996	METIMRHEENEIPSCDLSNPARPNPVVSPSPLTSPASSCAEKGP	1055						
Db	958	MDTLVMEKEENDIPSCDLSGFVRPNPIIVSSPLSTFFRSSPEDS	1017						
QY	1056	GCKMRLSYLSSRTPGYSVLRIISLTHPTIPFNLMKVHLMVAVEGR	1115						
Db	1018	GTDLKLSYLSRAAGYSVLKITMTQSIIPFNLMKVHLMVAVVGR	1077						
QY	1116	FIWDKTDVYNQKVFGLSEAFVSUGYEVYESCPDLILWEKRTTV	1175						
Db	1078	FIWDKTDAYNQKVYGLSEAAVSVGYEYESCLDLTLWEKRTAIL	1137						
QY	1176	HHAALNIQSGILHKNGENQFVSQQPPVIGSIMGNRRRRSISCP	1235						
Db	1138	HHVLDVQNGILYKNGENQFISQQPPVVSIMGNRRRRSISCP	1197						
QY	1236	TCGSDGSLYVGDFNYIRRIFFPSGNVTNILELRNKDFRSHSP	1295						
Db	1198	ACGIDGSLYVGDFNYVRRIFPSGNVTSVLELRNKDFRHSNPA	1257						
QY	1296	DSNSRRVFKIKSTVVVKDLVKNSEVAGTGDQCLPDDTRCGDG	1355						
Db	1258	DTNTRRIYRPKSLTGAKDLTKNAEVVAGTGEQCLPFDEARC	1317						
QY	1356	DKFGLIYFVDGTMIRRIDQNGIISTLLGSNDLTSARPLSCDS	1415						
Db	1318	DKNGLIYFVDGTMIRKVDQNGIISTLLGSNDLTSARPLTCD	1377						
QY	1416	PMDNSLYVLNNVVLQISENHQVRIVAGRPMHCQVPGIDHFL	1475						
Db	1378	PMDNSIYVLNNVVLQITENRQVRIAAGRPMHCQVPGVE-Y	1436						
QY	1476	SHNGVLYIAETDEKKINRIROVTTSGEISLVAGAPSGCDC	1535						
Db	1437	SYSGVLYITETDEKKINRIROVTTDGEISLVAGIPSECD	1496						
QY	1536	LNTPSSLAVCADGELYVADLGNIRIRFIRKNKPFNLTONM	1595						
Db	1497	LSAPSSLAASPDGTLIYIADLGNIRIRAVSKNKPLLSNM	1556						
QY	1596	LYTQSLPTGDYLYNFTYTGDGDTLITDNNGNMNVRRD	1655						
Db	1557	QYTVSLVTGDYLYNFYSYNDNDITAVTDSNGNTLRIRRD	1616						
QY	1656	TNSALKSVTTQGHELAMMTYHGNSGLLATKSNENGTWTF	1715						
Db	1617	TNGCLKGMTAQGLEVLFTYHGNSGLLATKSDETGTTFFD	1676						
QY	1716	FRSDTSSVHVQVETSSK-DDVHTITNLSASGAFYTLLOD	1774						
Db	1677	LHGDMDKAITVDIESSSREEDVSITSNLSSIDSFYTM	1736						
QY	1775	GMEVALQTEPHLLAGTVNPTVGKRNVTLPIDNGLNLV	1834						
Db	1737	GLDSHYQTEPHVLAGTANPTVAKRNMTLPGENGQNL	1796						
QY	1835	NRNLLSLDFDRVTRTEKIYDDHRKFTLRILYDQAGR	1894						
Db	1797	GRNLLSVDFDRTTKTEKIYDDHRKFLLR IAYDTS	1856						
QY	1895	GIQRGIMSERMEYDQACRITSRIFADGKTWSYTYLEK	1954						
Db	1857	SIQRTTSEKVDYDGGQGRIVSRVFADGKTWSYTYLEK	1916						
QY	1955	SVTMPNVARQTLETIRSVGYRNIYQPPPEGNASVTD	2014						
Db	1917	AITMPSVARHTMQTIRSIGYRNIYNPPESNASIITD	1976						
QY	2015	GKLSKLAETLYDTTKVSFTYDETAGMLKTNLQNEG	2074						

Db 1977 RRQTRLSEILYDSTRVSFTYDETAGVLKTVNLQSDGFICTIRYRQIGPLIDRQIFRFESED 2036

Qy 2075 GNVNARFDYNDNSFRVTSMQAVINETPLPIDLYRYDDVSGKTEQFGKFGVIYYDINQII 2134

Db 2037 GNVNARFDYSYDNSFRVTSMQGVINETPLPIDLYQFDDISGKVEQFGKFGVIYYDINQII 2096

Qy 2135 TTAVMTHTKHFDAYGRMKEVQYEIFRSLMYMTVQYDNGMRVVKELKVGVPYANTTRYSY 2194

Db 2097 STAVMTYTKHFDAGHRIKEIQYEIFRSLMYWITIQYDNGMRVTKREIKIGFPANTTKYAY 2156

Qy 2195 EYDADGLOQTVSINDKPLWRYSYDNLGNLHLLSPGNSARLTPLRYDIRDRITRLGDVQYK 2254

Db 2157 EYDVGLOQTIVYLNKIMWRNYNDLGNLHLLNPSNSARLTPLRYDLRDRITRLGDVQYR 2216

Qy 2255 MDEDFLQRGGDIFEYNSAGLLIKAYNRAGSWSVRYRYDGLGRRVSSKSSHHLQFFY 2314

Db 2217 LDEDFLQRGTETFEYSSKGLLTRVYSKSGWTVIYRYDGLGRRVSSKTSLGQHLQFFY 2276

Qy 2315 ADLTNPTKVTHLYNHSSSEITSLYDLOQHLFAMELSSGDEFYIACDNIQTPLAVFSGTG 2374

Db 2277 ADLTYPTRITHVYNHSSSEITSLYDLOQHLFAMEISSGDEFYIASDNTGTPLAVFSSNG 2336

Qy 2375 LMIKQILYTAYGEIYMDTNPNFQIIIGYHGGLYDPLTKLVHMGRRDYDVLAGRWTSPDHE 2434

Db 2337 LMLKQIQYTAYGEIYFDSNIDFQLVIGFHGGLYDPLTKLIHFGERDYDILAGRWTTPDIE 2396

Qy 2435 LMKHLSSNVMPFNLYMFKNNPNISNQDIKCFMTDVSNSWLLTFGFQLHNVIPGYPKPDM 2494

Db 2397 IWKRI-GKDPAPFNLYMFRNNPNASKIHDVKDYITDVNSWLVTFGFHLHNAIPGFPVPKF 2455

Qy 2495 DAMEPSYELIHTQMTQEWDNSSKSI LGVQCEVQKQKAFVTLERFDQLYGSTITSQQAP 2554

Db 2456 DLTEPSYELV----KSOQWDDIPPIFGVQQQVARQAKAFSLSLGMAEVQ-----VSRRRAG 2507

Qy 2555 KTKK---FASSGSVFGKGVKFAKDKGRVTTDIIISVANEDGRRVAAIILNHAHYLENLHFTI 2611

Db 2508 GAQSWLWFATVKSLLIGKVM LAVSQGRVQTNVNLNIANEDCIKVA AVLNNAFYLENLHFTI 2567

Qy 2612 DGVDTHYFVKPGPSEGLAILGLSGRRRTLENGVNVTVSQINTVLNGRTRRYTDIQLQYG 2671

Db 2568 EGKDTHYFIKTTTPESDLGTLRLTSGRKALENGINVTVSQSTTVNGRTRRPADVEMQFG 2627

Qy 2672 ALCLNTRYGTTLDEEKARVLELARQAVRQAWAREOQRLREGEEGLRAWTEGEKQQVLST 2731

Db 2628 ALALHVRYGMTLDEEKARILEQARQALARAWAREOQVRVDGEGARLWTEGEKQRLLSA 2687

Qy 2732 GRVQGYDGFVVISVEQPELSDSANNIHFMRQSEMGRR 2769

Db 2688 GKVQGYDGYVLSVEQPELADSANNIQFLRQSEIGRR 2725

RESULT 6

US-11-113-424-52

; Sequence 52, Application US/11113424

; Publication No. US20050260713A1

; GENERAL INFORMATION:

; APPLICANT: Gangolli et al.

; TITLE OF INVENTION: Polypeptides and Nucleic Acids Encoding Same

; FILE REFERENCE: 21402-225

; CURRENT APPLICATION NUMBER: US/11/113,424

; CURRENT FILING DATE: 2005-04-21

; PRIOR APPLICATION NUMBER: 60/256,704

; PRIOR FILING DATE: 2000-12-19

; PRIOR APPLICATION NUMBER: 60/311,590

; PRIOR FILING DATE: 2001-08-10

; PRIOR APPLICATION NUMBER: 60/257,314

; PRIOR FILING DATE: 2000-12-20

; PRIOR APPLICATION NUMBER: 60/311,613

; PRIOR FILING DATE: 2001-08-10

; PRIOR APPLICATION NUMBER: 60/315,617

; PRIOR FILING DATE: 2001-08-29

; PRIOR APPLICATION NUMBER: 60/307,506

; PRIOR FILING DATE: 2001-07-24

; PRIOR APPLICATION NUMBER: 60/322,358

; PRIOR FILING DATE: 2001-09-14

; PRIOR APPLICATION NUMBER: 60/294,075

; PRIOR FILING DATE: 2001-05-29

; PRIOR APPLICATION NUMBER: 60/288,153

; PRIOR FILING DATE: 2001-05-02

; NUMBER OF SEQ ID NOS: 190

; SOFTWARE: Patentin Ver. 2.1

; SEQ ID NO 52

; LENGTH: 2725

; TYPE: PRT

; ORGANISM: Homo sapiens

US-11-113-424-52

Query Match 64.4%; Score 9584; DB 7; Length 2725;

Best local Similarity 62.4%; Pred. No. 0;

Matches 1749; Conservative 404; Mismatches 538; Indels 112; Gaps 17;

Qy 1 MDVKERKPYRSLTR-RRDAERRYTSSSADSEEGKAPQKSYSSSETLKAYDQDARLAYGS- 58

Db 1 MEQTDCKPYQPLPKVKHEMDLAYTSSSEDESDGRKPRQSYNSRETLLHEYNQELRMVNSQ 60

Qy 59 --RVKDIVPQEA-B-EFCRTGANFTLRELGLEEVTPPHGTLYRTDI-GLPQCGYSMGAGSD 114

Db 61 SRKRKEVEKSTQEMEFCEHTSLC-----SGYQTDHMSVSRHGYQLEMGS 106

Qy 115 ADMEADTVLSPEHPVRLWGRSTRSGRSSCLSSRANSNLTLTDEHENTETDHPGGLQ--- 171

Db 107 VDTETGAASPDHALRMWIRGMKSEHSSCLSSRANSALSLTDTDHER-KSDGENGFKFSP 165

Qy 172 -----NHARLR--TPPPPLSHAHTPNQHHAAASINSLNRGNFTPRS 209

Db 166 VCCDMEAQAGSTQDVQSSPHNQFTFRPLPPPPPPHACTCARKPPPAADSLQRRSMTTRS 225

Qy 210 NPSPAPTDHLSLGEPPAGGAQEPAAHQENWLLNSNIPLETRNLGKQPFGLTLQDNLIEMD 269

Db 226 QPSA-----APAPPTSTQDSVHLHNSVWLLNSNIPLETR----- 259

Qy 270 ILGASRHDGAYSDGHFLFKPG-GTSPLFCFTTSPGYPLTSSTVSYSPPPRPLPRSTFARPAF 328

Db 260 -----HFLFKHGGSSAIFSAASQNYPLTSNTVSYSPPPRPLPRSTFSRPAF 305

Qy 329 NLKKPSKYCNWKAALSAIVISATLVILLAYFVAMHLFGLNWHLQPMEGQMYEITEDTAS 388

Db 306 TENKPYRCCNWKCTALSATAITVTLLALLAYVIAVHLFGLTLQLPVEGELYANGVSKGN 365

Qy 389 SWPVPTDVSLYPSGGTGLETPDRKKGKTTEGKPSFFPEDSFIDSGEIDVGRRASQKIPP 448

Db 366 RGTESMDTTYSPIGGKVSDKSEK-----VFQGRAIDTGEVDIGAQMVTIPP 414

Qy 449 GTFWRSQVFIHDPVHLKFNVSLGKAALVGIYGRKGLPPSHTQDFDVELLDGRLLTQEAR 508

Db 415 GLFWRFQITIHHPILYLFKNISLAKDSLGLGIYGRNIPPTHQTQDFDVKLMDGKQLVKQDSK 474

Qy 509 SLEGTPRQSRGTVPSPSSHETGFIQYLDSGIWHLAFYNDGKESEVVSFLTTALESVDNCPS 568

Db 475 GSDDTQHSRNLILTSLQETGFI EYMDQGPWYLA FYNDGKMEQVFLTTTAIEIMDDCST 534

Qy 569 NCYNGNDCISGTCFCFLGFLGPCGRASCPVLCSGNGQYMKGRCLCHSGWKAGABCDVPTN 628

Db 535 NCNGNGECISGHCHCFPGFLGPCDSCPVLCGGNGEYKGHCVCRHGWKGPECDVPEE 594

Qy 629 QCIDVACSNHGTCTGTCTICNPGYKGESCEEVDCMDPTCSGRGVCVRGECHCFVWGGETN 688

Db 595 QCIDPTCFGHGTCTMGVCICVPGYKGEICEEEEDCLDPMCSNHGICVKGECHCTGWWGVN 654

Qy 689 CETPRATCLDQCSGHGTFLPDTGLCSDPSTGHDCSIEICAADCGGHGVCVGGTCRCED 748

Db 655 CETPLPVCOEQCSGHGTFLLDAGVCSCDPKWTCSDCSTELCTMECGSHGVC SRGICQCEE 714

Qy 749 GWMGAACDQACHPRCAEHGTCRDGKCECSPGWNGEHTIAHYLDRVVKEGCPGLCNGNG 808

Db 715 GWVGPTCEERSCHSHCTEHGQCKDGKCECSPGWEGDHTIAHYLD-AVRDGCPLCFGNG 773





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; CURRENT APPLICATION NUMBER: US/11/096,051
; CURRENT FILING DATE: 2005-03-30
; PRIOR APPLICATION NUMBER: 10/038,854
; PRIOR FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 10/455,772
; PRIOR FILING DATE: 2003-06-04
; PRIOR APPLICATION NUMBER: 60/557,978
; PRIOR FILING DATE: 2004-03-30
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 4
; LENGTH: 2376
; TYPE: PRT
; ORGANISM: Homo sapiens
;
US-11-096-051-4

Query Match      62.4%; Score 9296; DB 7; Length 2376;
Best Local Similarity 69.6%; Pred. No. 0;
Matches 1673; Conservative 317; Mismatches 379; Indels 36; Gaps 9;

QY 372 LQPMEGQMYE---ITEDTASSWPVPTDVSLYPSGGTGLETPDRKKGKTTEGKPSFFPED 428
Db 1 LQQTENDTFENGKVNSDTR-----MPTNTVSLPSG-----DNGKLGGFQEN 41

QY 429 SFIDSGEIDVGRRASQKIPPTGFWRSQVFIDHPVHLKFNVSGLKAALVGIYGRKGLPPSH 488
Db 42 NTIDSGELDIGRRAIQIEIPGIFWRSOLFIDQPQFLKFNISLQDALIGVYGRKGLPPSH 101

QY 489 TQPDFVELLDGRRLLTQEARSLGTEPTQSRGTVPPSPSHETGFIQYLDSGIWHLAFYNDGK 548
Db 102 TQYDFVELLDGSRLLIAREQSRSLLETERAGRQARSVSLHEAGFIOYLDSGIWHLAFYNDGK 161

QY 549 ESEVVSFLTTAIESVDNCPSNCYNGDCCISGTCHCFGLGPDCCGRASCPVLCSGNGQYM 608
Db 162 NAEQVSFNTIVIESVVECPRNCHNGECVSGTCHCFGLGPDCCSRAACPVLCSGNGQYS 221

QY 609 KGRCLCHSGWGAECDPVPTNQCIDVACSNHGTCTGTCTCNPGYKGESCEEVDCMDPTCS 668
Db 222 KGRCLCFSGWKTECDVPTTQCIDPQCGRGICIMGSCACNSGYKGESCEEAADCIDPGCS 281

QY 669 GRGVCVRGECHCFVGWGTNCTEPTPRATCLDQCSGHGTFLPDTGLCSDRPSWTGHDCSIEI 728
Db 282 NHGVCIHGECHCSPGWGGSNCIEILKTMCPDQCSGHGTYLQESGCTCDPNWTGPDCSNEI 341

QY 729 CAADCGGHGVCVGGTCRCEDGWMGAACDQACHPRCAEHGTCRDGKCECSPGWNGEHCTI 788
Db 342 CSVDGCGSHGVMGGTCRCEEGTGPACNQACHPRCAEHGTCRDGKCECSPGWNGEHCTI 401

QY 789 AHYLDRVVKEGCPGLCNGNGRCTLDLNGWHCVQLGWRGAGCDTSMETACGDSKDNDDG 848
Db 402 AHYLDKIVKEGCPGLCNSNGRCTLQNGWHCVQPGWRGAGCDVAMETLCTDSKDNEDG 461

QY 849 LVDCMDPDCCLOPLCHINPLCLGSPNPLDIIQETQVPVSOQNLHSFYDRIKFLVGRDSTH 908
Db 462 LIDCMDPDCCLOQSSCQNPYCRGLPDPQDIIISQSLQSPSQAAKSFYDRISFLIGSDSTH 521

QY 909 IIPGENPFDGGHACVIRGQVMTSDGTPLVGNISFVNNPLFGYTIISRQDGSFDLVTNGGI 968
Db 522 VIPGESPFNKSLASVIRGQVLTADGTPLIGNVVSFFHYPEYGYTITRODGMFDLVANGGA 581

QY 969 SIILRFERAPFITQEHTLWLPWDRFFVWMETIIMRHEENETPSCDLSNFARNPNPVSPSPL 1028
Db 582 SLTLVFRSPFLTQYHTVWIPWNVYVMDTLVMKKEENDIPSCDLSGFVRPNPIIVSSPL 641

QY 1029 TSFASSCAEKGPIVPEIQALQOEIISGCKMRLSYLSRTPGYKSVLRISLTHPTIPFNL 1088
Db 642 STFRSSPEDSPIIPETQVLHEETIPGTDLKL SylSSRAAGYKSVLKITMTQSIIPFNL 701

QY 1089 MKVHLMVAVEGRLFRKWFAAAPDLSYFFIWDKTDVYNQKVFGLSEAFVSUGYEYESCDDL 1148
Db 702 MKVHLMVAVVGRLFQKWFASPANLAYTFIWDKTDAYNQKVYGLSEAVSVUGYEYESCDDL 761

QY 1149 ILWEKRTTVLQGEIDASKLGWSLDKXHALNIQSGILHKNGENQFVSQQPPVIGSIMG 1208
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Db 762 TLWEKRTAILQGYELDASNMGGWTLDKHVLVDVQNGILYKNGENQFISQQPPVWSSIMG 821

QY 1209 NGRRRSISCPSCNGLADGNKLLAPVALTCGSDGSLYVGDFNYIRRIFFPSGNVTNILELRN 1268
Db 822 NGRRRSISCPSCNGQADGNKLLAPVALACGIDGSLYVGDFNYVRRIFPSGNVTSVLELRN 881

QY 1269 KDFRHSHPAHKYIYLATDPMGSAVFLSDNSRRRVFKIKSTVVVKDLVKNSEVAVAGTDQC 1328
Db 882 KDFRHSSNPAHRYIYLATDPVTGDLYVSDTNRRIYRPKSLTGAKDLTKNAEVAAGTGEQC 941

QY 1329 LPFDDTRCGDGKATEATLTNPRGITVDKFGLIYFVDGTMIRRIDQNGIISTLLGSNDLT 1388
Db 942 LPFDEARCGDGKAVEATLMSPKGMADVKNGLIYFVDGTMIRKVDQNGIISTLLGSNDLT 1001

QY 1389 SARPLSCDSVMDISQVRLEWPTDLAINPMDNSLYVLDDNNVVLQISENHQVRIVAGRPMHC 1448
Db 1002 SARPLTCDTSMHISQVRLEWPTDLAINPMDNSIYVLDDNNVVLQITENQVRIAGRPMHC 1061

QY 1449 QVPGIDHFLLSKVAIHATLESATALAVSHNGVLYIAETDEKKINRIRQVTTSGEISLVAG 1508
Db 1062 QVPGVE-YPVGKHAVQTTLLESATAIAVSYGVLVITETDEKKINRIRQVTTDGEISLVAG 1120

QY 1509 APSGCDCKDANCDCFSGDDGYAKDAKLNTPSSLAVCADGELYVADLGNIRIFIRKNKP 1568
Db 1121 IPSECDCKDANCDCYQSGDGYAKDAKLSAPSSLAASPDGTLVIAIDLGNIRIRAVSKNKP 1180

QY 1569 FLNTQNMVELSSPIDQELYLFDTTGKHLVYQSLPTGDYLYNFTYTGDDITLITDNNNGM 1628
Db 1181 LLNSMNFYVASPTDQELYIFDINGTHQYTVSLVTGDYLYNFSYSDNDNITAVTDSNGNT 1240

QY 1629 VNVRDSTGMPLWLVPDQGVVWVTMGNTSALKSVTTQGHELAMVTYHSGSLLATKSNE 1688
Db 1241 LRIRRDPNRMPVRVVSVDNQVILWTIGTNGCLKSMTAQGLELVLFTHYHSGSLLATKSDE 1300

QY 1689 NGWTTFFEYDSFGRLTNVTFPTQGVSSFRSDTSSVHVQVETSSK-DDVTTITNLSASGA 1747
Db 1301 TGWTTFFDYDSEGLTNVTFPTGVVTLNHLGMDKAITVDIESSSREEDVSTNLSIDS 1360

QY 1748 FYTLQDQVRNSYIYGADGSLRLLLANGMEVALQTEPHLLAGTVNPTVGKRVNVTLPIDNG 1807
Db 1361 FYTMVQDQLRNSYQIGYDGLSLRIIYASGLDSHSHYQTEPHVLAGTANPTVAKRNMVLPGENG 1420

QY 1808 LNLVEWRQRKEAQGVTVFGRRLRVHNRNLLSLDFDVRVTRTEKIYDDHRKFTLRILYDQ 1867
Db 1421 QNLVEWRFRKEAQGVTVFGRKLRVNGRNLSSVDFDRTTKTEKIYDDHRKFTLRILAYDT 1480

QY 1868 AGRPSLWSPSSRLNGVNVTVSPGGYIAGIQRGIMSERMEYDQAGRITSRIFADGKTWSYT 1927
Db 1481 SGHPTLWLPSSKLMVNVTVSSTQGIASIQRGTTSEKVDYDGGQGRIVSRVFADGKTWSYT 1540

QY 1928 YLEKSMVLLHLSQRQYIFEFDKNDRLSSVVTMPNVARQTLTIRSVGYRNIYQPEGNAS 1987
Db 1541 YLEKSMVLLHLSQRQYIFEYDMWDLRLSAITMPSVARHTMQTIRSIGYRNIYNPPESNAS 1600

QY 1988 VIQDFTEDGHLHTFYLGTGRRVVIKYGKLSKLAETLYDTTKVSFTYDETAGMLKTINLQ 2047
Db 1601 IITDYNEEGLLLQTAFLGTSRRVLFKYRRQTRLSEILYDSTRVSFTYDETAGVLKTVNLQ 1660

QY 2048 NEGFTCTIRYRQIGPLIDRQIFRFTTEEGMVNARFDYNDVNSFRVTSMQAVINETPLPIDL 2107
Db 1661 SDGFICTIRYRQIGPLIDRQIFRFSDEGMVNARFDYSYDNSFRVTSMQGVINETPLPIDL 1720

QY 2108 YRYDDVSGKTEQFGKFGVIYYDINQIITTAVMTHTKHFDAYGRMKEVQYEIFRSLMYWMT 2167
Db 1721 YQFDDISGKVEQFGKFGVIYYDINQIISTAVMTYTKHFDAGHRIKEIQYEIFRSLMYWIT 1780

QY 2168 VOYDNMGRVVKKELKVGYPYANTTRYSEYEDADGQLQTVSINDKPLWRYSYDLNGLHLLS 2227
Db 1781 IQYDNMGRVTKREIKIGPFANTTKYAYEYDVGDLQTVYLNKIMWRNYDLNGLHLN 1840

QY 2228 PGNSARLTPLRYDIRDITRLGDVQYKMDDEGFLRQRGGDIFEYNSAGLLIKAYNRAGSW 2287
Db 1149 ILWEKRTTVLQGEIDASKLGWSLDKXHALNIQSGILHKNGENQFVSQQPPVIGSIMG 1208
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Db 1841 PSNSARLTPLRYDLRDRITRLGVDQYRLDDEDGFLRQRTGEIPEYSSKGLLTRVYSGSGW 1900

QY 2288 SVRYRYDGLGRRVSSKSSHHLQFFYADLTNPTKVTHLYNHSSEITSLYYDLQGHLPFA 2347

Db 1901 TVIYRYDGLGRRVSSKTSGLQHLQFFYADLTYPTRITHVYNHSSEITSLYYDLQGHLPFA 1960

QY 2348 MELSSGDEFYIACDNIGTPLAVFSGGLMIKQILYTAYGEIYMDTNPNFQIIIGYHGGLY 2407

Db 1961 MEISSGDEFYIASDNTGTPLAVFSSNGLMLKQIQYTAYGEIYFDSNIDFQLVIGFHGGLY 2020

QY 2408 DPLTKLVHMGRRDYDLAGRWTSPDHMLWKHLSSSNVMPENLYMFKNPNPISNSQDIKCF 2467

Db 2021 DPLTKLHPGERDYDILAGRWTTPDIEIWKRI-GKDPAPENLYMFRNNPASKIHDVKDY 2079

QY 2468 MTDVNSWLLTFGFQLHNVIPGYPKPDMDAMEPSYELIHTOMKTQEWDNKSILGVQCEVQ 2527

Db 2080 ITDVNSWLVTFGFHLHNAIPGFPVPKFDLTEPSYELV----KSQQWDDIPPIFGVQQQVA 2135

QY 2528 KQLKAFVTLERFDQLYGSTITSCQAPKTKK---FASSGSVFGKGVKFALKDGRVTTDII 2584

Db 2136 RQAKAFLSLGKMAEVQ---VSRRRAGGAQSWLWFATVKSLSLKGVM LAVSQGRVQTNVL 2191

QY 2585 SVANEDGRRVAAILNHAHYLENLHFTIDGVDTHTYFVKPGPSBGDLAILGLSGGRRTLENG 2644

Db 2192 NIANEDCIKVAAVLNNAFYLENLHFTIEGKDTHYFIKTTTPESDLGTLRLTSGRKALENG 2251

QY 2645 VNVTVSQINTVLNGRTRRYTDIQLQYGALCLNTRYGTTLDEKARVLELARQRAVRQAWA 2704

Db 2252 INVTVSQSTTVVNGRTRRFADVEMQFALALHVRYGMTLDEKARILEQARQARALAPAWA 2311

QY 2705 REQORLREGHEGLRAWTEGEKQQLVSTGRVQYDGFVFVISVEQYPELSDSANNIHFMRQS 2764

Db 2312 REQORVRDGEEGARLWTEGEKROLLSAGKVQGYDGYVLSVEQYPELADSANNIQFLRQS 2371

QY 2765 EMGRR 2769

Db 2372 EIGRR 2376

RESULT 8

US-10-821-234-1097

; Sequence 1097, Application US/10821234

; Publication No. US20050255114A1

; GENERAL INFORMATION:

; APPLICANT: Labat, Ivan

; APPLICANT: Stache-Crain, Birgit

; APPLICANT: Andarmani, Susan

; APPLICANT: Tang, Y. Tom

; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia

; FILE REFERENCE: 821A

; CURRENT APPLICATION NUMBER: US/10/821,234

; CURRENT FILING DATE: 2004-04-07

; PRIOR APPLICATION NUMBER: US 60/462,047

; PRIOR FILING DATE: 2003-04-07

; NUMBER OF SEQ ID NOS: 1704

; SOFTWARE: pt\_SEQ\_genes Version 1.0

; SEQ ID NO 1097

; LENGTH: 1094

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-821-234-1097

Query Match 28.0%; Score 4175.5; DB 6; Length 1094;

Best Local Similarity 69.3%; Pred. No. 2.3e-262;

Matches 764; Conservative 170; Mismatches 155; Indels 13; Gaps 5;

QY 1672 MMTYHGNSGLLATKSNENGWTTTFVEYDSFGRLTNVTFPTQGVSSFSRSDTSSVHVQVETS 1731

Db 2 LFTYHGNSGLLATKSDETGWTTFDYDSEGRLTNVTFPTGVVTVNLHGDMDKAITVDIESS 61

QY 1732 SK-DDVTITTNLSASGAFYTLQDQVRNSYYIGADGSLRLLLANGMEVALQTEPHLLAGT 1790

Db 62 SREEDVSITSNLSSIDSFYTMVQDQLRNSYQIGYDGSRLRIYASGLDSHYQTEPHVLAGT 121

QY 1791 VNPTVGKRNVTLPIDNGLNLVEWRQORKEAQGVTVFGRRLRVHNRNLLSLDFDRVTRTE 1850

Db 122 ANPTVAKRNMTLPGENGQNLVEWRKEQAQGVNVFGRKLRVNGRNLSSVDFDRTTKTE 181

QY 1851 KIYDDHRKFTRLRIYDQAGRPSLWSPPSSRLNGVNVITYSPGGYIAGIQRGINSERMEYDQA 1910

Db 182 KIYDDHRKFLRLIAYDTSGHPTLWLPSSKLMAVNVITYSSTGOIASIQRGITSEKVDYDGO 241

QY 1911 GRITSRIFADGKTWSYTYLEKSMVLLLHSHSQYIFEFDKNDRLSSVTPNVARQOTLETIR 1970

Db 242 GRIVSRVFADGKTWSYTYLEKSMVLLLHSHSQYIFEYDMMDRLSAITMPSVARHTMQTIR 301

QY 1971 SVGYRNIYQPPEGNASVIQDFTEDGHLHHTFYLGTGRRVIYKYGKLSKLAETLYDTTKV 2030

Db 302 SIGYRNIYNPPESNASIITDYNEEGLLLOTAFLGTSRRVLFKYRRQTRLSEILYDSTRV 361

QY 2031 SFTYDETAGMLKTINLQNEGFTCTIRYRQIGPLIDRQIFRFTTEGMVNARFDYNYDNSFR 2090

Db 362 SFTYDETAGVLKTVNLQSDGFICTIRYRQIGPLIDRQIFRSEDEGMVNARFDYSDNSFR 421

QY 2091 VTSMQAVINETPLPIDLYRYDDVSGKTEQFGKFGVIYYDINOIITTAVMTHTKHFDAYGR 2150

Db 422 VTSMQGVINETPLPIDLYQFDDISGKVEQFGKFGVIYYDINOIISTAVMTYTKHFDAGR 481

QY 2151 MKEVQYEIFRSLMYMTVQYDNMGRVVKKELKVGYPYANTTRYSEYEDADGQLQTVSINDK 2210

Db 482 IKEIQYEIFRSLMYWITIYQYDNMGRVTKREIKIGPFANTTKIAYEYDVGQLQTVYLNEK 541

QY 2211 PLWRYSYDLNGLNHLSPNSARLTPLRYDIRDRITRLGDVQYKMDDEGFLRQGGDIFE 2270

Db 542 IMWRNYDLNGLNHLNPSNSARLTPLRYDILDRITRLGDVQYRLDEDEGFLRQGTIFE 601

QY 2271 YNSAGLLIKAYNRAGSWSVRYRYDGLGRRVSSKSSHHLQFFYADLTNPTKVTHLYNHS 2330

Db 602 YSSKGLLTRVYSGSGWTVIYRYDGLGRRVSSKTSLGQHLQFFYADLTYPTRITHVYNHS 661

QY 2331 SSEITSLYYDLQGHLFAMELSSGDEFYIACDNIGTPLAVFSGTGLMIKQILYTAYGEIYM 2390

Db 662 SSEITSLYYDLQGHLFAMEISSGDEFYIASDNTGTPLAVFSSNGLMLKQIQYTAYGEIYF 721

QY 2391 DTNPNFQIIIGYHGGLYDPLTKLVHMGRRDYDLAGRWTSPDHMLWKHLSSSNVMPFNLY 2450

Db 722 DSNIDFQLVIGFHGGLYDPLTKLIHFGERDYDILAGRWTTPDIEIWKRI-GKDPAPFNLY 780

QY 2451 MFKNNNPISNODIKCFMTDVSNLLTFGQLHNVIPGYPKPDMDAMEPSYELIHTQMKT 2510

Db 781 MFRNNNPASKIHDVKDYITDVNSWLVTFGFHLHNAIPGFPVPKFDLTEPSYELV---KS 836

QY 2511 QEWDNKSILGVQCEVQKQLKAFVTLERFDQLYGSTITSCQAPKTKK---FASSGSVFG 2567

Db 837 QQWDDIPPIFGVQQQVARQAKAFLSLGKMAEVQ---VSRRRAGGAQSWLWFATVKSLIG 892

QY 2568 KGVKFALKDGRVTTDIIISVANEDGRRVAAILNHAHYLENLHFTIDGVDTHTYFVKPGPSEG 2627

Db 893 KGVMLAVSQGRVQTNVLNIANEDCIKVAAVLNNAFYLENLHFTIEGKDTHYFIKTTTPES 952

QY 2628 DLAILGLSGGRRTLENGVNVTVSQINTVLNGRTRRYTDIQLQYGALCLNTRYGTTLDEEK 2687

Db 953 DLGTLRLTSGRKALENGINVTVSQSTTVVNGRTRRFADVEMQFALALHVRYGMTLDEEK 1012

QY 2688 ARVLELARQRAVRQAWAREQORLREGEGLRAWTEGEKQQLVSTGRVQYDGFVFISVEQ 2747

Db 1013 ARILEQARQARALARAWAREQORVRDGEEGARLWTEGEKROLLSAGKVQGYDGYVLSVEQ 1072

QY 2748 YPELSDSANNIHFMRQSEMGR 2769

Db 1073 YPELADSANNIQFLRQSEIGRR 1094

RESULT 9

US-11-113-424-54

; Sequence 54, Application US/11113424

```

; Publication No. US20050260713A1
; GENERAL INFORMATION:
; APPLICANT: Gangolli et al.
; TITLE OF INVENTION: Polypeptides and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-225
; CURRENT APPLICATION NUMBER: US/11/113,424
; CURRENT FILING DATE: 2005-04-21
; PRIOR APPLICATION NUMBER: 60/256,704
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: 60/311,590
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/257,314
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: 60/311,613
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/315,617
; PRIOR FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: 60/307,506
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/322,358
; PRIOR FILING DATE: 2001-09-14
; PRIOR APPLICATION NUMBER: 60/294,075
; PRIOR FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: 60/288,153
; PRIOR FILING DATE: 2001-05-02
; NUMBER OF SEQ ID NOS: 190
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 54
; LENGTH: 1045
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-11-113-424-54

Query Match      26.7%; Score 3979.5; DB 7; Length 1045;
Best Local Similarity 69.2%; Pred. No. 1e-249;
Matches 729; Conservative 164; Mismatches 147; Indels 13; Gaps 5;

Qy 1721 DSSVHVQVETSSK-DDVTITNLSASGAFYTLTLLQDVNRNSYYIGADGSLRLLLLANGMEVA 1779
Db 2 DKAITVDIESSREEDVSITSNLSSIDSFYTMVQDQLRNSYQIGYDGSRLRIIYASGLDSH 61

Qy 1780 LQTEPHLLAGTVNPTVGKRNVTLPIDNGLNLVEWRQRKEARGQVTVFGRRLRVHNRNLL 1839
Db 62 YQTEPHVLGAGTANPTVAKRNWTLPGENGQNLVEWRFRKEAQGKVNFGFKLRVNGRNLL 121

Qy 1840 SLDPDRVTRTEKIYDDHRKFTLRLILYDQAGRPSLWSPSSRLNGVNVTVSPGGVIAGIQRG 1899
Db 122 SVPDFRRTTKTEKIYDDHRKFLRLIAYDTSGHPTLWLPSSKLMVNVTVSYSTGQIASIQRG 181

Qy 1900 IMSERMEYDQAGRITSRIFADGKTWSYTYLEKSMVLLLHSQRQYIFEFDKNDRLSSVTMP 1959
Db 182 TTSEKVDYDQGGRIVSRVFDGKTWSYTYLEKSMVLLLHSQRQYIFEYDMWDRLSAITMP 241

Qy 1960 NVARQTLETIRSVGYRNIYQPPEGNASVIOQFTEDGHLHLHTFYLGTGRRVIYKYGKLSK 2019
Db 242 SVARHTMQTIRSIGYRNIYNPPESNASIITDYNEEGLLQTAFLGTSRRVLFKYRRQTR 301

Qy 2020 LAETLYDTTKVSFTYDETAGMLKTINLQNEGFTCTIRYQIGPLIDRQIFRFTTEGMVNA 2079
Db 302 LSEILYDSTRVSFTYDETAGVLKTVNLQSDGFICTIRYQIGPLIDRQIFRSEDEGMVNA 361

Qy 2080 RFDVYDNSFRVTSMQAVINETPLPIDLYRDDVSGKTEQFGKFGVIYYDINQIITAVM 2139
Db 362 RFDYSYDNSFRVTSMQGVINETPLPIDLYQFDDISGKVEFGKFGVIYYDINQIITAVM 421

Qy 2140 THTKHFDAYGRMKEVQYEIFRSLMYWMTVQYDNMGRVVKELKVGPYANTTRYSEYDAD 2199
Db 422 TYTKHFDAGHRIKEIQYEIFRSLMYWITIYQDNMGRVTRKEIKIGPFANTTKYAYEYDVD 481

Qy 2200 GOLQTVSINDKPLWRYSYDLNGLNHLSPGNSARLTPLRYDIRDRITRLGDVQYKMDGDG 2259
Db 482 GOLQTVYLNKEIMWRNYNDLGNLHLLNPSNSARLTPLRYDLRDRITRLGDVQYRLDEGDG 541
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Qy 2260 FLRQRGGDIFEYNSAGLLIKAYNRAGSWSVRYRYDGLGRRRVSSKSSHHLQFFYADLTN 2319
Db 542 FLRQRGTETFEYSSKGLLTRVYSGSGWTVIYRYDGLGRRRVSSKTSLGQHLQFFYADLT 601

Qy 2320 PTKVTHLYNHSSEITSLYYDLQHLFAMELSSSGDEFYIACDNIGTPTPLAVFSGTGLMIK 2379
Db 602 PTRITHVYNHSSEITSLYYDLQHLFAMEISSGDEFYIASDNTGTPTPLAVFSSNGLMLK 661

Qy 2380 ILYTAYGEIYMDTNPNFQIIIGYHGGLYDPLTKLVHMGRRDYDVLAGRWTSPDHFWKHL 2439
Db 662 IQYTAYGEIYFDSNIDFQLVIGFHGGLYDPLTKLIHFERDYDILAGRWTTPDIEWKRI 721

Qy 2440 SSSNVMPENLYMFKNNNPISNSQDIKCFMTDVNSWLLTFGFQLHNVI PGYKPKDMDAMEP 2499
Db 722 -GKDPAPENLYMFRNNNPASKIHDVKDYITDVNSWLVTFGFHLHNAIPGFPVPKFDLTER 780

Qy 2500 SYELIHTQMKTQEWDNKSKILGVQCEVQKQKAFVTLERFDQLYGSTITSQQAPKTK- 2558
Db 781 SYELV---KSQWDDIPPIFGVQQQVARQAKAFSLGKMAEVQ---VSRRRAGGAQSW 832

Qy 2559 --FASSGSVFEGKGVKFALKDGRVTTDIISVANEDGRRVAAILNHAHYLENLHFTIDGVD 2616
Db 833 LWFATVKSLLIGKGVMLAVSQGRVQTNVLNIANEDCIKVAAVLNNAFLENLHFTIEGKDT 892

Qy 2617 HYFVKPGPSEGLAILGLSGRRRTLENGVNVTVSQINTVLNGRTRRYTDIQLQYGALCLN 2676
Db 893 HYFIKTTTPESDLGTLRLTSGRKALENGINVTVSQSTTVVNGRTRRFADVEMQFGALALH 952

Qy 2677 TRYGTTLDEEKARVLELARQRAVRQAWAREQQRLREGEGLRAWTEGKQQVLTSTGRVQG 2736
Db 953 VRYGMTLDEEKARILEQARQALARAWAREQQRVRDGEGARLWTEGKRQLLSAGKVQG 1012

Qy 2737 YDGFVFVISVEQYPELSDSANNIHFMROSEMGR 2769
Db 1013 YDGYVVLSEVEQYPELADSANNIQFLRQSEIGRR 1045

RESULT 10
US-11-113-424-50
; Sequence 50, Application US/11113424
; Publication No. US20050260713A1
; GENERAL INFORMATION:
; APPLICANT: Gangolli et al.
; TITLE OF INVENTION: Polypeptides and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-225
; CURRENT APPLICATION NUMBER: US/11/113,424
; CURRENT FILING DATE: 2005-04-21
; PRIOR APPLICATION NUMBER: 60/256,704
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: 60/311,590
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/257,314
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: 60/311,613
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/315,617
; PRIOR FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: 60/307,506
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/322,358
; PRIOR FILING DATE: 2001-09-14
; PRIOR APPLICATION NUMBER: 60/294,075
; PRIOR FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: 60/288,153
; PRIOR FILING DATE: 2001-05-02
; NUMBER OF SEQ ID NOS: 190
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 50
; LENGTH: 730
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-11-113-424-50
```



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Query Match      25.9%;   Score 3854;   DB 7;   Length 730;
Best Local Similarity 99.7%;   Pred. No. 7.8e-242;
Matches 728;   Conservative 1;   Mismatches 1;   Indels 0;   Gaps 0;

Qy 2040 MLKTLNLQNEGFTCTIRYRQIGBLIDRQIFRFTTEGMVNARFDYNDNSFRVTSMQAVIN 2099
    |||
Db 1 MLKTLNLQNEGFTCTIRYRQIGBLIDRQIFRFTTEGMVNARFDYNDNSFRVTSMQAVIN 60

Qy 2100 ETPLPIDLYRDDVSGKTEQFGKFGVIYYDINQIITTAVMTHTKHFDAYGRMKEVQYEIF 2159
    |||
Db 61 ETPLPIDLYRDDVSGKTEQFGKFGVIYYDINQIITTAVMTHTKHFDAYGRMKEVQYEIF 120

Qy 2160 RSLMYWMTVQYDNGMGRVVKELKVGYPYANTTRYSEYDADGQLQTVSINDKPLWYSYDL 2219
    |||
Db 121 RSLMYWMTVQYDNGMGRVVKELKVGYPYANTTRYSEYDADGQLQTVSINDKPLWYSYDL 180

Qy 2220 NGNLHLLSPGNSARLTPLRYDIRDRITRLGDVQYKMDDEGFLRQGGDIFEYNSAGLLIK 2279
    |||
Db 181 NGNLHLLSPGNSARLTPLRYDIRDRITRLGDVQYKMDDEGFLRQGGDIFEYNSAGLLIK 240

Qy 2280 AYNRAGWSVRYRDGLGRRVSSKSSHHLQFFYADLTNPTKVTHLYNHSSSEITSLYY 2339
    |||
Db 241 AYNRAGWSVRYRDGLGRRVSSKSSHHLQFFYADLTNPTKVTHLYNHSSSEITSLYY 300

Qy 2340 DLQHLFAMELSSGDEFYIACDNICTPLAVFSGTGLMIKQILYATYGEIYMDTNPNFQII 2399
    |||
Db 301 DLQHLFAMELSSGDEFYIACDNICTPLAVFSGTGLMIKQILYATYGEIYMDTNPNFQII 360

Qy 2400 IGYHGGLYDPLTKLVHMGRRDYDVLAGRWTSPDHELWKHLSSSNVMPFNLYMKNNPNIS 2459
    |||
Db 361 IGYHGGLYDPLTKLVHMGRRDYDVLAGRWTSPDHELWKHLSSSNVMPFNLYMKNNPNIS 420

Qy 2460 NSQDIKCFMTDVNSWLLTFGFQLHNVIPGYPKPDMDAMERSYELIHTQMKTQEWDNSKSI 2519
    |||
Db 421 NSQDIKCFMTDVNSWLLTFGFQLHNVIPGYPKPDMDAMERSYELIHTQMKTQEWDNSKSI 480

Qy 2520 LGVQCEVQKQKAFVTLERFDQLYGSTITSCQQAPKTKKFASSGSVFGKGVKFALKDGRV 2579
    |||
Db 481 LGVQCEVQKQKAFVTLERFDQLYGSTITSCQQAPKTKKFASSGSVFGKGVKFALKDGRV 540

Qy 2580 TTDIISVANEDGRRVAAILNHAHYLENLHFTIDGVDTHYFVKPGPSEGD LAILGLSGRR 2639
    |||
Db 541 TTDIISVANEDGRRVAAILNHAHYLENLHFTIDGVDTHYFVKPGPSEGD LAILGLSGRR 600

Qy 2640 TLENGVNVTVSQINTVLNGRTRRYTDIQLQYGALCLNTRYGTTLDEEKARVLELARQAV 2699
    |||
Db 601 TLENGVNVTVSQINTVLNGRTRRYTDIQLQYGALCLNTRYGTTLDEEKARVLELARQAV 660

Qy 2700 RQAWAREOQRLREGEGLRAWTEGEKQOVLSTGRVQGYDGFVVISVEQYPELSDSANNIH 2759
    |||
Db 661 RQAWAREOQRLREGEGLRAWTEGEKQOVLSTGRVQGYDGFVVISVEQYPELSDSANNIH 720

Qy 2760 FMRQSEMGRR 2769
    |||
Db 721 FMRQSEMGRR 730
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```
RESULT 11
US-11-113-424-53
; Sequence 53, Application US/11113424
; Publication No. US20050260713A1
; GENERAL INFORMATION:
; APPLICANT: Gangolli et al.
; TITLE OF INVENTION: Polypeptides and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-225
; CURRENT APPLICATION NUMBER: US/11/113,424
; CURRENT FILING DATE: 2005-04-21
; PRIOR APPLICATION NUMBER: 60/256,704
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: 60/311,590
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/257,314
; PRIOR FILING DATE: 2000-12-20
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; PRIOR APPLICATION NUMBER: 60/311,613
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/315,617
; PRIOR FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: 60/307,506
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/322,358
; PRIOR FILING DATE: 2001-09-14
; PRIOR APPLICATION NUMBER: 60/294,075
; PRIOR FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: 60/288,153
; PRIOR FILING DATE: 2001-05-02
; NUMBER OF SEQ ID NOS: 190
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 53
; LENGTH: 2515
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-11-113-424-53

Query Match      25.6%;   Score 3804.5;   DB 7;   Length 2515;
Best Local Similarity 33.2%;   Pred. No. 8.1e-238;
Matches 818;   Conservative 497;   Mismatches 969;   Indels 181;   Gaps 54;

Qy 384 EDTASSWPVPTDVSLYPSGGTGLETPDRKKGKTEGKPSFFPEDSFIDSGEIDVGRRAS 443
    |||
Db 131 EATSSAATSSSQSLTPSLSSSLANANNGGARTP---PARSFPPDG-TTFGQITLGQKLT 186

Qy 444 QKIPPGTFWRSQVFIIDHPVHLKFNVSGLKAALVYGRKGLPPSHTQDFDFVELLDGRRLL 503
    |||
Db 187 KEIQPYSYWNMQFYQSEPAYVKFDYTIIPRGASIGVYGRRNALPHTHTQYHFKEVLSGFSAS 246

Qy 504 TQEARS--LEGTPRQSRGTVPSPSSHETGFIQYLDSDGIWHLAFYN-DGKESEVVSFLT TAI 560
    |||
Db 247 TRTARAAHLSITREVTR-----YMEPGHWFVSLYNDGDDGVQELTFYAAVAE 292

Qy 561 ESVDNCPNSCYNGDCISGTCHCFLGLPDCGRASCPVLCSGNGQYMKGRCLCHSGWK 620
    |||
Db 293 DMTQNCNPGCSGNGQCLLGHQCNCNPGFGDDCSBSVCPVLCSEQHGEYTNCEICNPGWK 352

Qy 621 ABCDVPTNQCIDVACSNHGTCTGTCTICNPGYKBSCEEVDCMDPTCSGRGVCVRGECHC 680
    |||
Db 353 KECSLRHDECEVADCSGHGHCVSGKCQCQMRGYKGFCEEVDCPHPNCSGHGFCADGT C IC 412

Qy 681 FVGWGGTNCET---PRATCLDQCSGHGTFLPDTGLCSCDPSWTGHDCSIEICAADCGGHG 737
    |||
Db 413 KKGWKGPDCATMDQDALQCLPDCSGHGTFDLDTQTCTCEAKWSGDDCSKELCLDLCGQH 472

Qy 738 VCVGGTCRCEDGWMGAACDQACHPRCAEHGTCRDGKCECSPGWNGEHCTIAHVLDRVVK 797
    |||
Db 473 RCEGDACACDPEWGGEYCNTRLCDVRCNEHQCKNGTCLCVTGWNGKHCTI----- 523

Qy 798 EGCPLCNGNGRCTLDLNG-WHCVCQLGWRGAGCDTSMETACGDSKONDGDLVDCMDPD 856
    |||
Db 524 EGC PNSCAGHGQCRVSGEGQWECRCYEGWDGDCGIALELNCGDSKDNKDGLVDCEDPE 583

Qy 857 CCLQPLCHINPLCLGSPNPLDIIQETQVPVSQQNLHSPFYDRIKFLVGRDSTHIIPGENPF 916
    |||
Db 584 CCASHVCKTSQLCVSAPKPIDVLLRKQPPAITA---SFFERMKFLIDESLQNYAKLET F 640

Qy 917 DGGHACVIRGOVMTSDGTPLVGVNISFVNNPLFGYFISRQDGSFDLVTNGGISII LRPER 976
    |||
Db 641 NESRSAVIRGRVVTSLGMGLVGRVVS-TTTTLEGLFTRDDGWFDLMVNGGGGAVTLQFGR 699

Qy 977 APFITQEH TLWLPDRFFVMETIIMRHEENE-----IPSCDLSNFARPNPVVSPSLTS 1030
    |||
Db 700 APFRPQSRIVQVPWNEVVIIDLVMMSMSEKGLAVTTHTTCFAHDYDLMKPVVLASWKHG 759

Qy 1031 PASSCAEKGPVPEIQALQEEIISIGCKMRLSYLSRTPGYKSVLRISLTHPTIPFNLMK 1090
    |||
Db 760 FQGACPD RSAILAESQVIESLQIPGTGLNLVYHSSRAAGYLSTIKLQLTDPDVIPTSLHL 819

Qy 1091 VHLMWAVEGRLFRKWFAAAPDLSYYFIWDKTDVYNQKVFGLSEAFVSVGYEYESCPDLIL 1150
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Db 820 IHLRITIEGILFERIFEADPGIKFTYAWNRLNIYRQVYGVTTAVVKVGYQVTDCTD-IV 878  
QY 1151 WEKRTTVLQGYEIDASKLGWSLDKXHALNIQSGLILKXNGENQFVSQQPPVIGSIMNG 1210  
Db 879 WDIQTTLSGHDMSISEVGGWNLDIHHRYNFHEGILQKGDGNSIYLNRKPRILITMGDG 938  
QY 1211 RRRSISCPSCNGLADGNKLLAPVALTCGSDGSLYVGDENYIRRIFFPSGNVTNILELRNKD 1270  
Db 939 HQRPLECPDCGOATKORLLAPVALAAPDGSFLVGFENYIRRIIMTDGSI RTVVKL---- 994  
QY 1271 FRHSHSPAHKYYLATDPMGAVFLSDSNSRRVFKIKSTVVVKDLVKNSEVVAGTDQCCLP 1330  
Db 995 --NATRVSYRYHMAISPLDGTLYVSDPESHQIIRVRDITNDYSQPELNWEAVVSGGERCLP 1052  
QY 1331 FDDTRCGDGGKATEATLNPRTGTVDKFGLIYFVDTMIRRIDQNGIISTLLGSNDLTSA 1390  
Db 1053 GDEAHCGDGALAKDAKLAYPKGIAISSDNILYFADGTNIRMVDRDGI VSTLIGNHMHKSH 1112  
QY 1391 -RPLSCDSVMDISQVRLEWPTDLAINPMDNSLYVLNPNVVLQISENHQVRI VAGRPMHCQ 1449  
Db 1113 WKPIPCEGTLKLEEMHLRWPTELAVSPMDNTLHIIDHMLRMTPDGRVRVRISGRPLHCA 1172  
QY 1450 VPGIDHFLLSKVAIHATLESATALAVSHNGVLVYIAETDEKKINRIRQVTTSGEISLVAGA 1509  
Db 1173 TASTAYD--TDLATHATLVMPQSIAGFPLGELYVAESDSQRINRVRVIGTDGRIAPFAGA 1230  
QY 1510 PSGCDCKNDANCDFSGDDGYAKDAKALNTPTSSLAVCADGELYVADLGNIRIFIRKNKPF 1569  
Db 1231 ESKCNCL-ERGCDCFEAEHYLA TSAKFNTIAALAVTPDSHVHIADQANYRIKSVMSIPE 1289  
QY 1570 LNTQNMVELSSPIDQELYLFDTGKHLYTQSLPTGDLYNFTY--TG DGDITLITDNNG 1626  
Db 1290 ASPREYEIYAPDMQOEIYIFNRFQGVSTRNILTGETYVFTYNVNTSNGKLSVTDAAG 1349  
QY 1627 NMVNVRRDSTGMPLWLVPDQGVYVVTMGTNSALKSVTTQGHELAMMTYHGN SGILLATKS 1686  
Db 1350 NKVFLLRDYTSQVNSIENTKGQKCRLMTRMKMLHELSTPDNYNVTYEHGPTGLLRTKL 1409  
QY 1687 NENGWTTFEYDSFGRLTNVPTPTGOVSSFRSDTD-SSVHVQVETSSKDDVTITNLSAS 1745  
Db 1410 DSTGRSYVNYDEFGRLTSAVTPTRVIELSFDLSVKGAQVKVSENAQKEM-----SLLIQ 1465  
QY 1746 GAFYTLLODQVRNSYYIGADGSLRLLLLANGMEVALQTEPHLLAGTVNPTVG-----KR 1798  
Db 1466 GATVIVRNGAAESRTTVDMDGSTTSITPWGHNLMQMEVAPYTI LAEQSPLLGESYPVPAKQ 1525  
QY 1799 NVTLPIDNGLNLVEWR-----QRKEQARG---QVTVFGRRLRVHNRNLLSILD FDRV 1846  
Db 1526 RTEIAGDLA-NRFEWRYFVRBQQPLQAGKQSKGPPRPYTEVGRKLRVNGDNVLTLEYDRE 1584  
QY 1847 TRTEKIYDDHRKFTLRILYDQAGRPSLWSPSSRLNG----VNVYTSPPGGYIAGIQGIMS 1902  
Db 1585 TQSVVVMVDDKQELLNVTYDRTSRPISFRPQS---GDYAVVDLEYDRFGR LVSWKGVQLQ 1641  
QY 1903 ERNEYDQAGRITSRIFADGKTWSYTYLEK--SMVLLHSQRQ--YIFEFDKNDRLSSVTM 1958  
Db 1642 EAYSFDRNGRLNEIKYGDGSTMVYAFKDMFGSLPLKVTPRRSDYLLQYDDAGALQSLTT 1701  
QY 1959 P--NVARQTLETIRSVGYRNIIYQPPEGNASVIQDFTEDGHLHLTFYLGTRRRVIYKYGK 2016  
Db 1702 PRGHIHAFSLQT--SLGFFKYQYYSPINRHPFEILYNDEGQILAKIHPHQS GKVAFVHDT 1759  
QY 2017 LSKLAETLYDTTKVSFTYDETAGMLKTINLQNEGTCTIRYRQIGPLIDRQIFRF-TEEG 2075  
Db 1760 AGRLETILAGLSSTHYTYQDITSLVKSVEVQEPGFELRFBFKYHAGILKOEKLRFGSKNS 1819  
QY 2076 MVNARFDYNDNSFRVTSMQAVINETPLPIDLYRYDDVSGKTEQFGKFGVIYYDI----N 2131  
Db 1820 LASARYKYAYDGNARLSGIEMAIDDKELPTTRYKYKYSQNLQGLE-----VVQDLKITRN 1872  
QY 2132 QITTAVMTHTKHF-----DAYGRMKVEQYEIFRSLMYMTVQYDNMGRVVKELKVG P 2185

Db 1873 AFNRTVIODSAKQFAIVDYDQHGVRKSVLMNVKNIDVFRLELDYDLNRRIKSQKTTFG- 1931  
QY 2186 YANTTRYSEYDADGQ-LQTVSINDKPLWRYSYDLNGN-LHLLSPGNSARLTPLRYDIRD 2243  
Db 1932 -RSTAFDKINYNADGHVVEVLGTNN---WKYLFDENGNTVGVVDQGEKEN---LGYD IGD 1984  
QY 2244 RITRLGDVQY-KMDEDGFLRQGGDIFEVNSAGLLIKAYNRA--GSWSVRYRYDGLGRRV 2300  
Db 1985 RVIKVGDFEFNNYDARGFVVKRGEQKYRYNNRQGLIHSFERERFQSW---YY YDDRSRLV 2041  
QY 2301 SSKSSHSHLQFFYADLTNPTKVTHLYNHSSEITSLYYDLQGLHFAMELSSGDEFYIAC 2360  
Db 2042 AWHDNKGNTTQYVYANPRTPHLVTHVHPKISRMTKMLFYDDDRDMLIALE-HEDQRYYVAT 2100  
QY 2361 DNIGTPLAVESGTGLMIKQILYTAYGEIYMDTNPNFQIIIGYHGGLYDPLTKLVHMGRRD 2420  
Db 2101 DQGSPLAFFDQNGSIVKEMKRTPFGRIIKDTKPEFFVPIDFHGGLIDPHTKLVYTEQRQ 2160  
QY 2421 YDVLAGRWTSPDHELWKHLSSSNVMPFN--LYMFKNNPNPISNSQDIKCFMTD VNSSLTTF 2478  
Db 2161 YDPHVQWMT-----LWETLATEMSHPTDVFYRYHNNDPI-NPNKPQNTMIDLD SWLQLF 2216  
QY 2479 GFQLHNVIPGYPKPMDMAMEPSYELIHTQMTQCEWDNSKS-----ILGVOCEVQKQLK 2531  
Db 2217 GYDLNN-----MOSSRYTKLAQYTPQASIKSNTLAPDFGVISGLECIVEK--- 2261  
QY 2532 AFVTLERFDQLYGSTITSCQAPKTKKFASSGS----VFGKGVKFAKDKGRVTTDIISVA 2587  
Db 2262 --TSEKFSDFDFVPKPLLKTEPKMRNLLPRVSYRRGVFGEVLLSRIGGRALVSVWDGS 2318  
QY 2588 N---EDGRRVAAILNHAHYLENLHFTIDGVDPHYFVKPGPSEGD LAILGLSGGRTLENG 2644  
Db 2319 NSVVQD--VVSSVFNNSYFLD-LHFSIHDQDVFYFVK---DNVLKLRDDNEELRRLGGM 2371  
QY 2645 VNVTVSQINTVLNGRTRRYTDIQLQYGALCLNTRYGTTLDEEKARVLELARQAVRQAWA 2704  
Db 2372 FNISTHEISDHGSSAAK---ELRLHGPDAAVVIKYGVDPEQERHRLKHAKKRAVERAWE 2428  
QY 2705 REQRLREGEEGLRAWTEGEKQQVLSTGRVQVDCGFFVISVEQYPELSDSANNIHFMRQS 2764  
Db 2429 LEKQLVAAAGFQGRGDWTEEEKEELVQHGVDGWNIGIDIHSIHKYPQLADDPGNVAFORDA 2488  
QY 2765 EMGRR 2769  
Db 2489 KRKR 2493

RESULT 12

US-11-096-051-20  
; Sequence 20, Application US/11096051  
; Publication No. US20050244868A1  
; GENERAL INFORMATION:  
; APPLICANT: Kekuda, Ramesh  
; APPLICANT: MacLachlan, Timothy K  
; APPLICANT: Rastelli, Luca  
; APPLICANT: Vernet, Corine  
; APPLICANT: Eettenberg, Seth  
; TITLE OF INVENTION: Ten-M3 Polypeptides and Polynucleotides and their Methods of Use  
; FILE REFERENCE: Attorney Docket No. Cura 967  
; CURRENT APPLICATION NUMBER: US/11/096,051  
; CURRENT FILING DATE: 2005-03-30  
; PRIOR APPLICATION NUMBER: 10/038,854  
; PRIOR FILING DATE: 2001-12-31  
; PRIOR APPLICATION NUMBER: 10/455,772  
; PRIOR FILING DATE: 2003-06-04  
; PRIOR APPLICATION NUMBER: 60/557,978  
; PRIOR FILING DATE: 2004-03-30  
; NUMBER OF SEQ ID NOS: 38  
; SOFTWARE: CuraSeqList version 0.1  
; SEQ ID NO 20  
; LENGTH: 862  
; TYPE: PRT  
; ORGANISM: Homo sapiens

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US-11-096-051-20
Query Match      22.0%;   Score 3276;   DB 7;   Length 862;
Best Local Similarity 67.3%;   Pred. No. 2.4e-204;
Matches 567;   Conservative 94;   Mismatches 160;   Indels 22;   Gaps 3;

QY 369 NWHLQPMEGQMYE---ITEDTASSWPVPVPTDVSLYPSSGGTGLETPDRKGKGTTEGKPSFFF 425
Db 17 NWQLQQTENDTFENGKVNSDT-----MPTNTVSLPSG-----DNGKLGFT 57

QY 426 PEDSFIDSGEIDVGRRASQKIPPGTFWRSQVFIDHPVHLKFNVSIGKAAALVGIYGRKGLP 485
Db 58 QENNTIDSGELDIGRRALQEIPIPGIFWRSQQLFIDQPQFLKFNISLQKDALIGVYGRKGLP 117

QY 486 PSHTQDFVELLDGRRLLLTQEARSLGTPRQSRGTVPSPSSHETGFIQYLDSGIWHLAFYN 545
Db 118 PSHTQYDFVELLDGSRLLIAREQSRSLLETERAGRQARSVSLHEAGFIQYLDSGIWHLAFYN 177

QY 546 DGKESEVVSFLTTAIESVDNCPNSCYNGNDCISGTCHCFLGFLGPDGGRASCPVLCSGNG 605
Db 178 DGKNAEQVSFNTIVIESVVECPRNCHNGECVSGTCHCFPGFLGPDCSRACPVLCSGNG 237

QY 606 QYMKGRCLCHSGWKGAECDVPTNQCIDVACSNHGTCTGTCTICNPGYKGESCEEVDCMDP 665
Db 238 QYSGRCLCFSGWKGTEDVPTTQCIDPQCGGRGICIMGSCACNSGYKGESCEEADCIDP 297

QY 666 TCSGRGVCVRGECHCFVGGWGTNCETPRATCLDQCSGHGTFLPDTGLCSCDPSWTGHDCS 725
Db 298 GCSNHGVCIHGECHCSPGWGGSNCEILKTMCPDQCSGHGTYLQESGSCDTPNWTGPDCS 357

QY 726 IEICAADCGGHGVCVGGTCRCEDGWMGAACDQORACHPRCAEHGTCRDGKCECSPGWNGEH 785
Db 358 NEICSVDCSGSHGVCMGGTCTCRCEEGWTGPACNQORACHPRCAEHGTCRDGKCECSPGWNGEH 417

QY 786 CTIAHYLDRVVKEGCPGLCNGNRCRTLQNGWHCVQCLGWRGAGCDTSMETACGDSKND 845
Db 418 CTIAHYLDKIIVKEGCPGLCNSNGRCTLQNGWHCVQCPGWRGAGCDVAMETLCTDSKNE 477

QY 846 GDGLVDCMDPDCCLQPLCHINPLCLGSPNPLDIIQETQVPVSQQNLHSFYDRIKFLVGRD 905
Db 478 GDGLIDCMDPDCCLQSSCONQPYCRGLPDPQDIIISQLSPSQAAKSFYDRISFLIGSD 537

QY 906 STHIIPGENPFDGGHACVIRQVMTSDGTPLVGNVISFVNPLFGYTIISRQDGSFDLVN 965
Db 538 STHVIPGESPFNKSLASVIRGQVLTADGTPLIGVNVSFHYPEVGYTITRQDGMFDLVAN 597

QY 966 GGISIILRRERAPFITQEHTLWLPWDRFFVVMETIIMRHEENEIPSCDLSNFARPNPVVSP 1025
Db 598 GGASLTLVFERSPFLOTQYHTVWIPWNVFVYVMDTLVMKKEENDIPSCDLSGFVRPNPIVS 657

QY 1026 SPLTSFASSCAEKGPVPEIQALQEEISISGCKMRLSYLSRTPGYKSVLRISLTHPTIP 1085
Db 658 SPLSTFFRSPEDSPIIPETQVLHETTIPGTDLKL SYLSSRAAGYKSVLKITMTQSIIP 717

QY 1086 FNLMKVHLMVAVEGRLEFRKWFAPADLSYYFIWDKTDVYNQKVFGLSEAFVSUGYEYESC 1145
Db 718 FNLMKVHLMVAVVGRLFQKWFAPASPNLAYTFIWDKTDAYNQKVYGLSEAVVSUGYEYESC 777

QY 1146 PDLILWEKRTTVLQGYEIDASKLGWSLDKHHALNIQSGLIHKNGENQFVSQQPPVIGS 1205
Db 778 LDLTLWEKRTAILQGYELDASNMGWGTLDKHHVLDVQNGILYKNGENQFISQQPPVVS 837

QY 1206 IMG 1208
Db 838 LEG 840

RESULT 13
US-11-096-051-6
; Sequence 6, Application US/11096051
; Publication No. US20050244868A1
; GENERAL INFORMATION:
; APPLICANT: Kekuda, Ramesh
```

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; APPLICANT: MacLachlan, Timothy K
; APPLICANT: Rastelli, Luca
; APPLICANT: Vernet, Corine
; APPLICANT: Ettenberg, Seth
; TITLE OF INVENTION: Ten-M3 Polypeptides and Polynucleotides and their Methods of Use
; FILE REFERENCE: Attorney Docket No. Cura 967
; CURRENT APPLICATION NUMBER: US/11/096,051
; CURRENT FILING DATE: 2005-03-30
; PRIOR APPLICATION NUMBER: 10/038,854
; PRIOR FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 10/455,772
; PRIOR FILING DATE: 2003-06-04
; PRIOR APPLICATION NUMBER: 60/557,978
; PRIOR FILING DATE: 2004-03-30
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 6
; LENGTH: 821
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-11-096-051-6

Query Match      22.0%;   Score 3270;   DB 7;   Length 821;
Best Local Similarity 67.4%;   Pred. No. 5.5e-204;
Matches 566;   Conservative 93;   Mismatches 159;   Indels 22;   Gaps 3;

QY 369 NWHLQPMEGQMYE---ITEDTASSWPVPVPTDVSLYPSSGGTGLETPDRKGKGTTEGKPSFFF 425
Db 1 NWQLQQTENDTFENGKVNSDT-----MPTNTVSLPSG-----DNGKLGFT 41

QY 426 PEDSFIDSGEIDVGRRASQKIPPGTFWRSQVFIDHPVHLKFNVSIGKAAALVGIYGRKGLP 485
Db 42 QENNTIDSGELDIGRRALQEIPIPGIFWRSQQLFIDQPQFLKFNISLQKDALIGVYGRKGLP 101

QY 486 PSHTQDFVELLDGRRLLLTQEARSLGTPRQSRGTVPSPSSHETGFIQYLDSGIWHLAFYN 545
Db 102 PSHTQYDFVELLDGSRLLIAREQSRSLLETERAGRQARSVSLHEAGFIQYLDSGIWHLAFYN 161

QY 546 DGKESEVVSFLTTAIESVDNCPNSCYNGNDCISGTCHCFLGFLGPDGGRASCPVLCSGNG 605
Db 162 DGKNAEQVSFNTIVIESVVECPRNCHNGECVSGTCHCFPGFLGPDCSRACPVLCSGNG 221

QY 606 QYMKGRCLCHSGWKGAECDVPTNQCIDVACSNHGTCTGTCTICNPGYKGESCEEVDCMDP 665
Db 222 QYSGRCLCFSGWKGTEDVPTTQCIDPQCGGRGICIMGSCACNSGYKGESCEEADCIDP 281

QY 666 TCSGRGVCVRGECHCFVGGWGTNCETPRATCLDQCSGHGTFLPDTGLCSCDPSWTGHDCS 725
Db 282 GCSNHGVCIHGECHCSPGWGGSNCEILKTMCPDQCSGHGTYLQESGSCDTPNWTGPDCS 341

QY 726 IEICAADCGGHGVCVGGTCRCEDGWMGAACDQORACHPRCAEHGTCRDGKCECSPGWNGEH 785
Db 342 NEICSVDCSGSHGVCMGGTCTCRCEEGWTGPACNQORACHPRCAEHGTCRDGKCECSPGWNGEH 401

QY 786 CTIAHYLDRVVKEGCPGLCNGNRCRTLQNGWHCVQCLGWRGAGCDTSMETACGDSKND 845
Db 402 CTIAHYLDKIIVKEGCPGLCNSNGRCTLQNGWHCVQCPGWRGAGCDVAMETLCTDSKNE 461

QY 846 GDGLVDCMDPDCCLQPLCHINPLCLGSPNPLDIIQETQVPVSQQNLHSFYDRIKFLVGRD 905
Db 462 GDGLIDCMDPDCCLQSSCONQPYCRGLPDPQDIIISQLSPSQAAKSFYDRISFLIGSD 521

QY 906 STHIIPGENPFDGGHACVIRQVMTSDGTPLVGNVISFVNPLFGYTIISRQDGSFDLVN 965
Db 522 STHVIPGESPFNKSLASVIRGQVLTADGTPLIGVNVSFHYPEVGYTITRQDGMFDLVAN 581

QY 966 GGISIILRRERAPFITQEHTLWLPWDRFFVVMETIIMRHEENEIPSCDLSNFARPNPVVSP 1025
Db 582 GGASLTLVFERSPFLOTQYHTVWIPWNVFVYVMDTLVMKKEENDIPSCDLSGFVRPNPIVS 641

QY 1026 SPLTSFASSCAEKGPVPEIQALQEEISISGCKMRLSYLSRTPGYKSVLRISLTHPTIP 1085
Db 642 SPLSTFFRSPEDSPIIPETQVLHETTIPGTDLKL SYLSSRAAGYKSVLKITMTQSIIP 701
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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 11, 2005, 04:40:53 ; Search time 48 Seconds  
(without alignments)  
4769.353 Million cell updates/sec

Title: US-10-029-020-14  
Perfect score: 14887  
Sequence: 1 MDVKERKPYRSLTRRRDAER.....ELSDSANNIHFMRQSEMGRR 2769

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*  
1: /cgn2\_6/ptodata/1/iaa/5\_COMB.pep:\*  
2: /cgn2\_6/ptodata/1/iaa/6\_COMB.pep:\*  
3: /cgn2\_6/ptodata/1/iaa/H\_COMB.pep:\*  
4: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep:\*  
5: /cgn2\_6/ptodata/1/iaa/RE\_COMB.pep:\*  
6: /cgn2\_6/ptodata/1/iaa/baCkfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	2989	20.1	768	2	US-08-891-845-2 Sequence 2, Appli
2	2989	20.1	768	2	US-09-514-573-2 Sequence 2, Appli
3	2989	20.1	768	2	US-10-290-578-2 Sequence 2, Appli
4	2982	20.0	560	2	US-08-891-845-4 Sequence 4, Appli
5	2982	20.0	560	2	US-09-514-573-4 Sequence 4, Appli
6	2982	20.0	560	2	US-10-290-578-4 Sequence 4, Appli
7	1575	10.6	501	2	US-08-891-845-10 Sequence 10, Appl
8	1575	10.6	501	2	US-09-514-573-10 Sequence 10, Appl
9	1575	10.6	501	2	US-10-290-578-10 Sequence 10, Appl
10	649.5	4.4	2200	2	US-09-796-575-2 Sequence 2, Appli
11	648.5	4.4	2199	2	US-08-793-273C-2 Sequence 2, Appli
12	648.5	4.4	2199	4	PCT-US95-11684-2 Sequence 2, Appli
13	641	4.3	1810	2	US-08-793-273C-4 Sequence 4, Appli
14	641	4.3	1810	4	PCT-US95-11684-4 Sequence 4, Appli
15	585	3.9	2254	2	US-09-949-016-9270 Sequence 9270, Ap
16	440	3.0	2471	1	US-08-185-432-16 Sequence 16, Appl
17	440	3.0	2471	1	US-08-083-590A-19 Sequence 19, Appl
18	440	3.0	2471	2	US-08-532-384-19 Sequence 19, Appl
19	440	3.0	2471	2	US-08-899-232-1 Sequence 1, Appli
20	440	3.0	2471	2	US-09-121-457-1 Sequence 1, Appli
21	438.5	2.9	2703	1	US-08-185-432-19 Sequence 19, Appl
22	438.5	2.9	2703	2	US-08-899-232-4 Sequence 4, Appli
23	438.5	2.9	2703	2	US-09-121-457-4 Sequence 4, Appli
24	429	2.9	2523	1	US-08-185-432-18 Sequence 18, Appl
25	429	2.9	2523	2	US-08-899-232-3 Sequence 3, Appli
26	429	2.9	2523	2	US-09-121-457-3 Sequence 3, Appli
27	428	2.9	2556	1	US-08-083-590A-20 Sequence 20, Appl

28	428	2.9	2556	2	US-08-532-384-20 Sequence 20, Appl
29	425	2.9	494	2	US-09-949-002-373 Sequence 373, App
30	425	2.9	574	2	US-09-949-002-497 Sequence 497, App
31	423	2.8	1193	1	US-08-400-159-10 Sequence 10, Appl
32	423	2.8	1193	2	US-08-611-729A-10 Sequence 10, Appl
33	423	2.8	1193	2	US-09-195-524-10 Sequence 10, Appl
34	423	2.8	1193	2	US-09-310-685-8 Sequence 8, Appli
35	419.5	2.8	1219	2	US-08-882-046-5 Sequence 5, Appli
36	419.5	2.8	1219	2	US-09-566-047-5 Sequence 5, Appli
37	411.5	2.8	1036	2	US-09-068-740A-6 Sequence 6, Appli
38	411.5	2.8	1067	2	US-09-579-536C-18 Sequence 18, Appl
39	411.5	2.8	1187	2	US-09-068-740A-7 Sequence 7, Appli
40	411.5	2.8	1208	2	US-09-199-865-1 Sequence 1, Appli
41	411.5	2.8	1208	2	US-10-213-329-1 Sequence 1, Appli
42	411.5	2.8	1218	2	US-08-882-046-2 Sequence 2, Appli
43	411.5	2.8	1218	2	US-09-068-740A-11 Sequence 11, Appl
44	411.5	2.8	1218	2	US-09-566-047-2 Sequence 2, Appli
45	411.5	2.8	1218	2	US-09-917-254-85 Sequence 85, Appl

ALIGNMENTS

RESULT 1  
US-08-891-845-2  
; Sequence 2, Application US/08891845  
; Patent No. 6096873  
; GENERAL INFORMATION:  
; APPLICANT: Schaefer, Gabriele M.  
; APPLICANT: Sliwowski, Mark  
; TITLE OF INVENTION: Gamma-Heregulin  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 460 Point San Bruno Blvd  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPatin (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/891,845  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/021640  
; FILING DATE: 07/12/96  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Lee, Wendy M.  
; REGISTRATION NUMBER: 40,378  
; REFERENCE/DOCKET NUMBER: P1043  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415/225-1994  
; TELEFAX: 415/952-9881  
; TELEX: 910/371-7168  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 768 amino acids  
; TYPE: Amino Acid  
; TOPOLOGY: Linear  
US-08-891-845-2

Query Match 20.1%; Score 2989; DB 2; Length 768;  
Best Local Similarity 76.5%; Pred. No. 9.8e-215;  
Matches 598; Conservative 22; Mismatches 84; Indels 78; Gaps 10;  
QY 1 MDVKERKPYRSLTRRRDAERRYTTSSSADSEEGKAPQKSYSSSETLKAYDQDARLAYGSRV 60  
Db 1 MDVKERKPYRSLTRRRDAERRYTTSSSADSEEGKAPQKSYSSSETLKAYDQDARLAYGSRV 60



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QY      61 KDIVPQEAEEFCRTGANFTLRELGLEEVTPPHGTLTYRTDGLPQC GYSMGAGSDADMEAD 120
Db      61 KDIVPQEAEEFCRTGANFTLRELGLEEVTPPHGTLTYRTDGLPQC GYSMGAGSDADMEAD 120
QY     121 TVLSPEHPVRLWGRSTRSGRSSCLSSRANSNLTLTDEHENTETDHPGGLQN HARLRTPP 180
Db     121 TVLSPEHPVRLWGRSTRSGRSSCLSSRANSNLTLTDEHENTETDHPGGLQN HARLRTPP 180
QY     181 PPLSHAHTPNQHHAAASINSLNRGNFTPRSNPSPAPTDHSLSGEPPAGGAQEP AHAQENWL 240
Db     181 PPLSHAHTPNQHHAAASINSLNRGNFTPRSNPSPAPTDHSLSGEPPAGGAQEP AHAQENWL 240
QY     241 LNSNIPLETRNLGKQPFGLTQDNLIEMDILGASRHDGAYSDGHFLFKPGGTSPLFCTTS 300
Db     241 LNSNIPLETRNLGKQPFGLTQDNLIEMDILGASRHDGAYSDGHFLFKPGGTSPLFCTTS 300
QY     301 PGYPLTSSTVYSPPPRPLPRSTFARPAFNLKPKSKYCNWKCAALSAIVISATLVILLAYF 360
Db     301 PGYPLTSSTVYSPPPRPLPRSTFARPAFNLKPKSKYCNWKCAALSAIVISATLVILLAYF 360
QY     361 VAMHLFGLNWHLQPMEGQMYEITEDTASSWPVPTDVSLYPSGGTGLET PDRKKGTTGCK 420
Db     361 VAMHLFGLNWHLQPMEGQMYEITEDTASSWPVPTDVSLYPSGGTGLET PDRKKGTTGCK 420
QY     421 PSSFFPEDSFIDSGEIDVGRRASQKIPPGTFWRSQVFI DHPVHLKFNVSGLKAAALVGIY 480
Db     421 PSSFFPEDSFIDSGEIDVGRRASQKIPPGTFWRSQVFI DHPVHLKFNVSGLKAAALVGIY 480
QY     481 RKGLPPSHTQDFVELLDGRRLLTQEARSLGTPRQSRGTVP PSSHETGFIQYLDSGIWH 540
Db     481 RKGLPPSHTQDFVELLDGRRLLTQEARSLGTPRQSRGTVP PSSHETGFIQYLDSGIWH 540
QY     541 LAFYNDGKESEVVSFLTITAI---ESVDNCPSN CYNGD-----CISGTCHCFLGFL---- 588
Db     541 LAFYNDGKESEVVSFLTITAIALPRLKEMKQESAAGSKLVLCRETSS EYSSLRFKWPKN 600
QY     589 GPDCCGRASCP-----VLCSGNGQYMKGRCLCHSGWKGAEC DVPTNQ 630
Db     601 GNELNRKNKPQNIKIQKPKGKSELINKASLADSGEYM-----CKVISKLG 646
QY     631 IDVACSNHGTCTGTICINPGYKGESCEEVDCMDPTCSGRGV CVRGECHCFVWGWTNCE 690
Db     647 NDSASAN---ITIV-----ESNEIITGMPASTEGAYVSSESP IRISVSTEGANTS 693
QY     691 TPRAT-----CLDQ-----CSGHGTFL-----PDTGLCSCDPSW TGHDCSIEIC 729
Db     694 SSTSTSTGTSHLVKCAEKEKTEFCVNGGECFMVKDLSNP SRYLCKCPNEFTGDRCONYVM 753
QY     730 AA 731
Db     754 AS 755
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RESULT 2
US-09-514-573-2
; Sequence 2, Application US/09514573
; Patent No. 6500941
; GENERAL INFORMATION:
; APPLICANT: Schaefer, Gabriele M.
; APPLICANT: Slikowski, Mark
; TITLE OF INVENTION: Gamma-Herregulin
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
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;
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/514,573
; FILING DATE: 28 FEB 2000
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/891845
; FILING DATE: 10 JULY 1997
; APPLICATION NUMBER: 60/021640
; FILING DATE: 07/12/96
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P1043
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 768 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
;
US-09-514-573-2

Query Match      20.1%; Score 2989; DB 2; Length 768;
Best Local Similarity 76.5%; Pred. No. 9.8e-215;
Matches 598; Conservative 22; Mismatches 84; Indels 78; Gaps 10;

QY      1 MDVKERKPYRSLTRRRDAERRY TSSSADSEEGKAPQKSYSSSETLKAYDQDARLAYGSRV 60
Db      1 MDVKERKPYRSLTRRRDAERRY TSSSADSEEGKAPQKSYSSSETLKAYDQDARLAYGSRV 60
QY     61 KDIVPQEAEEFCRTGANFTLRELGLEEVTPPHGTLTYRTDGLPQC GYSMGAGSDADMEAD 120
Db     61 KDIVPQEAEEFCRTGANFTLRELGLEEVTPPHGTLTYRTDGLPQC GYSMGAGSDADMEAD 120
QY     121 TVLSPEHPVRLWGRSTRSGRSSCLSSRANSNLTLTDEHENTETDHPGGLQN HARLRTPP 180
Db     121 TVLSPEHPVRLWGRSTRSGRSSCLSSRANSNLTLTDEHENTETDHPGGLQN HARLRTPP 180
QY     181 PPLSHAHTPNQHHAAASINSLNRGNFTPRSNPSPAPTDHSLSGEPPAGGAQEP AHAQENWL 240
Db     181 PPLSHAHTPNQHHAAASINSLNRGNFTPRSNPSPAPTDHSLSGEPPAGGAQEP AHAQENWL 240
QY     241 LNSNIPLETRNLGKQPFGLTQDNLIEMDILGASRHDGAYSDGHFLFKPGGTSPLFCTTS 300
Db     241 LNSNIPLETRNLGKQPFGLTQDNLIEMDILGASRHDGAYSDGHFLFKPGGTSPLFCTTS 300
QY     301 PGYPLTSSTVYSPPPRPLPRSTFARPAFNLKPKSKYCNWKCAALSAIVISATLVILLAYF 360
Db     301 PGYPLTSSTVYSPPPRPLPRSTFARPAFNLKPKSKYCNWKCAALSAIVISATLVILLAYF 360
QY     361 VAMHLFGLNWHLQPMEGQMYEITEDTASSWPVPTDVSLYPSGGTGLET PDRKKGTTGCK 420
Db     361 VAMHLFGLNWHLQPMEGQMYEITEDTASSWPVPTDVSLYPSGGTGLET PDRKKGTTGCK 420
QY     421 PSSFFPEDSFIDSGEIDVGRRASQKIPPGTFWRSQVFI DHPVHLKFNVSGLKAAALVGIY 480
Db     421 PSSFFPEDSFIDSGEIDVGRRASQKIPPGTFWRSQVFI DHPVHLKFNVSGLKAAALVGIY 480
QY     481 RKGLPPSHTQDFVELLDGRRLLTQEARSLGTPRQSRGTVP PSSHETGFIQYLDSGIWH 540
Db     481 RKGLPPSHTQDFVELLDGRRLLTQEARSLGTPRQSRGTVP PSSHETGFIQYLDSGIWH 540
QY     541 LAFYNDGKESEVVSFLTITAI---ESVDNCPSN CYNGD-----CISGTCHCFLGFL---- 588
Db     541 LAFYNDGKESEVVSFLTITAIALPRLKEMKQESAAGSKLVLCRETSS EYSSLRFKWPKN 600
QY     589 GPDCCGRASCP-----VLCSGNGQYMKGRCLCHSGWKGAEC DVPTNQ 630
Db     601 GNELNRKNKPQNIKIQKPKGKSELINKASLADSGEYM-----CKVISKLG 646
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Db 481 RKGLPPSHTQDFVELLDGRRLLTQEARSLGTPRQSRGTVPPSSHETGFIQYLDSGIWH 540  
Qy 541 LAFYNDGKESEVVSFLTITAI 560  
Db 541 LAFYNDGKESEVVSFLTITAI 560

RESULT 6

US-10-290-578-4  
; Sequence 4, Application US/10290578  
; Patent No. 6916624  
; GENERAL INFORMATION:  
; APPLICANT: Schaefer, Gabriele M.  
; Sliwkowski, Mark  
; TITLE OF INVENTION: Gamma-Heregulin  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 460 Point San Bruno Blvd  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPatIn (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/290,578  
; FILING DATE: 08-No. 6916624-2002  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/891,845  
; FILING DATE: <Unknown>  
; APPLICATION NUMBER: 60/021640  
; FILING DATE: 12-Jul-96  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Lee, Wendy M.  
; REGISTRATION NUMBER: 40,378  
; REFERENCE/DOCKET NUMBER: P1043  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415/225-1994  
; TELEFAX: 415/952-9881  
; TELEX: 910/371-7168  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 560 amino acids  
; TYPE: Amino Acid  
; TOPOLOGY: Linear  
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:  
US-10-290-578-4

Query Match 20.0%; Score 2982; DB 2; Length 560;  
Best Local Similarity 99.8%; Pred. No. 1.9e-214;  
Matches 559; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MDVKERKPYRSLTRRRDAERYTSSSADSEEGKAPQKSYSSSETLKAYDQDARLAYGSRV 60  
Db 1 MDVKERKPYRSLTRRRDAERYTSSSADSEEGKAPQKSYSSSETLKAYDQDARLAYGSRV 60  
Qy 61 KDIVPQEAEEFCRTGANFTLRELGLEEVTPPHGTLTYRTDGLPCQCGYSMGAGSDADMEAD 120  
Db 61 KDIVPQEAEEFCRTGANFTLRELGLEEVTPPHGTLTYRTDGLPHCGYSMGAGSDADMEAD 120  
Qy 121 TVLSPEHPVRLWGRSTRSGRSSCLSSRANSNLTLDTEHENTETDHPGGLQNHARLRTPP 180  
Db 121 TVLSPEHPVRLWGRSTRSGRSSCLSSRANSNLTLDTEHENTETDHPGGLQNHARLRTPP 180  
Qy 181 PPLSHAHTPNQHHAA SINSLNRGNFTPRSNPSPAPTDHLSLSGEPPAGGAQEPAAHAQENWL 240  
Db 181 PPLSHAHTPNQHHAA SINSLNRGNFTPRSNPSPAPTDHLSLSGEPPAGGAQEPAAHAQENWL 240

Qy 241 LNSNIPLERNLGKQPFLGTLQDNLIEMDILGASRHDGAYSDGHFLFKPGCTSPFLCTTS 300  
Db 241 LNSNIPLERNLGKQPFLGTLQDNLIEMDILGASRHDGAYSDGHFLFKPGCTSPFLCTTS 300  
Qy 301 PGYPLTSSTVISPPPRPLPRSTFARPAFNLKKPSKYNWKCAALSAIVISATLVILLAYF 360  
Db 301 PGYPLTSSTVISPPPRPLPRSTFARPAFNLKKPSKYNWKCAALSAIVISATLVILLAYF 360  
Qy 361 VAMHLFGLNWLQPMEGQMEYEITEDTASSWPVPTDVSLYPSGGTGLETDRKGKGTTEGK 420  
Db 361 VAMHLFGLNWLQPMEGQMEYEITEDTASSWPVPTDVSLYPSGGTGLETDRKGKGTTEGK 420  
Qy 421 PSSFFPEDSFIDSGEIDVGRRASQKIPPGTFWRSQVFIHVPVHLKFNVSLGKAALVGIYG 480  
Db 421 PSSFFPEDSFIDSGEIDVGRRASQKIPPGTFWRSQVFIHVPVHLKFNVSLGKAALVGIYG 480  
Qy 481 RKGLPPSHTQDFVELLDGRRLLTQEARSLGTPRQSRGTVPPSSHETGFIQYLDSGIWH 540  
Db 481 RKGLPPSHTQDFVELLDGRRLLTQEARSLGTPRQSRGTVPPSSHETGFIQYLDSGIWH 540  
Qy 541 LAFYNDGKESEVVSFLTITAI 560  
Db 541 LAFYNDGKESEVVSFLTITAI 560

RESULT 7

US-08-891-845-10  
; Sequence 10, Application US/08891845  
; Patent No. 6096873  
; GENERAL INFORMATION:  
; APPLICANT: Schaefer, Gabriele M.  
; APPLICANT: Sliwkowski, Mark  
; TITLE OF INVENTION: Gamma-Heregulin  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 460 Point San Bruno Blvd  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPatIn (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/891,845  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/021640  
; FILING DATE: 07/12/96  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Lee, Wendy M.  
; REGISTRATION NUMBER: 40,378  
; REFERENCE/DOCKET NUMBER: P1043  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415/225-1994  
; TELEFAX: 415/952-9881  
; TELEX: 910/371-7168  
; INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 501 amino acids  
; TYPE: Amino Acid  
; TOPOLOGY: Linear  
US-08-891-845-10

Query Match 10.6%; Score 1575; DB 2; Length 501;  
Best Local Similarity 64.5%; Pred. No. 4.9e-109;  
Matches 332; Conservative 22; Mismatches 83; Indels 78; Gaps 10;

Qy 268 MDILGASRHDGAYSDGHFLFKPGGTSPFLCTTSGCYPLTSSTVSPPPRPLPRSTFARPA 327

Db 1 MDILGASRHDGAYSDGHFLFKPGGTSPLFCTTSPGYPLTSSVYSPPPRPLPRSTFARPA 60

QY 328 FNLKPKSKYCNWKAALSAIVISATLVILLAYFVAMHLFGLNWHLQPMEGOMYEITEDTA 387

Db 61 FNLKPKSKYCNWKAALSAIVISATLVILLAYFVAMHLFGLNWHLQPMEGOMYEITEDTA 120

QY 388 SSWPVPTDVSLYPSGGTGLETPDRKGKGTTEGKPSFFPEDSFIDSGEIDVGRRASQKIP 447

Db 121 SSWPVPTDVSLYPSGGTGLETPDRKGKGTTEGKPSFFPEDSFIDSGEIDVGRRASQKIP 180

QY 448 PGTFWRSQVFIHDPVHLKFNVSGLKKAALVGIYGRKGLPPSHTQDFVELLDGRRLLTQEA 507

Db 181 PGTFWRSQVFIHDPVHLKFNVSGLKKAALVGIYGRKGLPPSHTQDFVELLDGRRLLTQEA 240

QY 508 RSLEGTPRQSRGTVPSSSHETGFIQYLDSGIWHLAFYNDGKESEVVSFLTTAI---ESVD 564

Db 241 RSLEGTPRQSRGTVPSSSHETGFIQYLDSGIWHLAFYNDGKESEVVSFLTTAIALPRLK 300

QY 565 NCPSNCYNGD-----CISGTCHCFLGFL---GPDCCRASCP----- 598

Db 301 EMKSQESAAGSKLVLRCTSEYSSLRFKWFKNGNELNRKNKPQNIKIQKKPGKSELRLIN 360

QY 599 -VLCSGNGQYMKGRCLCHSGWKGAECVPTNQCIDVACSNHGTCITGTICNPGYKGESC 657

Db 361 KASLADSGEYM-----CKVISKLGNDASAN---ITIV-----ESN 393

QY 658 EEVDCMDPTCSGRGVCVRGECHCFVGGTNCETPRAT-----CLDQ-----CSG 702

Db 394 EIITGMPASTEGAYVSSSEPIRISVSTEGANTSSSTSTSTTGTSHLVKCAEKEKTFVCVNG 453

QY 703 HGTFL-----PDTGLCSCDPSWTGHDCSIEICAA 731

Db 454 GECFMVKDLSNPSRYLCKPCNFTGDRCONYVMAS 488

RESULT 8

US-09-514-573-10

; Sequence 10, Application US/09514573

; Patent No. 6500941

; GENERAL INFORMATION:

; APPLICANT: Schaefer, Gabriele M.

; APPLICANT: Sliwowski, Mark

; TITLE OF INVENTION: Gamma-Heregulin

; NUMBER OF SEQUENCES: 11

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Genentech, Inc.

; STREET: 460 Point San Bruno Blvd

; CITY: South San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94080

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: WinPatin (Genentech)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/514,573

; FILING DATE: 28 FEB 2000

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/891845

; FILING DATE: 10 JULY 1997

; APPLICATION NUMBER: 60/021640

; FILING DATE: 07/12/96

; ATTORNEY/AGENT INFORMATION:

; NAME: Lee, Wendy M.

; REGISTRATION NUMBER: 40,378

; REFERENCE/DOCKET NUMBER: P1043

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415/225-1994

; TELEFAX: 415/952-9881

; TELEX: 910/371-7168

; INFORMATION FOR SEQ ID NO: 10:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 501 amino acids

; TYPE: Amino Acid

; TOPOLOGY: Linear

US-09-514-573-10

Query Match 10.6%; Score 1575; DB 2; Length 501;

Best Local Similarity 64.5%; Pred. No. 4.9e-109;

Matches 332; Conservative 22; Mismatches 83; Indels 78; Gaps 10;

QY 268 MDILGASRHDGAYSDGHFLFKPGGTSPLFCTTSPGYPLTSSVYSPPPRPLPRSTFARPA 327

Db 1 MDILGASRHDGAYSDGHFLFKPGGTSPLFCTTSPGYPLTSSVYSPPPRPLPRSTFARPA 60

QY 328 FNLKPKSKYCNWKAALSAIVISATLVILLAYFVAMHLFGLNWHLQPMEGOMYEITEDTA 387

Db 61 FNLKPKSKYCNWKAALSAIVISATLVILLAYFVAMHLFGLNWHLQPMEGOMYEITEDTA 120

QY 388 SSWPVPTDVSLYPSGGTGLETPDRKGKGTTEGKPSFFPEDSFIDSGEIDVGRRASQKIP 447

Db 121 SSWPVPTDVSLYPSGGTGLETPDRKGKGTTEGKPSFFPEDSFIDSGEIDVGRRASQKIP 180

QY 448 PGTFWRSQVFIHDPVHLKFNVSGLKKAALVGIYGRKGLPPSHTQDFVELLDGRRLLTQEA 507

Db 181 PGTFWRSQVFIHDPVHLKFNVSGLKKAALVGIYGRKGLPPSHTQDFVELLDGRRLLTQEA 240

QY 508 RSLEGTPRQSRGTVPSSSHETGFIQYLDSGIWHLAFYNDGKESEVVSFLTTAI---ESVD 564

Db 241 RSLEGTPRQSRGTVPSSSHETGFIQYLDSGIWHLAFYNDGKESEVVSFLTTAIALPRLK 300

QY 565 NCPSNCYNGD-----CISGTCHCFLGFL---GPDCCRASCP----- 598

Db 301 EMKSQESAAGSKLVLRCTSEYSSLRFKWFKNGNELNRKNKPQNIKIQKKPGKSELRLIN 360

QY 599 -VLCSGNGQYMKGRCLCHSGWKGAECVPTNQCIDVACSNHGTCITGTICNPGYKGESC 657

Db 361 KASLADSGEYM-----CKVISKLGNDASAN---ITIV-----ESN 393

QY 658 EEVDCMDPTCSGRGVCVRGECHCFVGGTNCETPRAT-----CLDQ-----CSG 702

Db 394 EIITGMPASTEGAYVSSSEPIRISVSTEGANTSSSTSTSTTGTSHLVKCAEKEKTFVCVNG 453

QY 703 HGTFL-----PDTGLCSCDPSWTGHDCSIEICAA 731

Db 454 GECFMVKDLSNPSRYLCKPCNFTGDRCONYVMAS 488

RESULT 9

US-10-290-578-10

; Sequence 10, Application US/10290578

; Patent No. 6916624

; GENERAL INFORMATION:

; APPLICANT: Schaefer, Gabriele M.

; APPLICANT: Sliwowski, Mark

; TITLE OF INVENTION: Gamma-Heregulin

; NUMBER OF SEQUENCES: 11

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Genentech, Inc.

; STREET: 460 Point San Bruno Blvd

; CITY: South San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94080

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: WinPatin (Genentech)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/290,578

; FILING DATE: 08-No. 6916624-2002

CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/891,845  
FILING DATE: <Unknown>  
APPLICATION NUMBER: 60/021640  
FILING DATE: 12-Jul-96  
ATTORNEY/AGENT INFORMATION:  
NAME: Lee, Wendy M.  
REGISTRATION NUMBER: 40,378  
REFERENCE/DOCKET NUMBER: P1043  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415/225-1994  
TELEFAX: 415/952-9881  
TELEX: 910/371-7168  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 501 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 10:  
US-10-290-578-10

Query Match 10.6%; Score 1575; DB 2; Length 501;  
Best Local Similarity 64.5%; Pred. No. 4.9e-109;  
Matches 332; Conservative 22; Mismatches 83; Indels 78; Gaps 10;  
  
QY 268 MDILGASRHDGAYSDGHFLFKPGTSPFCFTTSPGYPLTSSVTYSPPPRPLPRSPARP 327  
DB 1 MDILGASRHDGAYSDGHFLFKPGTSPFCFTTSPGYPLTSSVTYSPPPRPLPRSPARP 60  
  
QY 328 FNLKKPSKYNWKCAALSAIVISATLVILLAYFVAMHLFGLNWHLQPMEGOMYEITEDTA 387  
DB 61 FNLKKPSKYNWKCAALSAIVISATLVILLAYFVAMHLFGLNWHLQPMEGOMYEITEDTA 120  
  
QY 388 SSWPVPTDVSLYPSGGTGLETPDRKKGKTTEGKPSFFPEDSFIDSGEIDVGRRASQKIP 447  
DB 121 SSWPVPTDVSLYPSGGTGLETPDRKKGKTTEGKPSFFPEDSFIDSGEIDVGRRASQKIP 180  
  
QY 448 PGTFWRSQVFIDHPVHLKFVNSLGAALVGIYGRKGLPPSHTQDFVELLDGRRLLTQEA 507  
DB 181 PGTFWRSQVFIDHPVHLKFVNSLGAALVGIYGRKGLPPSHTQDFVELLDGRRLLTQEA 240  
  
QY 508 RSLGTPRQSRGTVPSSSHETGFIQYLDGSIWHLAFYNDGKSEVWSFLTATAI---ESVD 564  
DB 241 RSLGTPRQSRGTVPSSSHETGFIQYLDGSIWHLAFYNDGKSEVWSFLTATAIALPRLK 300  
  
QY 565 NCPNSCYNGD-----CISGTCCHFLGFL----GPDCCGRASCP----- 598  
DB 301 EMKQESAAGSKLVLRCE TSSSYSLRPFKFWKNGNELNRKNQKIQKPKGKSELIN 360  
  
QY 599 -VLCGNGQYMKGRCLCHSGWKABCDVPTNQCIDVACNHGTCITGTICNPGYKGESC 657  
DB 361 KASLADSGEYM-----CKVISKLGNDSASAN----ITIV-----ESN 393  
  
QY 658 EEVDCMDPTCSGRGVCVRGECHCFVGWGGTNCETPRAT-----CLDQ-----CSG 702  
DB 394 EIITGMPASTEGAYVSSSPIRISVSTEGANTSSSTSTSTGTSHLVKCAEKEKTFVCVNG 453  
  
QY 703 HGTEL-----PDTGLCSCDPSWTGHDCSIEICAA 731  
DB 454 GECFMVKDLNPSRYLCKCPNEFTGDRCONYVMAS 488

RESULT 10  
US-09-796-575-2  
Sequence 2, Application US/09796575  
Patent No. 6632671  
GENERAL INFORMATION:  
APPLICANT: Geneseeques, Inc.  
TITLE OF INVENTION: NANOCAPSULE ENCAPSULATION SYSTEM AND METHOD  
FILE REFERENCE: G332.12-0001  
CURRENT APPLICATION NUMBER: US/09/796,575  
CURRENT FILING DATE: 2001-02-28

;; PRIOR APPLICATION NUMBER: US 60/185,282  
;; PRIOR FILING DATE: 2000-02-28  
;; NUMBER OF SEQ ID NOS: 5  
;; SOFTWARE: PatentIn version 3.1  
;; SEQ ID NO 2  
;; LENGTH: 2200  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
US-09-796-575-2  
  
Query Match 4.4%; Score 649.5; DB 2; Length 2200;  
Best Local Similarity 22.3%; Pred. No. 1.5e-38;  
Matches 310; Conservative 166; Mismatches 492; Indels 423; Gaps 64;  
  
QY 545 NDGKESEVVSVFLTTAIESVDNCPNSCYNGDCISGTCCHFLGFLGPDCCGRASCPVLCS-G 603  
DB 208 DDGFTGEDCSQLA-----CPSDCNDQKCVNGVCICFEGYAGADCSREICVPVPCSEE 259  
  
QY 604 NGQYMKGRCLCHSGWKABCDVPTNQCIDVACSNHGTCTITGTICNPGYKGESCEVDCM 663  
DB 260 HGTCVDGLCVCHDFAGDDCNKPL--CLN-NCYNRGRCVENECVDCDEGFTGEDCSSELICP 316  
  
QY 664 DPTCSGRGVCVRGECHCFVGWGGTNCETPRATCLDQCSDGHTFLPDTGLCSCDPSWTGHD 723  
DB 317 N-DCFDRGRINGTCYCEEFTGEDCGKP--TCPHACHTQGR--EEGQCVCDEGFAGLD 371  
  
QY 724 CSIEICAADCGGHGVCVGGTCRCEDGMMGAACDQACHPRCAEHGTCRDGKCECSPGWNG 783  
DB 372 CSEKRCPADCHNRGRVCVGRCECDDGFTGADCGELKCPNGCSGHGRVCVNGQCVCDEGYTG 431  
  
QY 784 EHCT-----IAHYLDRVVVKEG-----CPGLCNGNGRCTLDLNGWHCV 820  
DB 432 EDCSQLRCPNDCHSRGRCV-EGKVCCEQGFKGYDCSDMSCPNDCQHGRG---VNGM-CV 486  
  
QY 821 CQLGWRGAGC-----DTSMETACGDSKNDGDGLV--DCMDPDC-----CL--Q 860  
DB 487 CDDGYTGEDCRDRQCRPRDCSNRGLCVDGQCVCEDGFTGPDCAELSCPNDCHGQGRVCVNGQ 546  
  
QY 861 PLCH---INPLCLGSPNPLDIIQETQVPVSQQNLHSFYDRIKFLVGRDSTHIIIPGENPFD 917  
DB 547 CVCHEGFMGKDCKEQRCPSDCHGQGRVCVDQCICHEGF-----TGLDC----- 589  
  
QY 918 GGHAC-----VIRGQVMTSDGTPLVGVNISFVNNPLFGYTTISRQDGSFDLVTNCGI 968  
DB 590 GQHSCPSDCNNLGQCVSGRCICNEG--YSGEDCSEVSPPK-----DLV----- 630  
  
QY 969 SIILRFERAPFITQ--EHTLWLPWD-RFFVMTETIMRHEENEIPSCDLSNFARPNPVVSP 1025  
DB 631 -----VTEVTETVNLAWDNEMRVTEYLV-----VYTP 658  
  
QY 1026 SPLTSPASSCAEKGPVPEIQALQEEIISIGCKMRLSYLSRTPGYKSVLRISL---THP 1082  
DB 659 T-----HEGLEMQRVPGDQTS-----TIIQELEPGVEYFIRVFAILLENKK 700  
  
QY 1083 TIPFNLMKVHLMVAVEGRFLFRKWFAAAPDLSYYFIWDKTDV-----YNQKVF- 1130  
DB 701 SIPVSARVATYLPAPGLKFK----SIKETSVEVEWDPLDIAFETWEIIFRNMNKEDEGE 756  
  
QY 1131 -----LSEAFVSVGYEYESCPDLI-----LWEKRTTVLQG---YEI-----D 1164  
DB 757 ITKSLRRRPETSYRQTGLAPQGEYEISLHIVKNNTRGPKLRVTTTRLDAPSQIEVKDVTD 816  
  
QY 1165 ASKLGW--SLDKKHALNIQSGI-----LHKNGENQFVSQQPPVIGSIMGNRRR 1213  
DB 817 TTALITWFKPLAEIDGIELTYGIKDVPGDRTTIDLTEDENQY-----SIGNLKP-TEY 869  
  
QY 1214 SISCPCNGLADGNKLLAPVALTCGSDGSLYVGDFNIRRIFFPSGNVTNILELRNKDPRH 1273  
DB 870 EVSLISRRGDMSSNP--AKETFTTGLDAP-----PNLRRVSQTDNSITL-----EWRN 915  
  
QY 1274 SHSPAHHYYLATDFMSGAVFLSDSNSRRRVFKIKSTVVVKDLVKNSEVAVGTGDCQLPFDD 1333  
DB 916 GKAAIDSYRIKYAPISGG-----DHAEDVVPKSQLA----- 946



QY 1334 TRCGDGGKATEATLTNPRGITVDKFGLIYFVDGTMIRRIDQNGIISTLLGSNDLTSARPL 1393  
Db 947 -----TTKTLTGLRPGT--EYGI-----GVSARKEDKESNPATINAATELDTPKDL 991  
QY 1394 SCDVMDISQVRLEWPTDLA-----IN-----PMDNSLYVLDNNVVLQISE 1434  
Db 992 QVSETAETS-LTLLWKTPLAKFDRYRLNYSLPTGQWVGVLPRNTTSYVLRG---LEPGQ 1047  
QY 1435 NHQVRIVAGRPMHC-----QVPGIDHFLLSKVAIHATLESATAL--AVSHNGVL 1481  
Db 1048 EYNVLLTAEGRHKSKPARVKASTEQAPELENLTVTEVGWDLRLNWTAAADQAYEH--- 1103  
QY 1482 YIAETDE-KKINRIRQVTTSGEISLVAGAPSGCDCKNDANCDGDDGYAKDAKLNTPS 1540  
Db 1104 FIIQVQEAANKVEAARNLTVPG--SLRAVDIPGLKAATPYTVTSIYGVIOGY-----RTPV 1155  
QY 1541 SLAVCADGELYVADLGNIRIRFIRKNKPFNLNTQNMVELSSPIDQELYLFDTTGKHLYTQS 1600  
Db 1156 LSAEASTGE--TPNLGEVVVAEVEGWDALKLN-----WT 1186  
QY 1601 LPTGDYLYNFTYTGDDITLITDNNGNMNVNRRDSTGMPLWLVPDGOVYVWTMGTSAL 1660  
Db 1187 APEGAYEYFFIQVQEADTVEAAQN-----LTVPGGLRSTDLPLGLKAAT 1229  
QY 1661 K-SVTTQGHELAMMTYHGNSGLLATKSNENGTTFEYDSFGLTNVTFPTGQVSSFRSD 1719  
Db 1230 HYTITIRGVTDQFSTTPLSVEVLTEEVPDMGNLTVTEVSWDALRLNWTTPDGTYDQFT-- 1287  
QY 1720 TDSSVHVQVETSSKDDVTITTNLSAGAFYTLLODQVRNSYYIGADGSLRLLLANGMEVA 1779  
Db 1288 -----IQVQEA-----DQVEAHNLTVPGLSLR-----SMEI- 1313  
QY 1780 LQTEPHLLAGT 1790  
Db 1314 ----PGLRAGT 1320

RESULT 11  
US-08-793-273C-2  
; Sequence 2, Application US/08793273C  
; Patent No. 6482410  
; GENERAL INFORMATION:  
; APPLICANT: Crossin, Kathryn L.  
; APPLICANT: Phillips, Greg  
; APPLICANT: Prieto, Anne L.  
; TITLE OF INVENTION: CYTOTACTIN DERIVATIVES THAT STIMULATE ATTACHMENT AND  
; TITLE OF INVENTION: NEURITE OUTGROWTH, AND METHODS OF MAKING SAME  
; FILE REFERENCE: BEC0022S  
; CURRENT APPLICATION NUMBER: US/08/793,273C  
; CURRENT FILING DATE: 1997-05-22  
; PRIOR APPLICATION NUMBER: PCT/US95/11684  
; PRIOR FILING DATE: 1995-09-14  
; PRIOR APPLICATION NUMBER: 08/308,359  
; PRIOR FILING DATE: 1994-09-16  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 2199  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
US-08-793-273C-2  
  
Query Match 4.4%; Score 648.5; DB 2; Length 2199;  
Best Local Similarity 21.4%; Pred. No. 1.8e-38;  
Matches 280; Conservative 169; Mismatches 474; Indels 385; Gaps 55;  
  
QY 566 CPSCNYCNGDCCISGTCFLGFLGPDGGRASCPVLCSNGQYMKGRCLCHSGWKGAECD- 624  
Db 314 CPNDCFDRGRCINGTCYCEEGFTGDCGKPTCPHACHTQGRCEEQVCVDEGFAGVDCSE 373  
QY 625 --VPTN-----QCID-----VACSNHGTCITGTCTCNCNPGYKGESC 657

Db 374 KRCPADCHNRGRVCVDRCECDDGFTGADCGELKCPNGSGHGRCVNGQCVCDEGYTGEDC 433  
QY 658 EEVD CMDPTCSGRGVCVRGECHCFVWGWTNCETPRATCLDQC SGHGTFLPDTGLCSCDP 717  
Db 434 SQLRCPN-DCHSRGRVCVEGKVCCEQGFKYDCSD--MSCPNDC HQHGRCV--NGMCV added 488  
QY 718 SWTGHDCSI EICAADCGGHGVCVGGTCRCEDGWMGAACDQACHPRCAEHGTCRDKCEC 777  
Db 489 GYTGEDCDRDRQCPRDCSNRGLCVDGQCVCEDGFTGPDCAELSCPNDCHGQGRVCVNGQCVC 548  
QY 778 SPGWNGEHC TIAHYLDRVVKEGCPGLCNGNGRCRTLDLNGWHVCQLGWRGAGCDTSMETA 837  
Db 549 HEGFMGKDK-----EQRCPSDCHGQGR-----VDG-QCICHEGFTGLDCG---QHS 592  
QY 838 CGDSKDN DGLVDCMDPDCCCLQPLCHINPLCLG-----SPNPLDIIQETQVVPVQQNL 891  
Db 593 CPS-----DCNNLGQCVSGRCICNEGYSGEDCSEVSP-PKDLV---VTEVTEETV 638  
QY 892 HSFYDR-----IKFLVGRDSTHIIPGENPFDGGHACVIRGQVMTSDGTPLV-----GVN- 940  
Db 639 NLAWDNEMRVTEYLVVYTPH-----EGGLEMQFR--VPGDQTSTIIRELEPGVEY 687  
QY 941 ----ISFVNNPLFGYTI SRQDGSFDLVNTGGISIIILRFERAPFITQEHTLWLPWDRFFVM 996  
Db 688 FIRVFAILENKK-SIPVSARVATYLPAPEG-----LKFSIK-ETSVEVEWFLDIAFET 740  
QY 997 ETIIMRHEENEIPCDLSNFARPNPVPSPLTSFASSCAEKGPVPEIQALQEEISISG 1056  
Db 741 WEIIFRNMNKEDEGEITKSLRPE-----TSYRQTGLAPG-----QEYEIS- 781  
QY 1057 CKMRLSYLSSRTPGYKSVLRISLTHPTIPFNLMKVHLMVAVEGR LFRKWFAPAAADLSYF 1116  
Db 782 --LHIVKNNTRGPLKRVTTTRLDAPS-----QIEVKDVTDTTALITWFKPLAEID--- 830  
QY 1117 IWDKTDVYNQVFLSEAFVSVGYEYESCPDLILWEKRTTVLQGYEIDASKLGGWSLDKH 1176  
Db 831 -----GIELTYGIKDVP-----DRTTIDLTEDENQYSIGNLKPDTE 867  
QY 1177 HALNIQSGILHKNGENQFVSQQPPVIGSIMGNGRRRSISCPSCNGLADGNKLLAPVALT 1236  
Db 868 YEVS-----ISRRGD-----MSSNP-----AKETFT 889  
QY 1237 CGSDGSLYVGDFNYIRRI FSPGNVTNILELRNKDFRHSHPAHKYVLATDPM SGAVFLSD 1296  
Db 890 TGLDAP-----RNLRRVSQTDNSITL-----EWRNGKAAIDSYRIKYPISGG----- 932  
QY 1297 SNRRRVFKIKSTVVVKDLVKNSEVVAGTGDCQLPFDDTRCGDGGKATBATLTNPRGITVD 1356  
Db 933 -----DHAEVDVPKSOQA-----TTKTTLTGLRPGT-- 958  
QY 1357 KFLIYFVDGTMIRRIDQNGIISTLLGSNDLT SARPLCSDSVMDISQVRLEWPTDLA--- 1413  
Db 959 EYGI-----GVSARKEDKESNPATINAATELDTPKDLQVSETAETS-LTLLWKTPLAKFD 1012  
QY 1414 ---IN-----PMDNSLYVLDNNVVLQISENHQVRIVAGRPMHC----- 1448  
Db 1013 RYRLNYSLPTGQWVGVLPRNTTSYVLRG---LEPGQEYNVLLTAEGRHKSKPARVKAS 1069  
QY 1449 --QVPGIDHFLLSKVAIHATLESATAL--AVSHNGVLYIAETDE-KKINRIRQVTTSGEI 1503  
Db 1070 TEQAPELENLTVTEVGWDLRLNWTAAADQAYEH---FIIQVQEAANKVEAARNLTVPG-- 1123  
QY 1504 SLVAGAPSGCDCKNDANCDGDDGYAKDAKLNTPSSLAVCADGELYVADLGNIRIRFI 1563  
Db 1124 SLRAVDIPGLKAATPYTVSIYGVIOGY-----RTPVLSAEASTGE--TPNLGEVVVAEV 1175  
QY 1564 RKNKPFNLNTQNMVELSSPIDQELYLFDTTGKHLTYQSLPTGDYLYNFTYTGDDGITLITD 1623  
Db 1176 GWDALKLN-----WTAPEGAYEYFFIQVQEADTVEAAQ 1208  
QY 1624 NNGNMVNVRDSTGMPLWLVPDGOVYVWTMGTSALK-SVTTQGHELAMMTYHGNSGLL 1682  
Db 1209 N-----LTVPGGLRSTDLPLGLKAATHYITIRGVTDQFSTTPLSVEVL 1251

QY 1683 ATKSNENGWTTFFYEYDSFGRLTNVTFTPTQVSSFRSDTSSVHVQVETSSKDDVTITNL 1742  
Db 1252 TEEVPMGNLTVTEVSWDALRLNWTTPDGTVDQFT-----IQVQEA----- 1292

QY 1743 SASGAFYTLLOQVRNSYYIGADGSLRLLLANGMEVALQTEPHLLAGT 1790  
Db 1293 -----DQVEAHNLTVPGSLR-----SMEI-----PGLRAGT 1319

RESULT 12  
PCT-US95-11684-2  
; Sequence 2, Application PC/TUS9511684  
; GENERAL INFORMATION:  
; APPLICANT: THE SCRIPPS RESEARCH INSTITUTE  
; TITLE OF INVENTION: CYTOTACTIN DERIVATIVES THAT STIMULATE  
; TITLE OF INVENTION: ATTACHMENT AND NEURITE OUTGROWTH, AND METHODS OF MAKING  
; TITLE OF INVENTION: AND USING SAME  
; NUMBER OF SEQUENCES: 28  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: The Scripps Research Institute, Office of  
; ADDRESSEE: Patent Counsel  
; STREET: 10666 North Torrey Pines Road, TPC 8  
; CITY: La Jolla  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 92037  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US95/11684  
; FILING DATE: 14-SEP-1995  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/308,359  
; FILING DATE: 16-SEP-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Logan, April C.  
; REGISTRATION NUMBER: 33,950  
; REFERENCE/DOCKET NUMBER: BEC0019P  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 619-554-2937  
; TELEFAX: 619-554-6312  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2199 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
PCT-US95-11684-2

Query Match 4.4%; Score 648.5; DB 4; Length 2199;  
Best Local Similarity 21.4%; Pred. No. 1.8e-38;  
Matches 280; Conservative 169; Mismatches 474; Indels 385; Gaps 55;

QY 566 CPSCNYGNGDCISGTCFLGLPDCGRASCPVLCSNGQYMKGRCLCHSGWKGAECD- 624  
Db 314 CPNDCFDRGRCLNGTCYCEGFTGEDCGKPTCPHACTQGRCEEQVCVDEGAFGVCSE 373

QY 625 --VPTN-----QCID-----VACSNHGTCITGTICINPGYKGESC 657  
Db 374 KRCPADCHNRGRGVDCGRCECDGFTGADCGELKCPNGCSGHGRGVNGQVCDEGTGEDC 433

QY 658 EEVDCMDPTCSGRGVCVRGECHCFVWGWTNCETPRATCLDQCSGHGTFPLPDTGLCSCDP 717  
Db 434 SQRCPN-DCHSRGRVCVEGKCVEQGFKGYDCSD--MSCPNDCHQHGRCV--NGMVCVDD 488

QY 718 SWTGHDCSIICAADCGHGVCGGTCTCRCEGDGMGAACDQRACHPRCAEHGTCRDGKCEC 777  
Db 489 GYTGEDCDRQCPDRDCSNRGLCVDGQVCVEDGFTGPDCAELSCPNDCHGQGRGVNGQVCV 548

QY 778 SPGWNGEHCTIAHYLDRVVKEGCPGLCNGNGRCTLDLNGWHVCVQLGWRGAGCDTSMETA 837  
Db 549 HEGFMGKDK-----EQRCPDCHGQGR-----VDG-QCICHEGFTGLDCG---QHS 592

QY 838 CGDSKDNDDGLVDCMDPCCLQPLCHINPLCLG-----SPNPLDIIQETQVPVSQONL 891  
Db 593 CPS-----DCNNLGQCVSGRCICNEGYSGEDCSEVSP-PKDLV---VTEVTEETV 638

QY 892 HSFYDR-----IKFLVGRDSTHIIIPGENPFDGGHACVIRGQVMTSDGTPLV-----GVN- 940  
Db 639 NLAWDNEMRVTEYLVVYTPH-----EGGLEMQFR---VPGDQTSTIIRELEPGVEY 687

QY 941 ----ISFVNNPLFGYTIISRDGSGFDLVNTGGISIIILRFERAPFITQEHTLWLWDRFFVM 996  
Db 688 FIRVFAILNKK-SIPVSARVATYLPAPG-----LKFKSIK-ETSVEVEWDPLDIAFET 740

QY 997 ETIIMRHEENEIPCDLSNFARPNPVSPSPPLTSFASSCAEKGPVPEIQALQEEISISG 1056  
Db 741 WEIIFRNMNKEDEGEITKSLRPE-----TSYRQTGLAPG-----QEYEIS- 781

QY 1057 CKMRLSYLSSRTPGYKSVLRISLTHPTIPFNLMKVHLMVAVEGRLFRKWFAAAPDLSYF 1116  
Db 782 --LHIVKNNTRGPLKRVTTTRLDAPS-----QIEVKDVTDTTALITWFKPLAEID--- 830

QY 1117 IWDKTDVYNQKVFGLSEAFVSUGVEYESCPDLLLWEKRTTVLQGYEIDASKLGGWSLDKH 1176  
Db 831 -----GIELTYGIKDVPG-----DRTTIDLTEDENQYSIGNLKPDE 867

QY 1177 HALNIQSGILHKGNGENQFVSQQPPVIGSIMGNRRRSISCPSCNGLADGNKLLAPVALT 1236  
Db 868 YEVSL---ISRRGD-----MSSNP-----AKETFT 889

QY 1237 CGSDGSLXVGDFNYIRRIFFPSGNVTNILELRNKDFRHSHPAHKYIATDPMGSAVFLSD 1296  
Db 890 TGLDAP-----RNLRRVSQTDNSITL-----EWRNGKAAIDSYRIKYAPISGG----- 932

QY 1297 SNRRRVFKIKSTVVVKDLVKNSEVAVAGTGQCLPFDDTRCGDGGKATEATLTNPRGITVD 1356  
Db 933 -----DHAEVDVPKSQQA-----TTKTTLTGLRPGT-- 958

QY 1357 KFGLIYFVDGTMIRRIDONGIISTLLGSNDLT SARPLSCDSVMDISQVLEWPTDLA--- 1413  
Db 959 EYGI-----GVSARKEDKESNPATINATELDTPKDLQVSETAETS-LTLLWKTPLAKFD 1012

QY 1414 ---IN-----PMDNSLYVLDNNVVVLQISENHQVRIVAGRPMHC----- 1448  
Db 1013 RYRLNYSLPTGQWVGVLPRNTTSYVLRG---LEPGQEYNVLLTAEKGRHKSPPARVKAS 1069

QY 1449 --QVPGIDHFLLSKVAIHATLESATAL--AVSHNGVLYIAETDE-KKINRIQVTTSGEI 1503  
Db 1070 TEQAPELENLTVTEVGWDGLRLNWTAAADQAYEH---FIIQVQEAANKVEAARNLTVPG-- 1123

QY 1504 SLVAGAPSGCDCKNDANCDGSGDDGYAKDAKLNTPSSSLAVCADGELYVADLGNIRIRFI 1563  
Db 1124 SLRAVDIPGLKAATPYTVSIYGVIOGY-----RTPVLSAEASTGE--TPNLGEVWVAEV 1175

QY 1564 RKNKPFNLNTQNMVELSSPIDQELYLFDTTGKHLYTQSLPTGDYLYNFTYTGDDITLTD 1623  
Db 1176 GWDALKLN-----WTAPEGAYEYFFIQVQEADTVEAAQ 1208

QY 1624 NNGNMVNVRDRDSTGMPLWLVPDQVYVWVTMGNTNSALK-SVTTQGHELAMWTHGNSGLL 1682  
Db 1209 N-----LTVPGLRSTDLPLKAAATHYITIRGVTQDFSTPLSVEVL 1251

QY 1683 ATKSNENGWTTFFYEYDSFGRLTNVTFTPTQVSSFRSDTSSVHVQVETSSKDDVTITNL 1742  
Db 1252 TEEVPMGNLTVTEVSWDALRLNWTTPDGTVDQFT-----IQVQEA----- 1292

QY 1743 SASGAFYTLLOQVRNSYYIGADGSLRLLLANGMEVALQTEPHLLAGT 1790  
Db 1293 -----DQVEAHNLTVPGSLR-----SMEI-----PGLRAGT 1319







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Db      1503 SATEVQSETAVITWRPP-----RAPVTDYLLTYESIDGRVKEVILDPETTSYTLTE--- 1553
Qy      1934 VLLLSQRQYIFEFDKNDRLSSVTMPNVARQTLETIRSVGYRNIYQPPEGNASVIQDFT 1993
Db      1554 ---LSPSTQYTVKLQALSR-----SMRSKMIQTVFTTTGLLY----PYPKDCSQALLNGEV 1602
Qy      1994 EDGHLHLHTFYLGTR 2008
Db      1603 TSG--LYTIYLNDR 1615
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RESULT 15
US-09-949-016-9270
; Sequence 9270, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9270
; LENGTH: 2254
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-9270
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Query Match      3.9%; Score 585; DB 2; Length 2254;
Best Local Similarity 33.1%; Pred. No. 1.1e-33;
Matches 121; Conservative 33; Mismatches 136; Indels 76; Gaps 10;

Qy      562 SVDNCPNICYNGDCISGTCHCFGLGFLPDCGRASCPVLCSGNGQYMKGRCLCHSGWKGA 621
Db      320 STRTCPRDCRGRCEDEGECICDTGYSGDDCGVRS CPDGNQGRCEDEGRCVCWPYGTGT 379

Qy      622 ECDVPTNQCIDVACSNHGTCTGTCTCNPGYKGESCEEVDCMDPTCSGRGVCVRGECHCF 681
Db      380 DCG---SRACPRDCRGRRCENGVCVCNAGYSGEDCGVRS C-PGDCRGRRCESGRCMCW 435

Qy      682 VGWGGTNCET-----PRATCLD-----QCSGHGTFLPDTGL 712
Db      436 PGYTGRDCGTRACPGDCRGRRCVDRGRCVCPNPGFTGEDCGSRRCPCGDCRHHG--LCEDGV 493

Qy      713 CSCDPSWTGHDCSI EICAA DCGHGVGVGGTCRCEDGWMGAACDQACHPRCAEHGTCTRD 772
Db      494 CVCDAGYSGEDCSTRSCPGGCRGRGQQCLDGRVCVEDGYSGEDCGVRQCPNDCSQHGVQD 553

Qy      773 GKCECPGMNGEHCTIAHYLDRVVKEGCPGLCNGNGRCRTL DLNMGWHCVCCQLGWRGAGCDT 832
Db      554 GVCICWEGYVSEDCSI-----RTCPSNCHGRRC-----EEGRCLCDPGYTGPTCAT 600

Qy      833 SMETACGDSKNDGDGLVDCMDPDCCLPQ--LCHIN-----PLCLGSPNPLD 877
Db      601 RMCPA-----DCRGRGRVCVQGVCLCHVGVGGEDCGQEEPPASACPGGCGPRE 647

Qy      878 IIQETQ 883
Db      648 LCRAQ 653
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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 10, 2005, 15:51:23 ; Search time 178 Seconds  
(without alignments)  
6835.055 Million cell updates/sec

Title: US-10-029-020-14  
Perfect score: 14887  
Sequence: 1 MDVKERKPYRSLTRRDAER.....ELSDSANNIHFMRQSEMGRR 2769

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0  
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_21.\*  
1: Geneseqp1980s:\*  
2: Geneseqp1990s:\*  
3: Geneseqp2000s:\*  
4: Geneseqp2001s:\*  
5: Geneseqp2002s:\*  
6: Geneseqp2003as:\*  
7: Geneseqp2003bs:\*  
8: Geneseqp2004s:\*  
9: Geneseqp2005s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES				* Query		Description	
Result No.	Score	Match	Length	DB	ID		
1	14887	100.0	2769	5	ABG70388	Abg70388	Human TEN
2	14887	100.0	2769	7	ADP74830	Adf74830	Murine NO
3	14748.5	99.1	2758	5	ABG97359	Abg97359	Human CGD
4	14610	98.1	2775	7	ADP74842	Adf74842	Murine NO
5	14406.5	96.8	2794	5	ABB98401	Abb98401	Human NOV
6	10221	68.7	2721	5	ABP53587	Abp53587	Human NOV
7	10221	68.7	2721	8	ADH41969	Adh41969	Novel hum
8	10201	68.5	2725	5	ABP53586	Abp53586	Human NOV
9	10201	68.5	2725	8	ADH41995	Adh41995	Novel hum
10	10201	68.5	2725	8	ADH41991	Adh41991	Novel hum
11	10201	68.5	2725	8	ADH41933	Adh41933	Novel hum
12	10201	68.5	2725	8	ADH41997	Adh41997	Novel hum
13	10201	68.5	2725	8	ADH41999	Adh41999	Novel hum
14	10201	68.5	2725	8	ADH41973	Adh41973	Novel hum
15	10196	68.5	2725	8	ADH41993	Adh41993	Novel hum
16	9888.5	66.4	2628	5	ABP53588	Abp53588	Human NOV
17	9888.5	66.4	2628	8	ADH41949	Adh41949	Novel hum
18	9856	66.2	2613	5	ABP53589	Abp53589	Human NOV
19	9856	66.2	2613	8	ADH41977	Adh41977	Novel hum
20	9635	64.7	2765	8	ADH71220	Adh71220	Human pro
21	9616.5	64.6	2802	5	ADI16953	Adil6953	Chicken N
22	9610.5	64.6	2764	5	ADI16951	Adil6951	Murine NO
23	9610.5	64.6	2764	8	ADJ76262	Adj76262	Marker ge
24	9601	64.5	2765	5	ADI16952	Adil6952	Rat NOVX

25	9584	64.4	2725	7	ADJ69881	Adj69881	Human hea
26	9536	64.1	2733	4	AAU08680	Aau08680	Human FCT
27	9536	64.1	2733	8	ADH71250	Adh71250	Human pro
28	9536	64.1	2733	8	ADH71254	Adh71254	Human pro
29	9536	64.1	2733	8	ADH71240	Adh71240	Human pro
30	9536	64.1	2733	8	ADH71246	Adh71246	Human pro
31	9536	64.1	2733	8	ADH71258	Adh71258	Human pro
32	9531	64.0	2733	7	ADB32024	Adb32024	Human FCT
33	9530.5	64.0	2724	4	AAU08681	Aau08681	Human FCT
34	9530.5	64.0	2724	7	ADB32029	Adb32029	Human FCT
35	9530.5	64.0	2724	8	ADH71252	Adh71252	Human pro
36	9501	63.8	2725	5	ABG61913	Abg61913	Prostate
37	9501	63.8	2725	7	ADN39610	Adn39610	Cancer/an
38	9501	63.8	2725	8	ADQ21282	Adq21282	Human sof
39	9501	63.8	2725	8	ADU06625	Adu06625	Novel bro
40	9418	63.3	2759	5	ADI16608	Adi16608	Human NOV
41	9418	63.3	2759	8	ADH71272	Adh71272	Human pro
42	9314	62.6	2633	6	ABR58318	Abf58318	BCU0205B
43	9303	62.5	2590	5	ADI16954	Adil6954	Zebrafish
44	9165.5	61.6	2662	8	ADH71218	Adh71218	Human pro
45	9145	61.4	2346	5	ADI16955	Adil6955	Murine NO

ALIGNMENTS

RESULT 1  
ABG70388

ID	ABG70388	standard;	protein;	2769	AA.
XX	ABG70388;				
AC	ABG70388;				
XX	ABG70388;				
DT	05-NOV-2002	(first entry)			
XX	05-NOV-2002	(first entry)			
DE	Human	TEN-M4-like	protein.		
XX	Human	TEN-M4-like	protein.		
KW	Human; NOVX; NOVX-associated disorder; cardiomyopathy; atherosclerosis; cell signal processing; metabolic pathway modulation; metabolic disorder; obesity; diabetes; infectious disease; neurodegenerative disorder; acne; Alzheimer's disease; Parkinson's disease; immune disorder; cancer; haematopoietic disorder; cirrhosis; pancreatitis; learning defect; memory defect; infertility; congenital heart defect; hair growth; pigmentation disorder; endocrine disorder; respiratory disease; health; gastro-intestinal disease; reproductive; neurological disease; bone marrow transplantation; endocrine disease; allergy; inflammation; nephrological disorder; urinary system disorder; age-related disorder; neuropsychiatric disorder; EGF-related protein; SCUBE1; TEN-M4; adipocyte complement-related C1q tumour necrosis factor; out at first; beta adrenergic receptor kinase; EphA6/ehk-2; glucose transporter; type Ia membrane sushi-containing domain; butyrophilin; type Ia membrane sushi-containing domain containing; SNP; single nucleotide polymorphism.				
OS	Homo sapiens.				
XX	Homo sapiens.				
FH	Key	Location/Qualifiers			
FT	Misc-difference 28	/note= "Asp substituted by Gly as a result of a single nucleotide polymorphism (SNP)"			
FT	Misc-difference 64	/note= "Val substituted by Ala as a result of a single nucleotide polymorphism (SNP)"			
FT	Misc-difference 76	/note= "Ala substituted by Thr as a result of a single nucleotide polymorphism (SNP)"			
XX	WO200257453-A2.				
PD	25-JUL-2002.				
XX	19-DEC-2001; 2001WO-US050331.				
XX	19-DEC-2000; 2000US-0256704P.				





Db 1441 VAGRPMHCQVPGIDHFLLSKVAIHATLESATALAVSHNGVLVYIAETDEKKINRIRQVTTTS 1500

QY 1501 GEISLVAGAPSGCDCKNDANCDGFCGDDGYAKDAKLNTPSSLAVCADGELYVADLGNIRI 1560

Db 1501 GEISLVAGAPSGCDCKNDANCDGFCGDDGYAKDAKLNTPSSLAVCADGELYVADLGNIRI 1560

QY 1561 RFIRKNKPFNLNTQNMVELSSPIDQELYLFDFTGKHLYTQSLPTGDLYNFTYTGDGDIITL 1620

Db 1561 RFIRKNKPFNLNTQNMVELSSPIDQELYLFDFTGKHLYTQSLPTGDLYNFTYTGDGDIITL 1620

QY 1621 ITDNNGNMNVVRDSTGMPLWLVPDGVVYVWTMGNTSALKSVTTQGHELAMMTYHGNSG 1680

Db 1621 ITDNNGNMNVVRDSTGMPLWLVPDGVVYVWTMGNTSALKSVTTQGHELAMMTYHGNSG 1680

QY 1681 LLATKSNENGWTFEYDVSFGRLLTNVTFPTGQVSSFRSDTSSVHVQVETSSKDDVTIIT 1740

Db 1681 LLATKSNENGWTFEYDVSFGRLLTNVTFPTGQVSSFRSDTSSVHVQVETSSKDDVTIIT 1740

QY 1741 NLSASGAFYTLQDQVRNSYYIGADGSLRLLLANGMEVALQTEPHLLAGTVNPTVGKRVN 1800

Db 1741 NLSASGAFYTLQDQVRNSYYIGADGSLRLLLANGMEVALQTEPHLLAGTVNPTVGKRVN 1800

QY 1801 TLPIDNGLNLVEWRQKEQARGQVTVFGRRLRVHNRNLLSLDFDRVTRTEKIYDDHRKFT 1860

Db 1801 TLPIDNGLNLVEWRQKEQARGQVTVFGRRLRVHNRNLLSLDFDRVTRTEKIYDDHRKFT 1860

QY 1861 LRILYDQAGRPSLWSPSSRLNGVNVITYSPGGYIAGIQIGIMSERMEYDQAGRITSRIFAD 1920

Db 1861 LRILYDQAGRPSLWSPSSRLNGVNVITYSPGGYIAGIQIGIMSERMEYDQAGRITSRIFAD 1920

QY 1921 GKTWSYTYLEKSMVLLLSHQRYIFEFDKNDRLSSVTMPNVARQTLETIRSVGYRNIYQ 1980

Db 1921 GKTWSYTYLEKSMVLLLSHQRYIFEFDKNDRLSSVTMPNVARQTLETIRSVGYRNIYQ 1980

QY 1981 PPEGNASVIOQDFTEDGHLHHTFYLGTGRRVYKYGKLSKLAETLYDTTKVSFTYDETAGM 2040

Db 1981 PPEGNASVIOQDFTEDGHLHHTFYLGTGRRVYKYGKLSKLAETLYDTTKVSFTYDETAGM 2040

QY 2041 LKTINLQNEGFTCTIRYRQIGPLIDRQIFRFTBEGMVNARFDYNDNSFRVTSMQAVINE 2100

Db 2041 LKTINLQNEGFTCTIRYRQIGPLIDRQIFRFTBEGMVNARFDYNDNSFRVTSMQAVINE 2100

QY 2101 TPLPIDLYRYDDVSGKTEQFGKFGVIYYDINQIITTAVMTHTKHFDAYGRMKEVQYEIER 2160

Db 2101 TPLPIDLYRYDDVSGKTEQFGKFGVIYYDINQIITTAVMTHTKHFDAYGRMKEVQYEIER 2160

QY 2161 SLMYWMTVQYDNMGRVVKKELKVGPYANTTRYSEYDADGQLQTVSINDKPLWRYSYDLN 2220

Db 2161 SLMYWMTVQYDNMGRVVKKELKVGPYANTTRYSEYDADGQLQTVSINDKPLWRYSYDLN 2220

QY 2221 GNLHLLSPGNSARLTPLRYDIRDRITRLGDVQYKMDGDFLQRQGGDIFEYNSAGLLIKA 2280

Db 2221 GNLHLLSPGNSARLTPLRYDIRDRITRLGDVQYKMDGDFLQRQGGDIFEYNSAGLLIKA 2280

QY 2281 YNRAGSWSVRYRYDGLGRRVSSKSSHHLQFFYADLTNPTKVTHLYNHSSEITSLYYD 2340

Db 2281 YNRAGSWSVRYRYDGLGRRVSSKSSHHLQFFYADLTNPTKVTHLYNHSSEITSLYYD 2340

QY 2341 LQGHLFAMELSSGDEFYIACDNIGTPLAVFSGTGLMKQILYTAYGEIYMDTNPNFQII 2400

Db 2341 LQGHLFAMELSSGDEFYIACDNIGTPLAVFSGTGLMKQILYTAYGEIYMDTNPNFQII 2400

QY 2401 GYHGGLYDPLTKLVHMGRRDYDLVLAGRWTSPLDHELWKHLSSSNVMPFNLYMFKNNPNISN 2460

Db 2401 GYHGGLYDPLTKLVHMGRRDYDLVLAGRWTSPLDHELWKHLSSSNVMPFNLYMFKNNPNISN 2460

QY 2461 SQDIKCFMTDVNSWLLTFGFQLHNVIPGYPKPMDAMEPSYELIHTQMKTOBWDNSKSIL 2520

Db 2461 SQDIKCFMTDVNSWLLTFGFQLHNVIPGYPKPMDAMEPSYELIHTQMKTOBWDNSKSIL 2520

QY 2521 GVQCEVQQLKAFVTLERFDQLYGSTITSCQAPKTKKFASSGVSFGKGVKFAKDKGRVT 2580

Db 2521 GVQCEVQQLKAFVTLERFDQLYGSTITSCQAPKTKKFASSGVSFGKGVKFAKDKGRVT 2580

QY 2581 TDIISVANEDGRRVAAAILNHAHYLENLHFTIDGVDTHYFVKPGPSEGDLAAILGLSGGRRT 2640

Db 2581 TDIISVANEDGRRVAAAILNHAHYLENLHFTIDGVDTHYFVKPGPSEGDLAAILGLSGGRRT 2640

QY 2641 LENGVNVTVSQINTVLNGRTRRYTDIQLQYGALCLNTRYGTTLDEEKARVLELARQRAVR 2700

Db 2641 LENGVNVTVSQINTVLNGRTRRYTDIQLQYGALCLNTRYGTTLDEEKARVLELARQRAVR 2700

QY 2701 QAWAREQORLREGEGLRAWTEGEKQOVLSTGRVQYDGGFFVISVEQYPELSDSANNIHF 2760

Db 2701 QAWAREQORLREGEGLRAWTEGEKQOVLSTGRVQYDGGFFVISVEQYPELSDSANNIHF 2760

QY 2761 MRQSEMGR 2769

Db 2761 MRQSEMGR 2769

RESULT 2

ADF74830

ID ADF74830 standard; protein; 2769 AA.

XX

AC ADF74830;

XX

DT 26-FEB-2004 (first entry)

XX

DE Murine NOVX protein to treat human pathological conditions (SeqID 44).

XX

KW mouse; murine; NOVX; metabolic disorder; diabetes; anorexia; cancer;

KW cardiovascular; infectious; neurodegenerative; immune;

KW haematopoietic disease; dyslipidaemia; anorectic; virucide; nootropic;

KW antiinflammatory; neuroprotective; antilipaemic; anabolic; cardiant;

KW neurogenesis; wound healing; angiogenesis; chromosome mapping;

KW tissue typing; preventive medicine; pharmacogenomic;

KW single nucleotide polymorphism; SNP.

XX

OS Mus musculus.

XX

FH Key Location/Qualifiers

FT Misc-difference 168 /note= "Gly can be substituted for Ser by SNP"

FT Misc-difference 506 /note= "Glu can be substituted for Gln by SNP"

FT Misc-difference 2292 /note= "Arg can be substituted for Pro by SNP"

XX

PN WO2003076578-A2.

XX

PD 18-SEP-2003.

XX

PF 06-MAR-2003; 2003WO-US006794.

XX

PR 06-MAR-2002; 2002US-0361974P.

PR 08-MAR-2002; 2002US-00093463.

PR 08-MAR-2002; 2002WO-US007288.

PR 15-MAR-2002; 2002US-0365034P.

PR 19-MAR-2002; 2002US-0365477P.

PR 20-MAR-2002; 2002US-0365884P.

PR 20-MAR-2002; 2002US-0365984P.

PR 20-MAR-2002; 2002US-0365985P.

PR 22-MAR-2002; 2002US-0366928P.

PR 12-APR-2002; 2002US-0372018P.

PR 12-APR-2002; 2002US-0372022P.

PR 23-APR-2002; 2002US-0374682P.

PR 12-JUN-2002; 2002US-0388096P.

PR 14-JUN-2002; 2002US-0389143P.

PR 26-JUN-2002; 2002US-0391779P.

PR 15-AUG-2002; 2002US-0403743P.

PR 13-SEP-2002; 2002US-0410755P.

PR 23-SEP-2002; 2002US-0412957P.

PR 22-OCT-2002; 2002US-0420382P.

PR 05-MAR-2003; 2003US-00420382.

XX





QY 1501 GEISLVAGAPSGCDCKNDANCDFCGDDGYAKDAKALNTPSSLAVCADGELYVADLGNIRI 1560  
Db 1501 GEISLVAGAPSGCDCKNDANCDFCGDDGYAKDAKALNTPSSLAVCADGELYVADLGNIRI 1560  
QY 1561 RFIRKNKPFLNTQNMVELSSPIDQELYLFDFTGKHLYTQSLPTGDYLYNFTYTGDGDITL 1620  
Db 1561 RFIRKNKPFLNTQNMVELSSPIDQELYLFDFTGKHLYTQSLPTGDYLYNFTYTGDGDITL 1620  
QY 1621 ITDNNGMVNVRRDSTGMPLWLVPDGOVYVMTGNTSALKSVTTQGHELAMMTYHGNSG 1680  
Db 1621 ITDNNGMVNVRRDSTGMPLWLVPDGOVYVMTGNTSALKSVTTQGHELAMMTYHGNSG 1680  
QY 1681 LLATKSNENGWTTFYEYDSFGRLTNVTFFPTGOVSSFRSDTSSVHVQVETSSKDDVTIIT 1740  
Db 1681 LLATKSNENGWTTFYEYDSFGRLTNVTFFPTGOVSSFRSDTSSVHVQVETSSKDDVTIIT 1740  
QY 1741 NLSASGAFYTLLOQVRNSYYIGADGSLRLLLANGMEVALQTEPHLLAGTVNPTVGKRV 1800  
Db 1741 NLSASGAFYTLLOQVRNSYYIGADGSLRLLLANGMEVALQTEPHLLAGTVNPTVGKRV 1800  
QY 1801 TLPIDNGLNLVEWRQKEQARGQVTVFGRRLRVHNRNLLSLDFDRVTRTEKIYDDHRKFT 1860  
Db 1801 TLPIDNGLNLVEWRQKEQARGQVTVFGRRLRVHNRNLLSLDFDRVTRTEKIYDDHRKFT 1860  
QY 1861 LRILYDQAGRPSLWSPSSRLNGVNVITYSPGGYIAGIQRGIMSERMEYDOAGRITSRIFAD 1920  
Db 1861 LRILYDQAGRPSLWSPSSRLNGVNVITYSPGGYIAGIQRGIMSERMEYDOAGRITSRIFAD 1920  
QY 1921 GKTWSYTYLEKSMVLLHLSQRQYIFEFDKNDRLSSVTMPNVARQTLETIRSVGYRNIYQ 1980  
Db 1921 GKTWSYTYLEKSMVLLHLSQRQYIFEFDKNDRLSSVTMPNVARQTLETIRSVGYRNIYQ 1980  
QY 1981 PPEGNASVIQDFTDGHLLHTFYLGTGRRVIYKYGKLSKLAETLYDTTKVSFTYDETAGM 2040  
Db 1981 PPEGNASVIQDFTDGHLLHTFYLGTGRRVIYKYGKLSKLAETLYDTTKVSFTYDETAGM 2040  
QY 2041 LKTINLQNEGFTCTIRYRQIGPLIDRQIFRFTBEGMVNARFDYNDNSFRVTSMQAVINE 2100  
Db 2041 LKTINLQNEGFTCTIRYRQIGPLIDRQIFRFTBEGMVNARFDYNDNSFRVTSMQAVINE 2100  
QY 2101 TPLPIDLYRYDDVSGKTEQFGKFGVIYYDINQIITAVMTHTKHFDAYGRMKEVQYEIFR 2160  
Db 2101 TPLPIDLYRYDDVSGKTEQFGKFGVIYYDINQIITAVMTHTKHFDAYGRMKEVQYEIFR 2160  
QY 2161 SLMYWMTVQYDNMGRVVKKELKVGPYANTTRYSEYDADGQLQTVSINDKPLWRYSYDLN 2220  
Db 2161 SLMYWMTVQYDNMGRVVKKELKVGPYANTTRYSEYDADGQLQTVSINDKPLWRYSYDLN 2220  
QY 2221 GNLHLLSPGNSARLTPLRYDIRDRITRLGDVQYKXNDEGFLRQGGDIFEYNSAGLLIKA 2280  
Db 2221 GNLHLLSPGNSARLTPLRYDIRDRITRLGDVQYKXNDEGFLRQGGDIFEYNSAGLLIKA 2280  
QY 2281 YNRAGSWSVRYRYDGLGRRVSSKSSHHLQFFYADLTNPTKVTHLYNHSSEITSLYYD 2340  
Db 2281 YNRAGSWSVRYRYDGLGRRVSSKSSHHLQFFYADLTNPTKVTHLYNHSSEITSLYYD 2340  
QY 2341 LQGHLFAMELSSGDEFYIACDNIGTPLAVFSGTGLMIKQILYTAYGEIYMDTNPNFQIII 2400  
Db 2341 LQGHLFAMELSSGDEFYIACDNIGTPLAVFSGTGLMIKQILYTAYGEIYMDTNPNFQIII 2400  
QY 2401 GYHGGLYDPLTKLVHMGRRDYDLAGRWTSPDHKLWKLSSSNVMPFNLYMFKNNPISN 2460  
Db 2401 GYHGGLYDPLTKLVHMGRRDYDLAGRWTSPDHKLWKLSSSNVMPFNLYMFKNNPISN 2460  
QY 2461 SQDIKCFMTDVNSWLLTFGFQLHNVIPGYKPKMDAMEPSYELIHTQMKTOEWDNSKSIL 2520  
Db 2461 SQDIKCFMTDVNSWLLTFGFQLHNVIPGYKPKMDAMEPSYELIHTQMKTOEWDNSKSIL 2520  
QY 2521 GVQCEVQKQKAFVTLERFDQLYGSTITSCQAPTKKFASSGSVFGKGVKFAKXGRVT 2580  
Db 2521 GVQCEVQKQKAFVTLERFDQLYGSTITSCQAPTKKFASSGSVFGKGVKFAKXGRVT 2580  
QY 2581 TDIISVANEDGRRVAAILNHAHYLENLHFTIDGVDTHYFVKPGPSEGDLAILGLSGGRRT 2640

Db 2581 TDIISVANEDGRRVAAILNHAHYLENLHFTIDGVDTHYFVKPGPSEGDLAILGLSGGRRT 2640  
QY 2641 LENGVNVTVSQINTVLNGRTRRYTDIQLQYGALCLNTRYGTTLDEEKARVLELARQRAVR 2700  
Db 2641 LENGVNVTVSQINTVLNGRTRRYTDIQLQYGALCLNTRYGTTLDEEKARVLELARQRAVR 2700  
QY 2701 QAWAREQORLREGEGLRAWTEGEKQQVLSGTRVQGYDGGFFVSVSEQYPELSDSANNIHF 2760  
Db 2701 QAWAREQORLREGEGLRAWTEGEKQQVLSGTRVQGYDGGFFVSVSEQYPELSDSANNIHF 2760  
QY 2761 MRQSEMGRR 2769  
Db 2761 MRQSEMGRR 2769  
RESULT 3  
ABG97359  
ID ABG97359 standard; protein; 2758 AA.  
XX  
AC ABG97359;  
XX  
DT 16-DEC-2002 (first entry)  
XX  
DE Human CGDD10, INCYTE 7488573CD1.  
XX  
KW Human; cell growth; differentiation; death; CGDD; cancer;  
KW cell proliferative disorder; arteriosclerosis; atherosclerosis;  
KW cirrhosis; hepatitis; paroxysmal nocturnal haemoglobinuria; psoriasis;  
KW polycythaemia vera; primary thrombocytopaenia; developmental disorder;  
KW renal tubular acidosis; anaemia; mental retardation; epilepsy; AIDS;  
KW neurological disorder; Alzheimer disease; Parkinson's disease; asthma;  
KW reproductive disorder; infertility; autoimmune disorder; gout; allergy;  
KW inflammatory disorder; acquired immunodeficiency syndrome; uveitis;  
KW autoimmune thyroiditis; contact dermatitis; Crohn's disease; infection;  
KW diabetes mellitus; glomerulonephritis; irritable bowel syndrome;  
KW multiple sclerosis; osteoarthritis; osteoporosis; pancreatitis;  
KW rheumatoid arthritis.  
XX  
OS Homo sapiens.  
XX  
PN WO200272830-A2.  
XX  
PD 19-SEP-2002.  
XX  
PF 08-FEB-2002; 2002WO-US003715.  
XX  
PR 09-FEB-2001; 2001US-0268111P.  
PR 23-FEB-2001; 2001US-0271175P.  
PR 08-MAR-2001; 2001US-0274503P.  
PR 09-MAR-2001; 2001US-0274552P.  
XX  
PA (INCY-) INCYTE GENOMICS INC.  
XX  
PI Yue H, Yao MG, Ison CH, Lu Y, Warren BA, Elliott VS, Baughn MR;  
PI Ding L, Xu Y, Gietzen KJ, Tang TY, Lal PG, Duggan BM, Burford N;  
PI Lu DAM, Richardson TW, Tran UK, Khare R, Walia NK;  
DR WPI; 2002-723356/78.  
DR N-PSDB; ABS78652.  
XX  
PT New human proteins associated with cell growth, differentiation and  
PT death, useful for diagnosing, treating or preventing autoimmune or  
PT inflammatory disorders (e.g. AIDS, allergy or anemia), cancer,  
PT atherosclerosis or hepatitis.  
XX  
PS Claim 1; Page 155-161; 181pp; English.  
XX  
CC The invention relates to an isolated polypeptide comprising CGDD1-12  
CC (cell growth, differentiation and death), a naturally occurring amino  
CC acid sequence at least 90% identical to CGDD, a biologically active  
CC fragment or an immunogenic fragment. Also included are the  
CC polynucleotides encoding CGDD1-12, a recombinant polynucleotide

CC comprising a promoter sequence operably linked to the CGDD  
CC polynucleotides, a cell transformed with the recombinant polynucleotide,  
CC a transgenic organism comprising the recombinant polynucleotide, an anti-  
CC CGDD antibody, screening for compounds which bind to/modulate or are  
CC ant/agonists of CGDD or alter the expression of CGDD polynucleotide and a  
CC CGDD polynucleotide microarray. The polypeptides, polynucleotides,  
CC agonists and antagonists are useful for diagnosing, treating or  
CC preventing disorders associated with aberrant expression of CGDD,  
CC particularly cell proliferative (e.g. arteriosclerosis, atherosclerosis,  
CC cirrhosis, hepatitis, paroxysmal nocturnal haemoglobinuria, polycythaemia  
CC vera, psoriasis, primary thrombocytopaenia or cancer), developmental  
CC disorders (e.g. renal tubular acidosis, anaemia or mental retardation),  
CC neurological disorders (e.g. Alzheimer disease, Parkinson's disease or  
CC epilepsy), reproductive disorders (e.g. infertility or a disruption in  
CC the menstrual cycle), or autoimmune/inflammatory disorders (e.g. AIDS,  
CC (acquired immunodeficiency syndrome) allergies, asthma, autoimmune  
CC thyroiditis, contact dermatitis, Crohn's disease, diabetes mellitus,  
CC glomerulonephritis, gout, irritable bowel syndrome, multiple sclerosis,  
CC osteoarthritis, osteoporosis, pancreatitis, rheumatoid arthritis,  
CC uveitis, or viral, bacterial, fungal, parasitic, protozoal or helminthic  
CC infections. They are also useful in the assessment of the effects of  
CC exogenous compounds on the expression of nucleic acid and amino acid  
CC sequences of proteins associated with CGDD. The present sequence  
CC represents a CGDD protein  
XX  
SQ Sequence 2758 AA;

Query Match		99.1%;	Score 14748.5;	DB 5;	Length 2758;	
Best Local Similarity		99.3%;	Pred. No. 0;			
Matches 2751;		Conservative	0;	Mismatches	7;	
				Indels	11;	
				Gaps	3;	
QY	1	MDVKERKPYRSLTRRRDAERRY	TSSADSEEGKAPQKYS	SSSETLKAYDQDARLAYGSRV	60	
Db	1	MDVKERKPYRSLTRRRDAERRY	TSSADSEEGKAPQKYS	SSSETLKAYDQDARLAYGSRV	60	
QY	61	KDIVPQEAEEFCRTGANFTL	RELGLEEVTPPHGTL	YRTDIGLPQC	GYSMGAGSDADMEAD 120	
Db	61	KDIVPQEAEEFCRTGANFTL	RELGLEEVTPPHGTL	YRTDIGLPQC	GYSMGAGSDADMEAD 120	
QY	121	TVLSPEHPVRLWGRSTR	SGRSSCLSSRANSNLT	LTDTHEHENTETDHPGGLQNHARL	RTPP 180	
Db	121	TVLSPEHPVRLWGRSTR	SGRSSCLSSRANSNLT	LTDTHEHENTET--PGGLQNHARL	RTPP 178	
QY	181	PPLSHAHTPNQHHAAASIN	SLNRGNFTPRSNPSPAPT	DHLSLSGEPPAGGAQEP	PAHAQENWL 240	
Db	179	PPLSHAHTPNQHHAAASIN	SLNRGNFTPRSNPSPAPT	DHLSLSGEPPAGGAQEP	PAHAQENWL 238	
QY	241	LNSNIPLETNLGKQPF	LGTLDQNLJEMDILGAS	RHDGAYSDGHFLFKPGGT	SPLFCTTS 300	
Db	239	LNSNIPLETNLGKQPF	LGTLDQNLJEMDILGAS	RHDGAYSDGHFLFKPGGT	SPLFCTTS 298	
QY	301	PGYPLTSTTVYSP	PPRPLPRSTFARPAFNLK	KPSKYNWKAALS	SAIVISATLVILLAYF 360	
Db	299	PGYPLTSTTVYSP	PPRPLPRSTFARPAFNLK	KPSKYNWKAALS	SAIVISATLVILLAYF 358	
QY	361	VAMHLEGLNWHLQPM	EGQMYEITEDTASSWP	VPTDVS	LYPSGGTGLETPDRKGGTTEGK 420	
Db	359	VGKHLF--NWHLQPM	EGQMYEITEDTASSWP	VPTDVS	LYPSGGTGLETPDRKGGTTEGK 416	
QY	421	PSSFFPEDSFIDS	GEIDVGRRASQKIP	PGTFWR	SQVFDHPVHLKFNVS	LKAAALVGIIYG 480
Db	417	PSSFFPEDSFIDS	GEIDVGRRASQKIP	PGTFWR	SQVFDHPVHLKFNVS	LKAAALVGIIYG 476
QY	481	RKGLPPSHTQDF	VELLDGRRLLTQEAR	SLEGT	PROSRGTVPSSHETGFIQ	YLDSDGIWH 540
Db	477	RKGLPPSHTQDF	VELLDGRRLLTQEAR	SLEGT	PROSRGTVPSSHETGFIQ	YLDSDGIWH 536
QY	541	LAFYNDGKSEVVS	FLTTAIESVDNCP	SNCYNGDCIS	GTCHCFGLG	FLGPCGRASCPVL 600
Db	537	LAFYNDGKSEVVS	FLTTAIESVDNCP	SNCYNGDCIS	GTCHCFGLG	FLGPCGRASCPVL 596
QY	601	CSGNQYMKGRCLCH	SGWKGAEC	DVPTNQCIDVAC	SNHGTCTGT	CICNPGYKGESCEEV 660

Db	597	CSGNQYMKGRCLCHSGWKGAEC	DVPTNQCIDVACSNHGTCTIMGT	CICNPGYKGESCEEV	656
QY	661	DCMDPTCSGRGVCVRGECHCFV	GWGGTNCETPRATCLDQCSGHGTF	LPDTGLCSCDPSWT	720
Db	657	DCMDPTCSGRGVCVRGECHCFV	GWGGTNCETPRATCLDQCSGHGTF	LPDTGLCSCDPSWT	716
QY	721	GHDCSIEICAADCGGHGVCVGGT	CRCE	DGWMGAACDQACHPRCAEHGTCRDGKCECSPG	780
Db	717	GHDCSIEICAADCGGHGVCVGGT	CRCE	DGWMGAACDQACHPRCAEHGTCRDGKCECSPG	776
QY	781	WNGEHTTIAHYLDRVVKEGCPGL	CNGNGRCTLDLNGWHCVCQLGWRGAGCDTSMETACGD	840	
Db	777	WNGEHTTIAHYLDRVVKEGCPGL	CNGNGRCTLDLNGWHCVCQLGWRGAGCDTSMETACGD	836	
QY	841	SKNDGDLVDCMDPDCCLOPLCHINPL	CLGSPNPLDIIQETQVPVSQQNLHSFYDRIKF	900	
Db	837	SKNDGDLVDCMDPDCCLOPLCHINPL	CLGSPNPLDIIQETQVPVSQQNLHSFYDRIKF	896	
QY	901	LVGRDSTHIIIPGENPFDGGHACVIR	GQVMTSDGTPLVGNISFVNNPLFGYTISRQDGSF	960	
Db	897	LVGRDSTHIIIPGENPFDGGHACVIR	GQVMTSDGTPLVGNISFVNNPLFGYTISRQDGSF	956	
QY	961	DLVTNGGISIIILRFERAPFITQEH	TLWLPWDRFFVMETIIMRHEENEIPSCDLSNFARPN	1020	
Db	957	DLVTNGGISIIILRFERAPFITQEH	TLWLPWDRFFVMETIIMRHEENEIPSCDLSNFARPN	1016	
QY	1021	PVVSPLTSFASSCAEKGP	IVPEIQALQEEISISGCKMRLSYLSRTPGYKSVLRISLT	1080	
Db	1017	PVVSPLTSFASSCAEKGP	IVPEIQALQEEISISGCKMRLSYLSRTPGYKSVLRISLT	1076	
QY	1081	HPTIPFNLMKVHLMVA	VEGRLFRKWF	FAAADLSYYFIWDKTDVYNQKVFLSEAFVS	1140
Db	1077	HPTIPFNLMKVHLMVA	VEGRLFRKWF	FAAADLSYYFIWDKTDVYNQKVFLSEAFVS	1136
QY	1141	EYESCPDLILWEKRTTVLQGYE	IDASKLGGWSLDKHHALNIQSGILHKGNGENQFVSQQP	1200	
Db	1137	EYESCPDLILWEKRTTVLQGYE	IDASKLGGWSLDKHHALNIQSGILHKGNGENQFVSQQP	1196	
QY	1201	PVIGSIMGRRRSISCPSCNGLADGNKLLAP	VALTCGSDGSLYVGDFNYIRRI	FPSGNV 1260	
Db	1197	PVIGSIMGRRRSISCPSCNGLADGNKLLAP	VALTCGSDGSLYVGDFNYIRRI	FPSGNV 1256	
QY	1261	TNILELRNKDFRHSHSPA	KYYLATDPM	SGAVFLSDSNRRRVFKIKSTVVVKDLVKNSEV 1320	
Db	1257	TNILEL-----SHSPA	KYYLATDPM	SGAVFLSDSNRRRVFKIKSTVVVKDLVKNSEV 1309	
QY	1321	VAGTGDQCLPFDDTRCGDGGKATE	ATLTNPRGITVDKFG	LIYFVDGTMIRRIDQNGIIST 1380	
Db	1310	VAGTGDQCLPFDDTRCGDGGKATE	ATLTNPRGITVDKFG	LIYFVDGTMIRRIDQNGIIST 1369	
QY	1381	LLGSNDLT	SARPLSCDSVMDISQVRLEWPTDLAINPMDNSLYVLDDNNVVLQISENHQVRI 1440		
Db	1370	LLGSNDLT	SARPLSCDSVMDISQVRLEWPTDLAINPMDNSLYVLDDNNVVLQISENHQVRI 1429		
QY	1441	VAGRPMHCQVPGIDHFLLSKVAIHAT	LESATALAVSHNGVLYIAETDEKKINRIRQVTT	1500	
Db	1430	VAGRPMHCQVPGIDHFLLSKVAIHAT	LESATALAVSHNGVLYIAETDEKKINRIRQVTT	1489	
QY	1501	GEISLVAGAPSGCDCKNDANCDC	FGSGDDGYAKDAXLNT	PSSLAVCADGELYVADLGNIRI 1560	
Db	1490	GEISLVAGAPSGCDCKNDANCDC	FGSGDDGYAKDAXLNT	PSSLAVCADGELYVADLGNIRI 1549	
QY	1561	RFIRKNKPF	LNTQNMVELSSPIDQELYLFD	TGKHYTQSLPTGDYLYNFTYTGDG	DITL 1620
Db	1550	RFIRKNKPF	LNTQNMVELSSPIDQELYLFD	TGKHYTQSLPTGDYLYNFTYTGDG	DITL 1609
QY	1621	ITDNNGMVNVR	RDSTGMPLWLVPDQVY	WVTMTGNSALKSVTTQGH	ELAMTYHGNSG 1680
Db	1610	ITDNNGMVNVR	RDSTGMPLWLVPDQVY	WVTMTGNSALKSVTTQGH	ELAMTYHGNSG 1669
QY	1681	LLATKSNENGW	TTFYEDSFGRLTNVT	FPTGQVSSFRSDTSSVHVQVETSSKDD	VITTT 1740
Db	1670	LLATKSNENGW	TTFYEDSFGRLTNVT	FPTGQVSSFRSDTSSVHVQVETSSKDD	VITTT 1729





CC expression using antisense oligos, ribozymes and peptide nucleic acids.  
CC The polypeptides, nucleic acid molecules and antibodies are useful in the  
CC manufacture of a medicament for treating metabolic disorders, diabetes,  
CC anorexia, cancer, cardiovascular, infectious, neurodegenerative, immune  
CC and haematopoietic diseases as well as various dyslipidaemias.  
CC Accordingly, these molecules have many activities including anorectic,  
CC virucide, nootropic, antiinflammatory, neuroprotective, antilipaemic,  
CC anabolic and cardiant. Furthermore, they are useful in screening assays  
CC to identify small molecules that modulate or inhibit, for example,  
CC neurogenesis, wound healing and angiogenesis. The nucleic acids are also  
CC used as in chromosome mapping, tissue typing, preventive medicine and  
CC pharmacogenomics. This polypeptide is a murine NOVX protein of the  
XX invention.  
SQ Sequence 2775 AA;

Query Match		98.1%;	Score 14610;	DB 7;	Length 2775;		
Best Local Similarity		98.2%;	Pred. No. 0;				
Matches 2743; Conservative		2;	Mismatches 6;	Indels 42;	Gaps 12;		
QY	1	MDVKERKPYRSLTRRRDAERRY	TSSADSEEGKAPQKYS	SSSETLKAYDQDARLAYGSRV	60		
Db	1	MDVKERKPYRSLTRRRDAERRY	TSSADSEEGKAPQKYS	SSSETLKAYDQDARLAYGSRV	60		
QY	61	KDIVPOEAEFCRTGANFTL	RELGLEEVTPPHGTL	YRTDIGLPQC	GYSMGAGSDADMEAD 120		
Db	61	KDIVPOEAEFCRTGANFTL	RELGLEEVTPPHGTL	YRTDIGLPQC	GYSMGAGSDADMEAD 120		
QY	121	TVLSPEHPVRLWGRSTRSGRSS	CLSSRANSNLTLT	DEHENTETDHPGGLQNHARL	RTTP 180		
Db	121	TVLSPEHPVRLWGRSTRSGRSS	CLSSRANSNLTLT	DEHENTETDHPGGLQNHARL	RTTP 180		
QY	181	PPLSHAHTPNQHHAAASIN	SLNRGNFTPRSNPSPAPT	DHLSGEP	PAGGAQEP	HAQENWL 240	
Db	181	PPLSHAHTPNQHHAAASIN	SLNRGNFTPRSNPSPAPT	DHLSGEP	PAGGAQEP	HAQENWL 240	
QY	241	LNSNIPLERNLGKQP	FLGTLQDNLIEMDIL	GASRHDGAYS	SDGHFLFKPGGTSPL	FCCTS 300	
Db	241	LNSNIPLERNLGKQP	FLGTLQDNLIEMDIL	GASRHDGAYS	SDGHFLFKPGGTSPL	FCCTS 300	
QY	301	PGYPLTSSTVSPP	PRPLPRSTFARPAFLN	KKPSKYCNWKAALS	SAIVISATLVILLAYF	360	
Db	301	PGYPLTSSTVSPP	PRPLPRSTFARPAFLN	KKPSKYCNWKAALS	SAIVISATLVILLAYF	360	
QY	361	VAMHLFGLNWHLPQMEG	QMYEITEDTASSWPV	PTDVS	LYPSGGTGLETPDRK	GKGTTGK 420	
Db	361	VAMHLFGLNWHLPQMEG	QMYEITEDTASSWPV	PTDVS	LYPSGGTGLETPDRK	GKGTTGK 420	
QY	421	PSSFFPEDSFIDS	GEIDVGRASQKIPPGT	FWRSQVFDHPVHLKFN	VSGLKAAALVG	IYG 480	
Db	421	PSSFFPEASFIDS	GEIDVGRASQKIPPGT	FWRSQVFDHPVHLKFN	VSGLKAAALVG	IYG 480	
QY	481	RKGLPPSHTQDFVEL	LDGRLLTQEARSL	EGTPRQSRGTVP	SSSHETGFIQYLD	SGIWH 540	
Db	481	RKGLPPSHTQDFVEL	LDGRLLTQEARSL	EGTPRQSRGTVP	SSSHETGFIQYLD	SGIWH 540	
QY	541	LAFYNDGKESEVVS	FLTTAIESVDNCP	SNCYNGDCISGTC	HCFLGFLGPD	CGRASC	PVL 600
Db	541	LAFYNDGKESEVVS	FLSP--ESVDNCP	SNCYNGDCISGTC	HCFLGFLGPD	CGRASC	PVL 598
QY	601	CSNGQYMKGRCLCH	SGWKGAEC	DVPTNQCIDVACSNHGT	CI	TGTCICNPGYK	GESCEEV 660
Db	599	CSNGQYMKGRCLCH	SGWKGAEC	DVPTNQCIDVACSNHGT	CI	TGTCICNPGYK	GESCEE- 657
QY	661	DCMDPTCSGRGVC	VRGECHCFVGG	TNCETPRATCLD	QCSGHGT	FLPDTGLC	SDPSWT 720
Db	658	DCMDPTCSGRGVC	VRGECHCSVGG	TNCETPRATCLD	QCSGHGT	FLPDTGLC	SDPSWT 717
QY	721	GHDCSIEICAADCGGHG	VCVGGTCRC	EDGWMGAACD	QRACHPRCAEHG	TCRDGKCEC	SPG 780
Db	718	GHDCSIEICAADCGGHG	VCVGGTCRC	EDGWMGAACD	QRACHPRCAEHG	TCRDGKCEC	SPG 777
QY	781	WNGEHTI--AHYLD	RVVK--EGCPGL	CNGNGRCTL	DLNGWHCV	QCQLGWRG	AGCDTSMET 836

Db	778																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																					
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Db 1854 RVTRTEKIYDDHRKFTLRILYDQAGRPSLWSPSSRLNGVNVITYSPGGYTAGIQRGIMSER 1913

QY 1905 MEYDQAGRITSRIFADGKTWSYTYLEKSMVLLHSQRQYIFEFDKNDRLSSVTMPNVARQ 1964  
|||||

Db 1914 MEYDQAGRITSRIFADGKTWSYTYLEKAGV-----EFDKNDRLSSVTMPNVARQ 1962  
|||||

QY 1965 TLETIRSVGYRNIYQPEGNASVIQDFTEDGHLHTFYLGTRRRVIYKYGKLSKLAETL 2024  
|||||

Db 1963 TLETIRSVGYRNIYQPEGNASVIQDFTEDGHLHTFYLGTRRRVIYKYGKLSKLAETL 2022  
|||||

QY 2025 YDTTKVSFTYDETAGMLKTINLQNEGFTCTIRYRQIGPLIDRQIFRFTTEGMVNARFDYN 2084  
|||||

Db 2023 YDTTKVSFTYDETAGMLKTINLQNEGFTCTIRYRQIGPLIDRQIFRFTTEGMVNARFDYN 2082  
|||||

QY 2085 YDNSFRVTSMQAVINETPLPIDLYRYDDVSGKTEQFGKFGVIYYDINQIITAVMTHTKH 2144  
|||||

Db 2083 YDNSFRVTSMQAVINETPLPIDLYRYDDVSGKTEQFGKFGVIYYDINQIITAVMTHTKH 2142  
|||||

QY 2145 FDAYGRMKEVQYEIFRSILMYMWTVOYDNMGRVVKKELKVGYPYANTTRYSYEYDADGQLQT 2204  
|||||

Db 2143 FDAYGRMKEVQYEIFRSILMYMWTVOYDNMGRVVKKELKVGYPYANTTRYSYEYDADGQLQT 2202  
|||||

QY 2205 VSINDKPLWRYSYDLNGNLHLLSPGNSARLTPLRYDIRDRITRLGDVQYKMDDEGFLRQR 2264  
|||||

Db 2203 VSINDKPLWRYSYDLNGNLHLLSPGNSARLTPLRYDIRDRITRLGDVQYKMDDEGFLRQR 2262  
|||||

QY 2265 GGDIFEYNSAGLLIKAYNRAGSWSVRYRYDGLGRRVSSKSSHHLQFFYADLTNPTKVT 2324  
|||||

Db 2263 GGDIFEYNSAGLLIKAYNRAGSWSVRYRYDGLGRRVSSKSSHHLQFFYADLTNPTKVT 2322  
|||||

QY 2325 HLYNHSSEITSLYYDLQGHLPAMELSSGDEFYIACDNIGTPLAVFSGTGLMIKQILYTA 2384  
|||||

Db 2323 HLYNHSSEITSLYYDLQGHLPAMELSSGDEFYIACDNIGTPLAVFSGTGLMIKQILYTA 2382  
|||||

QY 2385 YGEIYMDTNPNFQIIIGYHGGLYDPLTKLVHMRDYYDLAGRWTSPDHELWKHLSSSNV 2444  
|||||

Db 2383 YGEIYMDTNPNFQIIIGYHGGLYDPLTKLVHMRDYYDLAGRWTSPDHELWKHLSSSNV 2442  
|||||

QY 2445 MPENLYMFKNNNPISNSQDIKCFMTDVNSWLLTFGQLHNVIPGYPKPDMDAMEPSYELI 2504  
|||||

Db 2443 MPENLYMFKNNNPISNSQDIKCFMTDVNSWLLTFGQLHNVIPGYPKPDMDAMEPSYELI 2502  
|||||

QY 2505 HTQMKTQEWDNK-----SILGVQCEVQKQLKAFVTLERFDQLYGSTITSCQQAPKT 2556  
|||||

Db 2503 HTQMKTQEWDNKSVIPAQCQSILGVQCEVQKQLKAFVTLERFDQLYGSTITSCQQAPKT 2562  
|||||

QY 2557 KKFASSGSVFGKGVKFPALKDGRVTTDIIISVANEDGRRVAAILNHAHYLENLHFTIDGVDT 2616  
|||||

Db 2563 KKFASSGSVFGKGVKFPALKDGRVTTDIIISVANEDGRRVAAILNHAHYLENLHFTIDGVDT 2622  
|||||

QY 2617 HYFVKPGPSEGDLAILGLSGRRRTLENGVNVTVSQINTVLNGRTRRYTDIQLQYGALCLN 2676  
|||||

Db 2623 HYFVKPGPSEGDLAILGLSGRRRTLENGVNVTVSQINTVLNGRTRRYTDIQLQYGALCLN 2682  
|||||

QY 2677 TRYGTTLDEEKARVLELARQAVRQAWAREQQRLREGEGRLAWTEGEKQQVLSTGRVQG 2736  
|||||

Db 2683 TRYGTTLDEEKARVLELARQAVRQAWAREQQRLREGEGRLAWTEGEKQQVLSTGRVQG 2742  
|||||

QY 2737 YDGFVFISVEQYPELSDSANNIHFMRQSEMGR 2769  
|||||

Db 2743 YDGFVFISVEQYPELSDSANNIHFMRQSEMGR 2775  
|||||

RESULT 5  
ABB98401  
ID ABB98401 standard; protein; 2794 AA.  
XX  
AC ABB98401;  
XX  
DT 21-OCT-2002 (first entry)  
XX  
DE Human NOV1, a TEN-M4 like protein.  
XX

KW Human; NOV1; cytostatic; Cardiant; Antiinflammatory; Immunosuppressive;  
KW Antiallergic; Haemostatic; Anti-HIV; Antidiabetic; Anorectic;  
KW Antiasthmatic; Nephrotropic; Hepatotropic; Neuroprotective; Nootropic;  
KW Antibacterial; Virucide; Antiparasitic; Relaxant; Anticonvulsant;  
KW Gene Therapy; NOV; cancer; heart disease; inflammation;  
KW autoimmune disorder; allergy; blood disorder; AIDS; diabetes; obesity;  
KW asthma; IGA nephropathy; cirrhosis; arthritis; Alzheimer's disease;  
KW infection; stroke; muscular dystrophy; epilepsy; wasting disorder;  
KW TEN-M4 like protein.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Misc-difference 379 /note= "Encoded by ATGACGGATT"  
XX  
PN WO200255704-A2.  
XX  
PD 18-JUL-2002.  
XX  
PF 09-JAN-2002; 2002WO-US000554.  
XX  
PR 09-JAN-2001; 2001US-0260417P.  
PR 10-JAN-2001; 2001US-0260831P.  
PR 28-FEB-2001; 2001US-0272338P.  
PR 09-MAR-2001; 2001US-0274876P.  
PR 18-APR-2001; 2001US-0284704P.  
XX  
PA (CURA-) CURAGEN CORP.  
XX  
PI Padigaru M, Li L, Zerhusen BD, Casman SJ, Shenoy S, Spytek KA;  
PI Zhong M, Gangolli EA, Burgess CE, Patturajan M, Vernet CAM;  
PI Taylor S, Tchernev VT, Miller CE, Guo X, Boldog FL, Grosse WM;  
PI Alsobrook JP, Gerlach V, Edinger S, Rothenberg ME, Ellerman K;  
PI Macdougall J, Malyankar U, Millet I, Peyman J, Smithson G;  
PI Gunther E, Stone DJ;  
XX  
DR WPI; 2002-590674/63.  
DR N-PSDB; ABN85378.  
XX  
PT NOVX polypeptides and encoding polynucleotides, useful for preventing or  
PT treating NOVX-associated disorders e.g. cancer, inflammation, or  
PT Alzheimer's disease, and in chromosome mapping, tissue typing or  
PT pharmacogenomics.  
XX  
PS Claim 1; Page 10-11; 358pp; English.  
XX  
CC The present sequence is the protein sequence for a NOV protein. The NOV  
CC proteins and coding sequences are useful for treating or preventing NOV-  
CC associated disorders or in the manufacture of a medicament for treating  
CC the disorders, such as cancer, heart disease, inflammation, autoimmune  
CC disorders, allergies, blood disorders, AIDS, diabetes, obesity, asthma,  
CC IGA nephropathy, cirrhosis, arthritis, Alzheimer's disease, infections  
CC (e.g. bacterial, viral, parasitic), stroke, muscular dystrophy, epilepsy,  
CC and other wasting disorders associated with chronic diseases. NOV1 is a  
CC TEN-M4 like protein and the NOV1 gene is localised to chromosome 11  
XX  
SQ Sequence 2794 AA;  
Query Match 96.8%; Score 14406.5; DB 5; Length 2794;  
Best Local Similarity 96.7%; Pred. No. 0;  
Matches 2704; Conservative 21; Mismatches 41; Indels 31; Gaps 11;

QY 1 MDVKERKPYRSLTRRRDAERRYTSSSADSEEGKAPQKSYSSSETLKAYDQDARLAYGSRV 60  
|||||  
Db 1 MDVKERKPYRSLTRRRDAERRYTSSSADSEEGKAPQKSYSSSETLKAYDQDARLAYGSRV 60  
|||||

QY 61 KDIVPQEAEEFCRTGANFTLRELGLEEVTPPHGTYRTDIGLPQCGYSMGAGSDADMEAD 120  
|||||

Db 61 KDIVPQEAEEFCRTGANFTLRELGLEEVTPPHGTYRTDIGLPQCGYSMGAGSDADMEAD 120  
|||||

QY 121 TVLSPHPVRLWGRSTRSGRSSCLSSRANSNLTLTDEHENTETDHPGGLQNHARLRTTP 180  
|||||



Db 121 TVLSPEHPVRLWGRSTRSGRSSCLSSRANSNLTLTDEHENTETDHPGGLQNHARLRTPP 180

Qy 181 PPLSHAHTPNQHHAAASINSLNRGNFTPRSNPSPAPT D H S L S G E P P A G G A Q E P A H A Q E N W L 240

Db 181 PPLSHAHTPNQHHAAASINSLNRGNFTPRSNPSPAPT D H S L S G E P P A G G A Q E P A H A Q E N W L 240

Qy 241 LNSNIPLETNRNLGKQPFGLGTLQDNLIEMDILGASRHDGAYS D G H F L F K P G G T S P L F C T T S 300

Db 241 LNSNIPLETNRNLGKQPFGLGTLQDNLIEMDILGASRHDGAYS D G H F L F K P G G T S P L F C T T S 300

Qy 301 PGYPLTSSTVSPPPRPLPRSTFARPAFNLLKPKPSKYNWKCAALSAIVISATLVILLAYF 360

Db 301 PGYPLTSSTVSPPPRPLPRSTFAWPAFNLLKPKPSKYNWKCAALSAIVISATLVILLAYF 360

Qy 361 VAMHLFGLNHLQPMEGQMYEITEDTASSWPVPTDVSLYPSGGTGLET PDRKKGTTTEGK 420

Db 361 VAMHLFGLNHLQPMEGQMYEITEDTASSWPVPTDVSLYPSGGTGLET PDRKKGTTTEGK 420

Qy 421 PSSFFPEDSFIDSGEIDVGRRASQKIPPGT F W R S Q V F I D H P V H L K F N V S L G K A A L V G I Y G 480

Db 421 PSSFFPEASFIDSGEIDVGRRASQKIPPGT F W R S Q V F I D H P V H L K F N V S L G K A A L V G I Y G 480

Qy 481 RKGLPPSHTQDFVELLDGRRLLTQEARSLLEGTPRQSRGTVPSSSHETGFIQYLDSGIWH 540

Db 481 RKGLPPSHTQDFVELLDGRRLLTQEARSLLEGTPRQSRGTVPSSSHETGFIQYLDSGIWH 540

Qy 541 LAFYNDGKESVVSLTTAIESVDNCPSNCYGNGDCISGTCHCFGLGFLGPD CGRASC PVL 600

Db 541 LAFYNDGKESVVSLTTAI--LDSW-ALCLGDGECVSGTCHCFGLGPD C S R A A C P V L 597

Qy 601 CSGNGOYMKGRCLCHSGWKGAECDPVTNQCIDVACSNHGTCITGTCTICNPGYKGESCEEV 660

Db 598 CSGNGOYSKGRCLCFSGWKGTGTECDVPTTQCIDPQCGGRGICIMGSCACNSGYKGESCEE 657

Qy 661 DCMDDPTCSGRGVCVRGECHCFVWGWTNCETPRATCLDQCSGHGTFLPDTGLCSCDPSWT 720

Db 658 DCIDPGCSNHGVCIHGECHCSPGWGGNCEILKTMCPDQCSGHGTYLQESGSC TCDPNWT 717

Qy 721 GHDCSIEICAADCGHGVCVGGTCRCEDGWMGAACDQ RACHPRCAEHGTCRDGKCECSPG 780

Db 718 GPDCSNEICSVDCSGSHGVCMGGTCRCBEGWGPACNQ RACHPRCAEHGTCRDGKCECSPG 777

Qy 781 WNGEHCTI--AHYLD R V V K --EGCPGLCNGNGRCTLDLNGWHCV C Q L G W R G A G C D T S M E T 836

Db 778 WNGEHCTISLAHYLD R V V K L S E G C P G L C N G N G R C T L D L N G W H C V C Q L G W R G A G C D T S M E T 837

Qy 837 ACGDSKNDGDGLVDCMDPCCLOPLCHINPLCLGSPNPLDIIQETQVPVSQQNLHSFYD 896

Db 838 ACGDSKNDGDGLVDCMDPCCLOPLCHINPLCLGSPNPLDIIQETQVPVSQQNLHSFYD 897

Qy 897 RIKFLVGRDSTHIIIPGENPFDGGHACVIRGOVMTSDGTPLVGVNISFVNPNPLFGYTISRQ 956

Db 898 RIKFLVGRDSTHIIIPGENPFDGGHACVIRGOVMTSDGTPLVGVNISFVNPNPLFGYTISRQ 957

Qy 957 DGSFDLVTNGGISIIILRFERAPFITQEH TLWLPWD R F V M E T I I M R H E E N E I P S C D L S N F 1016

Db 958 DGSFDLVTNGGISIIILRFERAPFITQEH TLWLPWD R F V M E T I I M R H E E N E I P S C D L S N F 1017

Qy 1017 ARPNPVVSPSPLTSFASSCAEKGPVPEIQALQEEISISGCKMRLSYLSSRTPGYKSVL R 1076

Db 1018 ARPNPVVSPSPLTSFASSCAEKGPVPEIQALQEEISISGCKMRLSYLSSRTPGYKSVL R 1077

Qy 1077 ISLTHTIPFNLMKVHLMVAVEGR LFRKWFAAAPDLSYFIW D K T D V Y N Q K V F G L S E A F V 1136

Db 1078 ISLTHTIPFNLMKVHLMVAVEGR LFRKWFAAAPDLSYFIW D K T D V Y N Q K V F G L S E A F V 1137

Qy 1137 SVGYEYESCPDLILWEKRTTVLQGYEIDASKLGWSLDKHHALNIQS-GILHKNGENQF 1195

Db 1138 SVGYEYESCPDLILWEKRTTVLQGYEIDASKLGWSLDKHHALNIQS G G I L H K N G E N Q F 1197

Qy 1196 VSQOPPVIGSIMNGRRRRSISCPSCNGLADGNKLLAPVALTCGSDGSLYVGDFNYIRRI F 1255

Db 1198 VSQOPPVIGSIMNGRRRRSISCPSCNGLADGNKLLAPVALTCGSDGSLYVGDFNYIRRI F 1257

Qy 1256 PSGNVTNILEL--RNKDFRSHSPAHKYYLATDMSGAVFLSDSNSRRRVFKIKSTVVVKD 1313

Db 1258 PSGNVTNILELRVRNKDFRSHSPAHKYYLATDMSGAVFLSDSNSRRRVFKIKSTVVVKD 1317

Qy 1314 LVKNSEVWAGTGDCQLPFDDTRCGDGGKATEATLTNPR--GITVDKFGLLIYFVDGTMIR 1370

Db 1318 LVKNSEVWAGTGDCQLPFDDTRCGDGGKATEATLTNPRGPPGITVDKFGLLIYFVDGTMIR 1377

Qy 1371 RIDQNGIISTLLGSNDLTSARPLSCDSVMDISQVR--LEWPTDLAINPMDNSLYVL DNN 1427

Db 1378 RIDQNGIISTLLGSNDLTSARPLSCDSVMDISQVRQVHLEWPTDLAINPMDNSLYVL DNN 1437

Qy 1428 VVLQISENHQVRIVAGRPMHCQVPGIDHFLLSKVAIHATLESATALAVSHNGVLYIAETD 1487

Db 1438 VVLQISENHQVRIVAGRPMHCQVPGIDHFLLSKVAIHATLESATALAVSHNGVLYIAETD 1497

Qy 1488 EKKINRIRQVTTSGEISLVAGAPSGCDCKNDANCD CFSGDDGYAKDAKLNTPSSLAVCAD 1547

Db 1498 EKKINRIRQVTTSGEISLVAGAPSGCDCKNDANCD CFSGDDGYAKDAKLNTPSSLAVCAD 1557

Qy 1548 GELYVADLGNIRIRFIRKNKPF LNTQNMYBELSSPIDQELYLFDTTGKHLYTQSLPTGDYL 1607

Db 1558 GELYVADLGNIRIRFIRKNKPF LNTQNMYBELSSPIDQELYLFDTTGKHLYTQSLPTGDYL 1617

Qy 1608 YNFTYTGDGDI TLTDNNGNMVNVRDSTGMPLWLVPDGOVYVWTMG TNSALKS VTTQG 1667

Db 1618 YNFTYTGDGDI TLTDNNGNMVNVRDSTGMPLWLVPDGOVYVWTMG TNSALKS VTTQG 1677

Qy 1668 HELAMMTYHGNSGLLATKSNENGWTTTFEYD SFGRLTNVTFTPTQGVSSFRSDT DSSVHVQ 1727

Db 1678 HELAMMTYHGNSGLLATKSNENGWTTTFEYD SFGRLTNVTFTPTQGVSSFRSDT DSSVHVQ 1737

Qy 1728 VETSSKDDVTITTNLSASGAFYTL LQDQVRNSYYIGADGSLRLL L L L A N G M E V A L Q T E P H L L 1787

Db 1738 VETSSKDDVTITTNLSASGAFYTL LQDQVRNSYYIGADGSLRLL L L L A N G M E V A L Q T E P H L L 1797

Qy 1788 AGTVNPTVGKRNVTLPIDNGLNLVEWRQKEQARGQVTFGRRLR--VHNRLNLSLDFD 1844

Db 1798 AGTVNPTVGKRNVTLPIDNGLNLVEWRQKEQARGQVTFGRRLRVLQVHNRNLLSLDFD 1857

Qy 1845 RVTRTEKIYDDHRKFTLRILYDQAGRPSLWSPSSRLNGVNVTYSPGGYIAGIQRGIMSER 1904

Db 1858 RVTRTEKIYDDHRKFTLRILYDQAGRPSLWSPSSRLNGVNVTYSPGGYIAGIQRGIMSER 1917

Qy 1905 MEYDQAGRITSRIFADGKTWSYTYLEK---SMVLLLLHSQRQYIFEFDKNDRLSSVTMPN 1960

Db 1918 MEYDQAGRITSRIFADGKTWSYTYLEKAGVQSMVLLLLHSQRQYIFEFDKNDRLSSVTMPN 1977

Qy 1961 VARQTLETIRSVGYRNIYQPPEGNASVIQDFTEDGHL LHTFVLGTGRRVIYKYGKLSKL 2020

Db 1978 VARQTLETIRSVGYRNIYQPPEGNASVIQDFTEDGHL LHTFVLGTGRRVIYKYGKLSKL 2037

Qy 2021 AETLYD TTKVSFTYDETAGMLKTINLQNEGFTCTIRYRQIGPLIDRQIFRFTEEGMVNAR 2080

Db 2038 AETLYD TTKVSFTYDETAGMLKTINLQNEGFTCTIRYRQIGPLIDRQIFRFTEEGMVNAR 2097

Qy 2081 FDYNYDNSFRVTSMQAVINETPLPIDLYR D D V S G K T E Q F G K F G V I Y Y D I N Q I I T T A V M T 2140

Db 2098 FDYNYDNSFRVTSMQAVINETPLPIDLYR D D V S G K T E Q F G K F G V I Y Y D I N Q I I T T A V M T 2157

Qy 2141 HTKHFDAYGRMKEVQYEIFRSLMYMVTVQYDNMGRVVKELKVGPPYANTTRYSEYDADG 2200

Db 2158 HTKHFDAYGRMKEVQYEIFRSLMYMVTVQYDNMGRVVKELKVGPPYANTTRYSEYDADG 2217

Qy 2201 QLQTVSINDKPLWRYSYDLNGLNHL LSPGNSARLTPLRYDIRDRITRLGDVQYKMD E D G F 2260

Db 2218 QLQTVSINDKPLWRYSYDLNGLNHL LSPGNSARLTPLRYDIRDRITRLGDVQYKMD E D G F 2277

Qy 2261 LRQRGGDIFEYNSAGLLIKAYNRAGSWSVRYRYDGLGRRVSSKSSHHLQFFYADLTNP 2320

Db 2278 LRQRGGDIFEYNSAGLLIKAYNRAGSWSVRYRYDGLGRRVSSKSSHHLQFFYADLTNP 2337







Db 2397 I-GKDPAPFNLYMFRNNPNASKIHVDKDYITDVSWSLVTFGFHLHNAIPGFPVPKFDLTE 2455

QY 2499 PSYELIHTQMKTOEWDNSKSI LGVQCEVQKQLKAFVTLERFDQLYGSTITSCQQAPKTKK 2558

Db 2456 PSYELV----KSQWDDPIPIFGVQQQVARQAKAFLSLGKMAEVQ-----VSRRRAGGAQS 2507

QY 2559 ---FASSGSVFGKGVKPAKDKGRVTTDIIISVANEDGRRVAAILNHAHYLENLHFTIDGVD 2615

Db 2508 WLWFATVKSLIGKGVMLAVSQGRVQTNVLNIANEDCIKVAAVLNNAFYLENLHFTIEGKD 2567

QY 2616 THYFVKPGPSEGDLA ILGLSGGRRRTLENGVNVTVSQINTVLNGRTRRRYTDIQLQYGALCL 2675

Db 2568 THYFIKTTTPESDLGTLRLTSGRKALENGINVTVSQSTTVWNGRTRRFADVEMQFGALAL 2627

QY 2676 NTRYGTTLDEEKARVLELARQAVRQAWAREQQRLREGEGLRAWTEGEKQVLSGTRVQ 2735

Db 2628 HVRYGMTLDEEKARILEQARQALARAWAREQQRVDRDGEGARLWTEGEKRLLSAGKVQ 2687

QY 2736 GYDGFVFVISVEQYPELSDSANNIHFMROSEMGR 2769

Db 2688 GYDGYVLSVEQYPELADSANNIQFLRQSEIGRR 2721

RESULT 7

ID ADH41969

XX ADH41969 standard; protein; 2721 AA.

AC ADH41969;

XX

DT 25-MAR-2004 (first entry)

XX Novel human protein NOV40s.

KW cardiovascular; antiarteriosclerotic; hypotensive; cytostatic; anorectic;  
KW antidiabetic; immunosuppressive; anti-HIV; neuroprotective; nootropic;  
KW antiparkinsonian; antiasthmatic; antiinfertility; cardiomyopathy;  
KW atherosclerosis; hypertension; cancer; obesity; diabetes; AIDS;  
KW multiple sclerosis; graft-versus-host disease; Alzheimer's disease;  
KW Parkinson's disease; asthma; fertility disorder; chromosome mapping;  
KW tissue typing; preventive medicine; pharmacogenomic; vaccine.

XX Homo sapiens.

XX WO2003102159-A2.

XX

PD 11-DEC-2003.

XX

PF 04-JUN-2003; 2003WO-US017573.

XX

PR 04-JUN-2002; 2002US-0385490P.

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PR 07-JUN-2002; 2002US-0387078P.

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(CURA-) CURAGEN CORP.

PI Alsobrook JP, Anderson DW, Baumgartner JC, Berghs C, Boldog FL;  
PI Burgess CE, Casman SJ, Catterton E, Dhanabal M, Edinger SR;  
PI Ellerman K, Ettenberg S, Gangolli EA, Gerlach VL, Gorman L;  
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PI Khrantsov NV, Larochelle WJ, Li L, Liang H, Low K, Macdougall JR;  
PI Maclachlan T, Malyankar UM, Mcqueeney K, Mezick AJ, Miller CE;  
PI Millet I, Padigar M, Patturajan M, Peyman JA, Qian X, Rastelli L;  
PI Rieger DK, Rothenberg ME, Shenoy SG, Shimkets RA, Smithson G;  
PI Spytek KA, Stone DJ, Sukumaran S, Szekeres ES, Vernet CAM, Voss EZ;  
PI Wolenc AR, Zhong M, Zhong H;

WPI; 2004-053467/05.

N-PSDB; ADH41968.

New NOVX polypeptides and nucleic acid molecules useful for preventing or treating NOVX-associated disorders, e.g. cancer, cardiomyopathy, atherosclerosis or diabetes, in chromosome mapping, tissue typing or in pharmacogenomics.

Claim 2; SEQ ID NO 522; 1503pp; English.

The invention relates to 566 new isolated human polypeptides and their encoding genes, sequences that are at least 95% identical to these or sequences comprising one or more conservative substitutions in these. The polypeptide, polynucleotide and antibodies against the polypeptides are useful in diagnosing, treating or preventing NOVX-associated disorders, e.g. cardiomyopathy, atherosclerosis, hypertension, cancer, obesity, diabetes, AIDS, multiple sclerosis, graft-versus-host disease, Alzheimer's disease, Parkinson's disease, asthma, or fertility disorders. The nucleic acids are further used as hybridization probes, in chromosome mapping, tissue typing, preventive medicine, and pharmacogenomics. The polypeptides are also useful as vaccines. This sequence represents an example of the polypeptide of the invention.

Sequence 2721 AA;

XX SQ



Query Match		68.7%;	Score 10221;	DB 8;	Length 2721;
Best Local Similarity		67.0%;	Pred. No. 0;		
Matches 1873;		Conservative 362;	Mismatches 461;	Indels 98;	Gaps 20;
Qy	1	MDVKERKPYRSLTR-RRDAERRYTSSSADSEEGKAP-QKSYSSETLKAYDQD-ARLAYG	57		
Db	1	MDVKERRPYCSLTKSRREKERRYNTSSADNEECRVPTQKSYSSETLKAFDHDSSRLLYG	60		
Qy	58	SRVKDIVPQEAEEFCRTGANFTLRELGLBEVTPPHGTLYRTDGLPCQGYSMGAGSDADM	117		
Db	61	NRVKDLVHREADFTROQNFTLRQLGVCEPATRRGLAFCAEMGLPHRGYSISAGSDADT	120		
Qy	118	EADTVLSPPEHVRWLGRSTRSGRSSCLSSRANSNLTLTDTEHEN---TETDHPGGLQNH	174		
Db	121	ENEAVMSPEHAMRLWGRGVKSGRSSCLSSRSNSALTTLTDTEHENSSENEQPASNQOS	180		
Qy	175	RLRTPPPPLSHAHTPNQHAAASINSLNRGNFTPRSNPSPAPTDHLSGEPPAGGAQ----	230		
Db	181	TLQPLPP---SHKQHSAQHH-PSITSLNRNSLNTNRRNQSPAP-----PAALPAELQTT	229		
Qy	231	-EPAHAQENWLLNSNIPLETRNLGKQPFGLGTLQDNLIEMDILGASRHDGAYSDBGHFLFKP	289		
Db	230	PESVOLQDSVWVLSNVPLESR-----HFLFKT	256		
Qy	290	G-GTSPLFCTTSPGYPLTSSVYSPPPRPLPRSTFARPAFNLKKPSKYCNWKCAALSAIV	348		
Db	257	GTGTTPLFSTATPGYTMASGSVYSPPTPLPRNTLSRAFKPKSSKYCSWKCTALCAVG	316		
Qy	349	ISATLVILLAYFVAMHLFGLNWHLQPMEGQMYE---ITEDTASSWPVPTDVSLYPSGGTG	405		
Db	317	VSVLLAILLSYFIAMHLFGLNWLQQTENDTFENGKVNSDT-----MPTNTVSLPSG---	368		
Qy	406	LETDPDRKGKGTTEGKPSFFPEDSFIDSGEIDVGRRASQKIPPGTFWRSQVFIDHPVHLK	465		
Db	369	-----DNGKLGFTQENNTIDSGELDIGRRAOIEIPPGIFWRSQLFIDQPFQFLK	417		
Qy	466	FNVSLGKAALVGIYGRKGLPPSHTQDFVELLDGRRLLTQBARSLLEGTPRQSRGIVPPSS	525		
Db	418	FNISLQDALIGVYGRKGLPPSHTQYDFVELLDGSRLLIARQRSLLETERAGRQARSVSL	477		
Qy	526	HETGFIQYLDSGIWHLAFYNDGKESVVSFLTTAIESVDNCPSNICYNGDCISGTCHCFL	585		
Db	478	HEAGFIQYLDSGIWHLAFYNDGKNAEQVSFNTIVIESVVECPRNCNGECVSGTCHCFP	537		
Qy	586	GFLGPDGGRASCPVLCSGNGQYMKGRCLCHSGWKGAECDVPTNQCIDVACSNHGTITGT	645		
Db	538	GFLGPDCSRAAACPVLCSGNGQYSGKRCCLCFSGWKGTGTECDVPTTQCIDPQCGRGICIMS	597		
Qy	646	CICNPGYKGESCEEVDCMDPTCSGRGVCVRGECHCFVGGWGTNCETPRATCLDQCSGHT	705		
Db	598	CACSSGYKGESCEEADCIDPGCSNHGVCIHGECHCSPGWGGSNCEILKTMCPDQCSGHT	657		
Qy	706	FLPDTGLCSCDPSPWTGHDCSIIEICAADCGHGVCVGGTCRCEDGWMGAACDQACHPRCA	765		
Db	658	YLQESGSTCDPNWTGPDCCSNEICSVDCSGSHGVCMMGGTCRCIEGWTGPACNQACHPRCA	717		
Qy	766	EHGTCRDGKCECSPGWNGEHCTIAHYLDRVV-----KEGCPGLCNGNGRCTLDLNGWHC	819		
Db	718	EHGTCRDGKCECSQGWNGEHCTIAHYLDKIVKOKIGYKEGCPGLCSNNGRCTLDQGGHC	777		
Qy	820	VCQLGWRGAGCDTSMETACGDSKNDGDGLVDCMDPDCCLOPLCHINPLCLGSPNPLDII	879		
Db	778	VCQPGWRGAGCDVAMETLCTDSKDNEGDGLIDCMDPDCCLOQSSCQNPQYCRGLPDPQDII	837		
Qy	880	QETQVPVSQNLHSHFYDRIKFLVGRDSTHIIPGENPFDGGHACVIRGOVMTSDGTPLVG	939		
Db	838	SQSLQSPSQQAASFYDRISFLIGSDSTHVIPGESPFNKSLASVIRGOVLTADGTFPLIG	897		
Qy	940	NISFVNNPLFGYTIISRQDGSFDLVTNGGISIILRFERAPFITQEHLLWLPWDRFFVMETI	999		
Db	898	NVSFPHYPEYGYTITRQDGMFDLVANGGASLTLVFERSEFLTQYHTWIPWNVFMVMDTL	957		

Qy	1000	IMRHEENEIPSCDLSNFARPNPVVSPSPLTSPASSCAEKGPVPEIQALQEEHISISGCKM	1059
Db	958	VMEKEENDIPSCDLSGCFVRPNPIIVSSPLSTFFRSSPEDSPIIPETQVHLHEETIPGTDL	1017
Qy	1060	RLSYLSSRTPGYKSVLRISLTHPTIPFNLMKVHLMVAVEGRLEFRKWFAPAAPDLSYYFIWD	1119
Db	1018	KLSYLSSRAAGYKSVLKITMTQSIIPFNLMKVHLMVAVVGRLFQKQFPASPENLAYTFIWD	1077
Qy	1120	KTDVYNQKVFGLSEAFVSVGYEYESCPDLILWEKRTTVLQGYEIDASKLGWSLDKHHAL	1179
Db	1078	KTDAYNQKVYGLSEAVVSVGYEYESCLDLTLWEKRTAILQGYELDASNMGWTLDKHHVL	1137
Qy	1180	NIQSGILHKNGENQFVSQQPPVIGSIMGNRRRRSISCPSCNGLADGNKLLAPVALTCGS	1239
Db	1138	DVQNGILYKNGENQFISQQPPVSSIMGNRRRRSISCPSCNGQADGNKLLAPVALACGI	1197
Qy	1240	DGSLYVGDFNYIRRIFFPSGNVTNILELRNKDPRHSHSPAHKYYLATDPMSCAVFLSDSNS	1299
Db	1198	DGSLYVGDFNYVRRIFFPSGNVTSVLELRNKDFRHSSNPAHRYYLATDPVTGDLVYSDTNT	1257
Qy	1300	RRVFKIKSTVVVKDLVKNSEVVAGTGDQCLPFDDTRCGDGGKATEATLTNPRGITVDKFG	1359
Db	1258	RRYRPKSLTGAKDLTKNAEVVAGTGEQCLPFDEARCGDGGKAVEATLMSPKGMAVDKNG	1317
Qy	1360	LIYFVDGTMIRRIDQNGIISTLLGSNDLTSARPLSCDSVMDISQVRLEWPTDLAINPMDN	1419
Db	1318	LIYFVDGTMIRKVDQNGIISTLLGSNDLTSARPLTCDTSMHISQVRLEWPTDLAINPMDN	1377
Qy	1420	SLYVLDNNVVLQISENHQVRIVAGRPMHCQVPGIDHFLLSKVAIHATLESATALAVSHNG	1479
Db	1378	SIYVLDNNVVVLQITENRQVRIAAGRPMHCQVPGVE-YPVGKHAVQTTLESATAIAVSYSG	1436
Qy	1480	VLYIAETDEKKINRIQVTTSGEISLVAGAPSGCDCKNANDCFSGDDGYAKOAKLNTP	1539
Db	1437	VLYITETDEKKINRIQVTTDGEISLVAGIPSECDCKNDANCDCYSGDGYAKDAKLSAP	1496
Qy	1540	SSLAVCADGELYVADLGNIRIRFIRKNKPPFLNTQNMVELSSPIDQELYLFDTTGKHLYTQ	1599
Db	1497	SSLAASPDGTLIYADLGNIRIRAVSKNKPLLNSMNFYEVASPTDQELYIFDINGTHQYTV	1556
Qy	1600	SLPTGDYLYNFTYTGDDITLITDNNGNMNVNRRDSTGMPLWLVPDQGVVWVTMTGNSA	1659
Db	1557	SLVTGDYLYNFSYNDNDITAVTDSNGNTLRIRRDPNRMPVRVVSFDNQVILWTIGTNGC	1616
Qy	1660	LKSVTTQGHELAMWTHGNSGLLATKSNENGWTTTFEYDYSFGRLTNVTFTPTGOVSSFRSD	1719
Db	1617	LKGMTAQGLELVLFYTHGNSGLLATKSDETGWTTFDYDSEGRLTNVTFTPTGVVTLNHGD	1676
Qy	1720	TDSSVHVQVETSSK-DDVTITTNLSAGAFYTLQDOVRNSYYIGADGSLRLLLANGMEV	1778
Db	1677	MDKAITVDIESSSREEDVSITSNLSSIDSFYTMVQDQLRNSYQIGYDGSRLRIYASGLDS	1736
Qy	1779	ALQTEPHLLAGTVNPTVGKRNVTLPIDNGLNLVEWRQKQARGQVTFGRRLRVHNRNL	1838
Db	1737	HYQTEPHVLAGTANPTVAKRNMTLPGENGQNLVEWRFRKEQAQGVNVEGRKLRVNGRNL	1796
Qy	1839	LSLDFDRVTRTEKIYDDHRKFTRLRLIYDQAGRPSSLWSPSSRLNGVNVVYSPGGYIAGIQ	1898
Db	1797	LSVDFDRTTKTEKIYDDHRKFLRLIAYDTSGHPTLWLPSSKLMVNVVYSSSTGQIASIQ	1856
Qy	1899	GIMSERMEYDQAGRITSRIFADGKTWSYTYLEKSMVLLLLHSQRYIFEFDKNDRLSSVTM	1958
Db	1857	GTTSEKVDYDQGRIVSRVAFADGKTWSYTYLEKSMVLLLLHSQRYIFEYDMWDRLSAITM	1916
Qy	1959	PNVARQTLLETIRSVGYRYNIYQPPEGNASVIOQFTEDGHLHLHTFVLGTGRRVIYKYGKLS	2018
Db	1917	PSVARHTMOTIRSIGYRYNIYNPPESNASIITDYNEEGLLLQTAFLGTSRRVLFKYRRQT	1976
Qy	2019	KLAETLYDTTKVSFTYDETAGMLKTINLQNEGFTCTIRYRQIGPLIDRQIFRFTTEGMVN	2078
Db	1977	RLSEILYDSTRVSFTYDETAGVLKTVNLQSDGFICTIRYRQIGPLIDRQIFRSEDEGMVN	2036
Qy	2079	ARFDYNYDNSFRVTSMQAVINETPLPIDLYRDDVSGKTEQFGKFGVIYYDINQIITAV	2138









Db 2157 EYDVGQLQTVYLNKIMWRNYNDLNGNLHLNLPENSARLTPLRYDLRDRITRLGDVQYR 2216

QY 2255 MDEDFLQRGGDIFEYNSAGLLIKAYNRAGSWSVRYRYDGLGRRVSSKSHSHLQFFY 2314

Db 2217 LDEDFLQRQGTIFEYSSKGLLTRVYSKGSWTVIYRYDGLGRRVSSKTSILGQHLQFFY 2276

QY 2315 ADLTNPTKVTHLYNHSSEITSLYYDLQHLFAMELSSGDEFYIACDNIGTFLAVFSGTG 2374

Db 2277 ADLTYPTRITHVYNHSSSEITSLYYDLQHLFAMEISSGDEFYIASDNTGTFLAVFSSNG 2336

QY 2375 LMIKQILYTAYGEIYMDTNPNFQIIIGYHGGLYDPLTKLVHMGRRDYDVLAGRWTSPDHE 2434

Db 2337 LMLKQIQYTAYGEIYFDSNIDQLVIGFHGGLYDPLTKLIHFGERDYDILAGRWTTPDIE 2396

QY 2435 LWKHLSSSNMFPNLYMFKNNPNISNSQDIKCFMTDVNSWLLTFGFQLHNVIPGYPKPDm 2494

Db 2397 IWKRI-GKDPAPFNLYMFRNNPNASKIHDVKDYITDVNSWLVTGFFHLHNAIPGFPVPKF 2455

QY 2495 DAMEPSYELIHTQMKTOEWDNSKSIILGVQCEVQKQKAFVTLERFDQLYGSTITSCQAP 2554

Db 2456 DLTEPSYELV---KSQQWDDIPPIFGVQQQVARQAKAFSLGKMAEVQ----VSRRRAG 2507

QY 2555 KTKK---FASSGSVFGKGVKPFALKDGRVTTDIISVANEDGRRVAAIILNHAHYLENLHFTI 2611

Db 2508 GAQSWLWFATVKSILGKGYMLAVSQGRVQTNVLNIANEDCIKVAAVLNNAFYLENLHFTI 2567

QY 2612 DGVDTHYFVKPGPSEGLAILGLSGGRRRTLENGVNVTVSQINTVLNGRTRRRYTDIQLQYG 2671

Db 2568 EGKDTHYFIKTTTPESDLGLRLTSGRKALENGINVTVSQSTTVNGRTRRRFADVEMQFG 2627

QY 2672 ALCLNTRYGTTLDEEKARVLELARQRAVROAWAREQORLREGEBGLRAWTEGEKQOVLST 2731

Db 2628 ALALHVRYGMTLDEEKARILEQARQALARAWAREQORVRDGEAGRLWTEGEKQQLLSA 2687

QY 2732 GRVQGYDGGFFVISVEQYPELSDSANNIHFMRQSEMGR 2769

Db 2688 GKVQGYDGYVLSVEQYPELADSANNIQFLRQSEIGRR 2725

RESULT 9

ADH41995

ID ADH41995 standard; protein; 2725 AA.

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AC ADH41995;

XX

25-MAR-2004 (first entry)

XX

Novel human protein NOV40f #2.

DE

cardiovascular; antiarteriosclerotic; hypotensive; cytostatic; anorectic;

XX

antidiabetic; immunosuppressive; anti-HIV; neuroprotective; nootropic;

KW

antiparkinsonian; antiasthmatic; antiinfertility; cardiomyopathy;

KW

atherosclerosis; hypertension; cancer; obesity; diabetes; AIDS;

KW

multiple sclerosis; graft-versus-host disease; Alzheimer's disease;

KW

Parkinson's disease; asthma; fertility disorder; chromosome mapping;

KW

tissue typing; preventive medicine; pharmacogenomic; vaccine.

XX

Homo sapiens.

OS

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PN

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PD

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PF

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PR

PR 06-JUN-2002; 2002US-0386465P.

PR 06-JUN-2002; 2002US-0386864P.

PR 07-JUN-2002; 2002US-0386701P.

PR 07-JUN-2002; 2002US-0386796P.

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PR 07-JUN-2002; 2002US-0387081P.

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PR 10-JUN-2002; 2002US-0387429P.

PR 10-JUN-2002; 2002US-0387540P.

PR 10-JUN-2002; 2002US-0387866P.

PR 11-JUN-2002; 2002US-0387866P.

PR 11-JUN-2002; 2002US-0387610P.

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PR 13-SEP-2002; 2002US-0410505P.

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PR 30-SEP-2002; 2002US-0415195P.

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(CURA-) CURAGEN CORP.

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WPI; 2004-053467/05.

N-PSDB; ADH41994.

New NOVX polypeptides and nucleic acid molecules useful for preventing or  
treating NOVX-associated disorders, e.g. cancer, cardiomyopathy,  
atherosclerosis or diabetes, in chromosome mapping, tissue typing or in  
pharmacogenomics.

Claim 2; SEQ ID NO 548; 1503pp; English.

XX The invention relates to 566 new isolated human polypeptides and their  
CC encoding genes, sequences that are at least 95% identical to these or  
CC sequences comprising one or more conservative substitutions in these. The  
CC polypeptide, polynucleotide and antibodies against the polypeptides are  
CC useful in diagnosing, treating or preventing NOVX-associated disorders,  
CC e.g. cardiomyopathy, atherosclerosis, hypertension, cancer, obesity,  
CC diabetes, AIDS, multiple sclerosis, graft-versus-host disease,  
CC Alzheimer's disease, Parkinson's disease, asthma, or fertility disorders.  
CC The nucleic acids are further used as hybridization probes, in chromosome  
CC mapping, tissue typing, preventive medicine, and pharmacogenomics. The  
CC polypeptides are also useful as vaccines. This sequence represents an  
CC example of the polypeptide of the invention.

XX  
SQ Sequence 2725 AA;

Query Match 68.5%; Score 10201; DB 8; Length 2725;  
Best Local Similarity 66.9%; Pred. No. 0;  
Matches 1872; Conservative 362; Mismatches 462; Indels 102; Gaps 21;

QY	1	MDVKERKPYRSLTR-RRDAERRYTSSADSEEGKAP-QKSYSSSETLKAYDQD-ARLAYG	57
Db	1	MDVKERRPYCSLTKSRREKERRYTNSSADNEECRVPTQKSYSSSETLKAFDHDSSRLLYG	60
QY	58	SRVKDIVPOBAEEFCRTGANFTLRELGLEEVTPPHGTLTYRTDGLPQCGYSMGAGSDADM	117
Db	61	NRVKDLVHREADEFTRQGNFTLRQLGVCCEPATRRGLAFCAEMGLPHRGYSISAGSDADT	120
QY	118	EADTVLSPHPVRLWGRSTRSGRSSCLSSRANSNLTLTDTHEHENTETDHPGGGLQNH	174
Db	121	ENEAVMSPHAMRLWGRGVKSGRSSCLSSRSNSALTTLTDEHENSSENEQPASNOGQS	180
QY	175	RLRTPPPPLSHAHTPNQHHAAASINSLNRGNFTPRSNPSPARTDHSLSGEPAGGAQ----	230
Db	181	TLQPLPP--SHKQHSAAQH-PSITSLNRNSLTNRRNQSPAP-----PAALPAELQTT	229
QY	231	-EPAHAQENWLLNSNIPLETNRNLGKQPFGLGTLQDNLIEMDILGASRHDGAYS	289
Db	230	PESVQLQDSWVLGNSVPLESR-----HPLFKT	256
QY	290	G-GTSPLECTSPGYPLTSTVYSPPPRPLPRSTFARPAFLNKKPSKYCNWKCAALSAIV	348
Db	257	GTGTTPLFSTATPGYTMASGSVYSPTRPLPRNTLSRSAPFKKSSKYCSWKCTALCAVG	316
QY	349	ISATLVILLAYFVAMHLFGLNHLQPMEGQMYE---ITEDASSWPVPTDVS	405
Db	317	VSVLLAILLSYFIAMHLFGLNWQLQQTENDTFENGKVNST-----MPTNTVSLPSG---	368
QY	406	LETDRKGKGTTEGKPSFFPEDSFIDSGEIDVRRASQKIPPGTFWRSQVFIDHPVHLK	465
Db	369	-----DNGKLGFTQENNTIDSSELGELDIGRRAIQEIPPGIFWRSQLFIDQPQFLX	417
QY	466	FNVSIGKAALVGIYGRKGLPPSHT----QFDFVELLDGRLLTQEARSL	521
Db	418	FNISLQDALIGVYGRKKLPPSHTQSSPYDFVELLDGRLLAREQ	477
QY	522	PPSSHETGFIQYLDSGIWHLAFYNDGKESEVVSFLTTAIESVDNCPSN	581
Db	478	SVSLHEAGFIQYLDSGIWHLAFYNDGKNAEQVSFNTIVIESVVECP	537
QY	582	HCFLGFLGPDCCGRASCPVLCGNGQYMKGRCLCHSGWKGAEC	641
Db	538	HCFPGLGPDCSRACPVLCGNGQYSGKRCCLCFSGWKGT	597
QY	642	ITGTICNPGYKGESCEEVDCMDPTCSGRGVCVRGECHFCFVGWGT	701
Db	598	IMGSCACSSGYKGESCEEADCDIPGCSNHGVCIHGECHSPGWG	657
QY	702	GHGTFLPDTGLCSDPSPWTHDCSIEICAADCGGHGVCVGGTC	761
Db	658	GHGTYLQESGSCTCDPNWTGPDCSNEICSVDCSGSHGVC	717
QY	762	PRCAEHGTCRDGKCECSPGWNGEHCTIAHYLDRVV-----KEG	815

Db	718	PRCAEHGTCRDGKCECSPGWNGEHCTIAHYLDKIVDKIKIGYKEGCPGLCNSNGRCTL	777
QY	816	GWHCVCQLGWRGAGCDTSMETACGDSKDNDDGLVDCMDPDCCLOPLCHINPLCLGSPNP	875
Db	778	GGHCVCQPGWRGAGCDVAMETLCTDSKDNDDGLVDCMDPDCCLOSSCQNPYCRGLPDP	837
QY	876	LDIIQETQVPVSQQNLHSHFYDRIKFLVGRDSTHIIIPGENPFDGGHACVIRGQVMTSDGTP	935
Db	838	QDIISQSLQSPSQAAKSFYDRISFLIGSDSTHVIPGESPFNKSLASVIRGOVLTA	897
QY	936	LVGWNISFVNNPLFGYTISRQDGSFDLVTNGGISIILRERAPFITQEH	995
Db	898	LIGVNVSFFHYPEGYTITRQDGMEDLVANGGASLTLVFERSPFLTQYHTVWIPWNVFYV	957
QY	996	METIIMRHEENEIPSCDLSNFARPNPVVSPLTSFASSCAEKGP	1055
Db	958	MDTLVMEKEENDIPSCDLSGFVRPNPIIVSSPLSTFFRSSPEDSPIIPETQVLHEETIP	1017
QY	1056	GCKMRLSYLSSRTPGYKSVLRISLTHPTIPFNLMKVHLMVAVEGR	1115
Db	1018	GTDLKLSYLSSRAAGYKSVLKITMTQSIIPFNLMKVHLMVAVGR	1077
QY	1116	FIWKTDTVYNQKVFGLSEAFVSUGVEYESCPDLILWEKRTTVLQ	1175
Db	1078	FIWKTDAYNQKVYGLSEAVSVUGVEYESCLDLTLWEKRTAILQ	1137
QY	1176	HHA	1235
Db	1138	HHVLDVQNGILYKNGENQFISQPPVSSIMGNRRRSISPCSCNGQADGNKLLAPVAL	1197
QY	1236	TCGSDGSLYVGDFNYIRRIFFPSGNVTNILELNKDFRSHSHPAHKYV	1295
Db	1198	ACGIDGSLYVGDFNYVRRIFPSGNVTSLVLELNKDFRSHSNPAHRYV	1257
QY	1296	DSNSRRRVFKIKSTVVVVKLVKNSEVVAGTGDQCLPFDDTRCGDGGKATEATLTNPRGITV	1355
Db	1258	DTNTRRIYRPKSLTGAKDLTKNAE	1317
QY	1356	DKFGLIYFVDGTMIRRIDONGIISTLLGSNDLTSARPLSCDSVMDISQVRLEWPTDLAIN	1415
Db	1318	DXNGLIYFVDGTMIRKVDQNGIISTLLGSNDLTSARPLTCDTSMHISQVRLEWPTDLAIN	1377
QY	1416	PMDNSLYVLDDNNVVLQISENHQVRIVAGRPMHCQVPGIDHFLLSKVAIHATLESATALAV	1475
Db	1378	PMDNSIYVLDDNNVVLQITENRQVR	1436
QY	1476	SHNGVLYIAETDEKKINRIRQVTTSGEISLVAGAPSGCDCKNANDANCFSGDDGYAKDAK	1535
Db	1437	SYSGVLYITETDEKKINRIRQVTTDGEISLVAGIPSECDCKNDANCDYQSGDGYAKDAK	1496
QY	1536	LNTPSSLAVCADGELYVADLGNIRIRFIRKNKPPFLNTQNMYELSSPIDQELYLFDTTGKH	1595
Db	1497	LSAPSSLAASP	1556
QY	1596	LYTQSLPTGDYLYNFTYTGDDITLITDNGNMMVNVRRDSTGMPLWLVPDQGVYVVTMG	1655
Db	1557	QYTVSLVTGDYLYNFSYSDNDNITAVTDSNGNTLRIRRD	1616
QY	1656	TNSALKSVTTQGH	1715
Db	1617	TNGCLKGMTAQGLELVLF	1676
QY	1716	FRSDTSSVHVQVETSSK-DDVTITNLSASGAFYLLQDQVRNSYYIGADGSLRLLLAN	1774
Db	1677	LHGDMDKAITVDIESSREEDVSITSNLSSIDSFYTMVQQDLRNSYQIGYDGSRLRIYAS	1736
QY	1775	GMEVALQTEPHLLAGTVNPTVGKRNVTLPIDNGLNLVEWRQRKEARGQVTVFGRRRLRVH	1834
Db	1737	GLDSHYQTEPHVLAGTANPTVAKRNMTLPGENGQNLVEWFRFRKEAQGQKVN	1796
QY	1835	NRNLLSLDFDRVTRTEKIYDDHRKFTLRILYDQAGRPSLWSPSSRLNGVNVITYSPGGYIA	1894

Db 1797 GRNLLSVDFDRTTTEKIYDDHRKFLLR IAYDTSGHPTLWLPSSKLMVNVVTSYSTGQIA 1856

Qy 1895 GIORGIMSERMEYDOAGRITSRIFADGKTWSYTYLEKSMVLLLSHQRYIFEFDKNDRLS 1954

Db 1857 SIQRTTSEKVDYDGGQIRIVSRVADGKTWSYTYLEKSMVLLLSHQRYIFEYDMWDRLS 1916

Qy 1955 SVTMPNVARQTLETIRSVGYRNIYQPEGNASVIQDFTEDGHLHTFVLGTGRRVIYKY 2014

Db 1917 AITMPSVARHTMQTIRSIGYRNIYNPPESNASITDYNEEGLLQTAFLGTSRRVLFKY 1976

Qy 2015 GKLSKLAETLYDTTKVSFTYDETAGMLKTINLQNEGFTCTIRYRQIGPLIDRQIFRFTEE 2074

Db 1977 RRQTRLSEILYDSTRVSFTYDETAGVLKTVNLQSDGFICTIRYRQIGPLIDRQIFRFS 2036

Qy 2075 GMVNAREFDYNDNSFRVTSMQAVINETPLPIDLYRYDDVSGKTEQFGKFGVIYYDINQII 2134

Db 2037 GMVNAREFDYSYDNSFRVTSMQGVINETPLPIDLYQFDDISGKVEQFGKFGVIYYDINQII 2096

Qy 2135 TTAVMTHTKHFDAYGRMKEVQYEIFRSLMYMTVQYDNMGRVVKKELKVGPGYANTTRYSY 2194

Db 2097 STAVMTYTKHFDAGRIKEIQYEIFRSLMYWITIYQDNMGRVTREIKIGPFANTTKYAY 2156

Qy 2195 EYDADGLOQTVSINDKPLWRYSYDNLGNLHLSPNSARLTPLRYDIRDRTRLGDVQYK 2254

Db 2157 EYDVGLOQTVLYLNEKIMWRNYDNLGNLHLSPNSARLTPLRYDLDRITRLGDVQYR 2216

Qy 2255 MDEDFLQRGGDIFEYNSAGLLIKAYNRAGSWRYRYDGLGRRVSSKSHSHHLQFFY 2314

Db 2217 LDDEDFLQRGRTEIFEYSSKGLLTRVYSKSGWTVIYRYDGLGRRVSSKSLGQHLQFFY 2276

Qy 2315 ADLTNPTKVTHLYNHSSEITSLSYDLOGLHFLAMELSSGDEFYIACDNIGTFLAVFSGTG 2374

Db 2277 ADLTYPTRITHVYNHSSEITSLSYDLOGLHFLAMEISSGDEFYIASDNTGTFLAVFSSNG 2336

Qy 2375 LMIKQILYTAYGEIYMDTNPNFQIIIGYHGGLYDPLTKLVHMGRRDYDVLAGRWTSPDHE 2434

Db 2337 LMLKQIQYTAYGEIYFDSNIDQLVIGFHGGLYDPLTKLIHFGERDYDILAGRWTTPDIE 2396

Qy 2435 LWKHLSSNVMPENLYMPKNNPNISNSQDIKCFMTDVNSWLLTTFGQLHNVIPGYPKPDM 2494

Db 2397 IWKRI-GKDPAPFNLVYFRNNPNPASKIHDVKDYITDVNSWLVTFGFHLHNAIPGFPVPKF 2455

Qy 2495 DAMEPSYELIHTQMTQEWDNSSKILGVQCEVQKQLKAFVTLERFDQLYGSTITSQQAP 2554

Db 2456 DLTEPSYELV----KSQQWDDIPPIFGVQQQVARQAKAFLSLGKMAEVQ----VSRRRAG 2507

Qy 2555 KTKK---PASSGSVFGKGVKFPALKDGRVTTDIIISVANEDGRRVAAIILNHAHYLENLHFTI 2611

Db 2508 GAQSWLWFATVKSLLIGKWM LAVSQGRVQTNVLNIANEDCIKVA AVLNNAFYLENLHFTI 2567

Qy 2612 DGVDTHYFVKPGPSEGDLAILGLSGRRRTLENGVNVTVSQINTVLNGRTRRYTDIQLQYG 2671

Db 2568 EGKDTHYFIKTTTPESDLGTLRLTSGRKALENGINVTVSQSTTVNGRTRRFADVEMQFG 2627

Qy 2672 ALCLNTRYGTTLDEEKARVLELARQAVRQAWAREOQRLREGEEGLRAWTEGKQQVLST 2731

Db 2628 ALALHVRYGMTLDEEKARILEQARQALARAWAREOQVRDGEGARLWTEGKRQLLSA 2687

Qy 2732 GRVQGYDGFVVISVEQYPELSDSANNIHFMRQSEMGRR 2769

Db 2688 GKVQGYDGYVVLVVEQYPELADSANNIQFLRQSEIGRR 2725

RESULT 10

ADH41991

ID ADH41991 standard; protein; 2725 AA.

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AC ADH41991;

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DT 25-MAR-2004 (first entry)

XX

DE Novel human protein NOV40d #2.

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KW cardiovascular; antiarteriosclerotic; hypotensive; cytostatic; anorectic; antidiabetic; immunosuppressive; anti-HIV; neuroprotective; nootropic; antiparkinsonian; antiasthmatic; antiinfertility; cardiomyopathy; atherosclerosis; hypertension; cancer; obesity; diabetes; AIDS;

KW multiple sclerosis; graft-versus-host disease; Alzheimer's disease; Parkinson's disease; asthma; fertility disorder; chromosome mapping; tissue typing; preventive medicine; pharmacogenomic; vaccine.

XX Homo sapiens.

OS

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PN WO2003102159-A2.

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PD 11-DEC-2003.

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PF 04-JUN-2003; 2003WO-US017573.

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PR 04-JUN-2002; 2002US-0385490P.

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PR 07-JUN-2002; 2002US-0386796P.

PR 07-JUN-2002; 2002US-0386931P.

PR 07-JUN-2002; 2002US-0387078P.

PR 07-JUN-2002; 2002US-0387081P.

PR 07-JUN-2002; 2002US-0387083P.

PR 10-JUN-2002; 2002US-0387429P.

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PR 11-JUN-2002; 2002US-0387606P.

PR 11-JUN-2002; 2002US-0387610P.

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PR 11-JUN-2002; 2002US-0387668P.

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PR 11-JUN-2002; 2002US-0387859P.

PR 12-JUN-2002; 2002US-0387934P.

PR 12-JUN-2002; 2002US-0387960P.

PR 12-JUN-2002; 2002US-0388022P.

PR 12-JUN-2002; 2002US-0388096P.

PR 12-JUN-2002; 2002US-0388432P.

PR 12-JUN-2002; 2002US-0388479P.

PR 13-JUN-2002; 2002US-0389123P.

PR 14-JUN-2002; 2002US-0389120P.

PR 14-JUN-2002; 2002US-0389146P.

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PR 18-JUN-2002; 2002US-0389604P.

PR 18-JUN-2002; 2002US-0389884P.

PR 19-JUN-2002; 2002US-0390006P.

PR 19-JUN-2002; 2002US-0390144P.

PR 19-JUN-2002; 2002US-0390209P.

PR 25-JUN-2002; 2002US-0391726P.

PR 06-AUG-2002; 2002US-0401628P.

PR 09-AUG-2002; 2002US-0402268P.

PR 12-AUG-2002; 2002US-0402822P.

PR 13-AUG-2002; 2002US-0403458P.

PR 15-AUG-2002; 2002US-0403617P.

PR 15-AUG-2002; 2002US-0403732P.

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PR 13-SEP-2002; 2002US-0410505P.

PR 23-SEP-2002; 2002US-0412955P.

PR 30-SEP-2002; 2002US-0415195P.

PR 23-OCT-2002; 2002US-0420627P.

PR 23-OCT-2002; 2002US-0420718P.

PR 24-OCT-2002; 2002US-0420852P.

PR 31-OCT-2002; 2002US-0422750P.

PR 01-NOV-2002; 2002US-0423095P.





Db 1437 SYSGVLYITETDEKKINRQVTTDGEISLVAGIPSECDCKNDANCDYQSGDGYAKDAK 1496

Qy 1536 LNTPSSLAVCADGELYVADLGNIRIRFIRKKNKPFNTQNMVELSSPIDOELYLFDTTGKH 1595

Db 1497 LSAPSSLAASPDTLYIADLGNIRIRAVSKNKPLLNSMNFYEVASPTDQELYIFDINGTH 1556

Qy 1596 LYTQSLPTGDYLYNFTYTGDDITLITDNNGMVNVRRDSTGMPLWLVPDGOVYVWTMG 1655

Db 1557 QYTVSLVTGDYLYNFSYSDNDNITAVTDSNGNTLIRRPDPNRMFVRVVSQVWQVILWTIG 1616

Qy 1656 TNSALKSVTTQGHELAMTYHGNSGLLATKSNENGWTFYFEYDYSFGRLLTNVTPTGOVSS 1715

Db 1617 TNGCLKGMTAQGLELVLFYHGNSGLLATKSDETGWTFYFDYDSEGRLLTNVTPTGVVTN 1676

Qy 1716 FRSDTSSVHVQVETSSK-DDVTITTNLSASGAFYTLLODQVRNSYYIGADCSLRLLLAN 1774

Db 1677 LHGDMDKAITVDIESSSREEDVSITSNLSSIDSFYTMVQDQLRNSYQIGYDGSURIIYAS 1736

Qy 1775 GMEVALQTEPHLLAGTVNPTVGKRNVTLPIDNGLNLVWVRQRKEQARGQVTVFGRRLRVH 1834

Db 1737 GLDSHYQTEPHVLAGTANPTVAKRNMWTLPGENGQNLVWRFRKEQAQGKVNVPGRKLRVN 1796

Qy 1835 NRLLSLDFDRVTRTEKIYDHRKFTLRILLYDQAGRPSLWSPSSRLNGVNVTVSPGGYIA 1894

Db 1797 GRNLLSVDFDRTTKTEKIYDHRKFLLRIRIAYDTSGHPFLWLPSSKLMVNVTVSSTGQIA 1856

Qy 1895 GIORGIMSERMEYDQAGRITSRIPADGKTWSYTYLEKSMVLLLHSORQYIFEFKNDRLS 1954

Db 1857 SIQRGTTSEKVDYDGGQGRIVSRVFADGKTWSYTYLEKSMVLLLHSORQYIFEYDMWDRLS 1916

Qy 1955 SVTMPNVARQTLTIRSVGYRNIYQPPEGNASVIOQFTEDGHLHLLTFFYLGTRRVIYKY 2014

Db 1917 AITMPSVARHTMQTIRSIGYRNIYNPPESNASIITDYNEGLLLQTAFLGTSRRVLFKY 1976

Qy 2015 GKLSKLAETLYDTTKVSFTYDETAGMLKTINLQNEGFTCTIRYRQIGPLIDRQIFRFTEE 2074

Db 1977 RRQTRLSEILYDSTRVSFTYDETAGVLKTVNLQSDGFICTIRYRQIGPLIDRQIFRPSED 2036

Qy 2075 GMVNARFDYNDNSFRVTSMQAVINETPLPIDLYRYDDVSGKTEQFGKFGVIYVDINQII 2134

Db 2037 GMVNARFDYSYDNSFRVTSMQGVINETPLPIDLYQFDDISGKVEQFGKFGVIYVDINQII 2096

Qy 2135 TTAVMTHTKHFDAYGRMKEVQYEIFRSLMYWMTVOYDNMGRVVKELKVGYPYANTTRYSY 2194

Db 2097 STAVMTYTKHFDAGRIKEIQYEIFRSLMYWITIYQDNMGRVTKREIKIGPFANTTKYAY 2156

Qy 2195 EYDAGQLQTVSINDKPLWRYSDVLNGNLHLLSPGNSARLTPLRYDIRDRITRLGDVOYK 2254

Db 2157 EYDVBGLQTVYLNKIMWRNYDLNGNLHLLNPSNSARLTPLRYDLRDRITRLGDVOYR 2216

Qy 2255 MDEDFLRQRGGDIFEYNSAGLLIKAYNRAGSWSVRYRYDGLGRRVSSKSSHHLQFFY 2314

Db 2217 LDEDFLRQRGTEIFEYSSKGLLTRVYSKSGSGWTVIYRYDGLGRRVSSKTSLGHLQFFY 2276

Qy 2315 ADLTNPTKVTHLYNHSSEITSLYVDLQGHLFAMELSSGDEFYIACDNIGTPLAVFSGTG 2374

Db 2277 ADLTYPTRITHVYNHSSSEITSLYVDLQGHLFAMEISSGDEFYIASDNTGTPLAVFSNG 2336

Qy 2375 LMIKQILYTAYGEIYMDTNPNFQIIGYHGGLYDPLTKLVHMGRRDYDVLAGRWTSPDHE 2434

Db 2337 LMLKQIQYTAYGEIYFDSNIDFQLVGFHGGLYDPLTKLIHGERDYYDILAGRWTTPDIE 2396

Qy 2435 LWKHLSSSNVMPFNLYMFKNNNPISNSQDIKCFMTDVNSWLLTFGFQLHNVIPGYKPD 2494

Db 2397 IWKRI-GKDPAPFNLVYMFERNNNPASKIHDVKDYITDVNSWLVTFGFHLHNAIPGFPVPKF 2455

Qy 2495 DAMEPSYELIHTQMKTOEWDNSKSIILGVQCEVQKQLKAFVTLERFDQLYSTITSCQAP 2554

Db 2456 DLTEPSYELV---KSQQWDDIPPIPGVQQVARQAKAFLSLGKMAEVQ----VSRRRAG 2507

Qy 2555 KTKK---PASSGSVFGKGVKFAKDGRTTDDIISVANEDGRRVAAIILNHAHYLENLHFTI 2611

Db 2508 GAQSWLWFATVKSLLIGKVMLAVSQGRVQTNVLNIANEDCIKVAALVNNAFYLENLHFTI 2567

Qy 2612 DGVDTHYFVKPGPSEGDLAAILGLSGRRTLENGVNVTVSQINTVLNGRTRRYTDIQLQYG 2671

Db 2568 EGKDTHYFIKTTTPESDLGTLRLTSGRKALENGINVTVSQSTTVVNGRTRRFADVEMQFG 2627

Qy 2672 ALCINTRYGTTLDDEEKARVLELARQRAVRQAWAREQQRLREGEGLRAWTEGEKQQVLST 2731

Db 2628 ALALHVRYGMTLDDEEKARILEQARQARALARAWAREQQVRDGEEGARLWTEGEKROLLSA 2687

Qy 2732 GRVQGYDGFVVISVEQYPELSDSANNIHFMRQSEMGR 2769

Db 2688 GKVQGYDGYVVLVSVEQYPELADSANNIQFLRQSEIGRR 2725

RESULT 11  
ADH41933

ID ADH41933 standard; protein; 2725 AA.

XX

AC ADH41933;

XX

DT 25-MAR-2004 (first entry)

XX

Novel human protein NOV40a.

DE

XX

KW cardiovascular; antiarteriosclerotic; hypotensive; cytostatic; anorectic;

KW antidiabetic; immunosuppressive; anti-HIV; neuroprotective; nootropic;

KW antiparkinsonian; antiasthmatic; antiinfertility; cardiomyopathy;

KW atherosclerosis; hypertension; cancer; obesity; diabetes; AIDS;

KW multiple sclerosis; graft-versus-host disease; Alzheimer's disease;

KW Parkinson's disease; asthma; fertility disorder; chromosome mapping;

KW tissue typing; preventive medicine; pharmacogenomic; vaccine.

XX

OS Homo sapiens.

XX

PN WO2003102159-A2.

XX

PD 11-DEC-2003.

XX

PF 04-JUN-2003; 2003WO-US017573.

XX

PR 04-JUN-2002; 2002US-0385490P.

PR 04-JUN-2002; 2002US-0385615P.

PR 04-JUN-2002; 2002US-0385755P.

PR 05-JUN-2002; 2002US-0386041P.

PR 06-JUN-2002; 2002US-0386355P.

PR 06-JUN-2002; 2002US-0386357P.

PR 06-JUN-2002; 2002US-0386447P.

PR 06-JUN-2002; 2002US-0386459P.

PR 06-JUN-2002; 2002US-0386465P.

PR 06-JUN-2002; 2002US-0386864P.

PR 07-JUN-2002; 2002US-0386701P.

PR 07-JUN-2002; 2002US-0386796P.

PR 07-JUN-2002; 2002US-0386931P.

PR 07-JUN-2002; 2002US-0387078P.

PR 07-JUN-2002; 2002US-0387081P.

PR 07-JUN-2002; 2002US-0387083P.

PR 10-JUN-2002; 2002US-0387429P.

PR 10-JUN-2002; 2002US-0387540P.

PR 10-JUN-2002; 2002US-0387866P.

PR 11-JUN-2002; 2002US-0387606P.

PR 11-JUN-2002; 2002US-0387610P.

PR 11-JUN-2002; 2002US-0387659P.

PR 11-JUN-2002; 2002US-0387668P.

PR 11-JUN-2002; 2002US-0387696P.

PR 11-JUN-2002; 2002US-0387859P.

PR 12-JUN-2002; 2002US-0387934P.

PR 12-JUN-2002; 2002US-0387960P.

PR 12-JUN-2002; 2002US-0388022P.

PR 12-JUN-2002; 2002US-0388096P.

PR 12-JUN-2002; 2002US-0388432P.

PR 12-JUN-2002; 2002US-0388479P.

PR 13-JUN-2002; 2002US-03889123P.

PR 14-JUN-2002; 2002US-03889120P.





Db 1078 FIWDKTDAYNQVYGLSEAVVSVGYEYESCLDLTLWEKRTAILQGYELDASNMGWTLDK 1137

QY 1176 HHALNIQSGILHKNGENQFVSQQPPVIGSIMGNRRRSISCPSCNGLADGNKLLAPVAL 1235

Db 1138 HHVLDVQNGILYKNGENQFISQQPPVSSIMGNRRRSISCPSCNGQADGNKLLAPVAL 1197

QY 1236 TCGSDGSLYVGDFNYIRRIFFPSGNVTNILELRNKDFRSHSPAHKYYLATDPMGAVFLS 1295

Db 1198 ACGIDGSLYVGDFNYVRRIFPSGNVTSVLELRNKDFRHSNPAHRYYLATDPVTGLYVS 1257

QY 1296 DSNRRRVFKIKSTVVVKDLVKNSEVVAGTDQCCLPFDDTRCGDGGKATEATLTNPRGITV 1355

Db 1258 DNTRRRIYRPKSLTGAKDLTKNAEVVAGTGEQCLPFDEARCGDGGKAVEATLMSPKGMAY 1317

QY 1356 DKFGLIYFVDGTMIRRIDQNGIISTLLGSNDLTSARPLSCDSVMDISQVRLEWPTDLAIN 1415

Db 1318 DKNGLIYFVDGTMIRKVDQNGIISTLLGSNDLTSARPLTCDTSMHISQVRLEWPTDLAIN 1377

QY 1416 PMDNSLYVLDNNVVLQISENHQVRIVAGRPMHCQVPGIDHFLLSKVAIHATLESATALAV 1475

Db 1378 PMDNSIYVLDNNVVQLITENQVRIAAGRPMHCQVPGVE-YPVGKHAVQTTLESATAIAV 1436

QY 1476 SHNGVLYIAETDEKKINRIRQVTTSGEISLVAGAPSGCDCKNDANCDFCSDGDGYAKDAK 1535

Db 1437 SYSGVLYITETDEKKINRIRQVTTDGEISLVAGIPSECDCKNDANCDYQSGDGYAKDAK 1496

QY 1536 LNTPSSSLAVCADGELYVADLGNIRIRFIRKNKPFINTQNMVELSSPIDQELYLEDFTGKH 1595

Db 1497 LSAFSSLAASPDTGLYIADLGNIRIRAVSKNKPLLNSMNFYEVASPTDQELYIFDINGTH 1556

QY 1596 LYTQSLPTGDYLYNFTYTGDGIDITLITDNNGMNVNRRDSTGMPLWLVPDGVVWTMG 1655

Db 1557 QYTVSLVTGDYLYNFSYNDNDITAVTDSNGNTLRIRRDNRMFVRVVSPPDNQVILWTIG 1616

QY 1656 TNSALKSVTTQGHELAMTYHGNSGLLATKSNENGWTTFYEDSFGRLTNVTFTPGQVSS 1715

Db 1617 TNGCLKGMTAQGLELVLFITYHGNSGLLATKSDETGWTTFFDYDSEGRLTNVTFTPGVVTN 1676

QY 1716 FRSDTSSVHVQVETSSK-DDVTITTNLSASGAFYTLQDQVRNSYYIGADGSLRLLLAN 1774

Db 1677 LHGDMDKAITVDIESSSREEDVSITSNLSSIDSFYTMVQDQLRNSYQIGYDGLRIIYAS 1736

QY 1775 GMEVALQTEPHLLAGTVNPTVGKRNVTLPIDNGLNLVEWRQKEAQGVTVFGRRLRVH 1834

Db 1737 GLDSHYQTEPHVLAGTANPTVAKNNMTLPGENGQNLVEWRFRKEAQGKVNVFGRKLRVN 1796

QY 1835 NRNLSLDFDRVTRTEKIYDDHRKFTRLIRILYDQAGRPSLWSPSSRLNGVNVTYSPGGYIA 1894

Db 1797 GRNLLSVDFDRTTKTEKIYDDHRKFLLRIAYDTSGHPTRLWLPSSKLMAVNVTYSSTGQIA 1856

QY 1895 GIORGIMSERMEYDQAGRITSRIFADGKTWSYTYLEKSMVLLHLSQRQYIFEFDKNDRLS 1954

Db 1857 SIQRTGTSEKVDYDQGRIVSVPADGKTWSYTYLEKSMVLLHLSQRQYIFEYDMWDRLS 1916

QY 1955 SVTMPNVARQTLTIRSVGYRNIYQOPPEGNASVIQDFTEDGHLLHTFYLGTGRRRIYKY 2014

Db 1917 AITMPSVARHTMQTIRSIGYRNIYNPPESNASIITDYNEEGILLQTAFLGTSRRVLFKY 1976

QY 2015 GKLSKLAETLYDTTKVSFTYDETAGMLKTINLQNEGFTCTIRYRQIGPLIDRQIFRFTEE 2074

Db 1977 RRQTRLSEILYDSTRVSFTYDETAGVLKTVNLQSDGFICTIRYRQIGPLIDRQIFRSED 2036

QY 2075 GMVNAREDYNVDNSFRVTSMAVINETPLPIDLYRYDDVSGKTEQFGKFGVIYYDINQII 2134

Db 2037 GMVNAREDYSYDNSFRVTSMQGVINETPLPIDLYQFDDISGKVEQFGKFGVIYYDINQII 2096

QY 2135 TTAVMTHTKHFDAYGRMKEVQYEIFRSLMYWMTVQYDNMGRVVVKELKVGYPYANTTRYSY 2194

Db 2097 STAVMTYTKHFDAGRIKEIQYEIFRSLMYWITIQYDNMGRVTKREIKIGPFANTTKYAY 2156

QY 2195 EYDADGQLQTSVINDKPLWRYSYDLNGLNHLSPGNSARLTPLRYDIRDRITRLGDVOYK 2254

Db 2157 EYDVGQLQTVYVINEKIMWRNYNDLNGNLHLLNPSNSARLTPLRYDLRDIRTRLDGVQVR 2216

QY 2255 MDEDGFLRQGGDIFEYNSAGLLIKAYNRAGSWSVRYRDGLRRRVSSKSSHHLQFFY 2314

Db 2217 LDEDGFLRQGTETFEYSSKGLLTRVYSKSGSWTVIYRYDGLRRRVSSKTSLGQHLQFFY 2276

QY 2315 ADLTNPTKVTHLYNHSSEITSLSYYDLQGHLPAMELSSGDEFYIACDNIGTPLAVFSGTG 2374

Db 2277 ADLTYPTRITHVYNHSSEITSLSYYDLQGHLPAMEISSGDEFYIASDNTGTPLAVFSSNG 2336

QY 2375 LMIKQILYTAIGEYMDTNPNFQIIIGYHGGLYDPLTKLVHMGRRRDYDVLAGRWTSPDHE 2434

Db 2337 LMLKQIQYTAIGEYFDSNIDFQLVIGFHGGLYDPLTKLIHFGERDYDILAGRWTTPDIE 2396

QY 2435 LMKHLSSSNVMPFNLYMFKNNPNISNSQDIKCFMTDVNSWLLTFGFQLHNVIPGYPKPDM 2494

Db 2397 IWKRI-GKDPAPFNLYMFRNNNPASKIHVDKDYITDVNSWLVTFGFHLHNAIPGFVPKF 2455

QY 2495 DAMEPSYELIHTQMKTQEWDNKSILGVQCEVQKQLKAFVTLERFDQLYGSTITSQQAP 2554

Db 2456 DLTEPSYELV----KSQQWDDIPPIFGVQQQVARQAKAFSLSGKMAEVQ----VSRRRAG 2507

QY 2555 KTKK--FASSGSVFGKGVKFALKDGRVTTDIISVANEDGRRVAAILNHAHYLENLHFTI 2611

Db 2508 GAQSWLWFATVKSILGKGMVLAVSQGRVQTVNLNIANEDCIKVA AVLNNAFYLENLHFTI 2567

QY 2612 DGVDTHYFVKPGPSEGLAILGLSGRRRTLENGVNVTVSQINTVLNGRTRRYTDIQLQYG 2671

Db 2568 EGKDTHYFIKTTTPESDLGTLRLTSGRKALENGINVTVSQSTTVVNGTRRRFADVEMQFG 2627

QY 2672 ALCLNTRYGTTLDEKARVLELARQRAVRQAWAREQQORLREGEEGLRAWTEGEKQVLST 2731

Db 2628 ALALHVRYGMTLDEKARILEQARQARALARAWAREQQORVRDGEGARLWTEGEKQQLLSA 2687

QY 2732 GRVQGYDGGFFVISVEQYPELSDSANNIHFMRQSEMGR 2769

Db 2688 GKVQGYDGYVLSVEQYPELADSANNIQFLRQSEIGRR 2725

RESULT 12  
ADH41997

ID ADH41997 standard; protein; 2725 AA.

XX ADH41997;

DT 25-MAR-2004 (first entry)

XX Novel human protein NOV40g #2.

DE cardiovascular; antiarteriosclerotic; hypotensive; cytostatic; anorectic;  
XX antidiabetic; immunosuppressive; anti-HIV; neuroprotective; nootropic;  
KW antiparkinsonian; antiasthmatic; antiinfertility; cardiomyopathy;  
KW atherosclerosis; hypertension; cancer; obesity; diabetes; AIDS;  
KW multiple sclerosis; graft-versus-host disease; Alzheimer's disease;  
KW parkinson's disease; asthma; fertility disorder; chromosome mapping;  
KW tissue typing; preventive medicine; pharmacogenomic; vaccine.

OS Homo sapiens.

PN WO2003102159-A2.

XX 11-DEC-2003.

PF 04-JUN-2003; 2003WO-US017573.

XX 04-JUN-2002; 2002US-0385490P.

PR 04-JUN-2002; 2002US-0385615P.

PR 04-JUN-2002; 2002US-0385755P.

PR 05-JUN-2002; 2002US-0386041P.

PR 06-JUN-2002; 2002US-0386355P.

PR 06-JUN-2002; 2002US-0386357P.

PR 06-JUN-2002; 2002US-0386447P.

PR 06-JUN-2002; 2002US-0386459P.

PR 06-JUN-2002; 2002US-0386465P.



Dbb 718 PRCAEHGCTCKGKCECSQGMNGEHCTIAHYLDKIIVKDKIGYKEGCPGLCNSNGRCTLDQN 777

Qy 816 GWHCVQLGWRGAGCDTSMETACGDSKONDGDLVDCMDPDCCLOPLCHINPLCLGSPNP 875

Dbb 778 GGHCVCQPGWRGAGCDVAMETLCTDSKONEGDGLIDCMDPDCCLOQSSCQNPYCRGLPDP 837

Qy 876 LDIIQETQVPVSQONLHFSFYDRIKFLVGRDSTHIIIPGENPFDGGHACVIRGQVMTSDGTP 935

Dbb 838 QDIISQLSQSPSQAAKSFYDRISFLIGSDSTHVIPEGSPFNKSLASVIRGOVLTDGTP 897

Qy 936 LVGVNISFVNNPLFGYTI SRQDSFDLVNTGGISIILRFERAPFITQEHTLWLWPDRFFV 995

Dbb 898 LIGVNVFFHYPEYGYTITRQDGMFDLVANGGASLTLVFERSPFLTQYHTVWIPNVFVY 957

Qy 996 METIIMRHEENEIPSCDLSNFARNPNVVPSPPLTSFASSCAEKGPIVPEIQALQEEISIS 1055

Dbb 958 MDTLVMEKEENDIPSCDLSGFVRPNPIIVSSPLSTFFRSSPEDSPIIPEIQVLHEETTIP 1017

Qy 1056 GCKMRLSYLSSRTPGYKSVLRISLSLTHPTIPFNLMKVHLMVAVEGRLFRKWFAAAPDLSYY 1115

Dbb 1018 GTDLKLSYLSSRAAGYSVLKITMTQSIIPFNLMKVHLMVAVVGRFLQKWFPPASPNLAYT 1077

Qy 1116 FIWKTDVYNQKVFGLSEAFVSUGYEYESCPDLILWEKRTTVLQYEIDASKLGWSLDK 1175

Dbb 1078 FIWKTDAYNQKVYGLSEAVVSUGYEYESCLDLTLWEKRTAILQGYELDASMGWTLDK 1137

Qy 1176 HHALNIQSGILHKNGENQFVSQOPPVGISIMGNRRRSISCPSCNGLADGNKLLAPVAL 1235

Dbb 1138 HHVLDVQNGILYKNGENQFISQOPPVSSIMGNRRRSISCPSCNGQADGNKLLAPVAL 1197

Qy 1236 TCGSDGSLYVGDFNYIRRIFFPSGNVTNILELRNKDPRHSHSPAKEYYLATDPMSCAVFLS 1295

Dbb 1198 ACGIDGSLYVGDFNYVRRIRFPSPGNVTSVLELRNKDPRHSSNPAHRYYLATDPVTGDLVVS 1257

Qy 1296 DSNRRRVFKIKSTVVVKDLVKNSEVAGTGDQCLPFDDTRCGDGGKATEATLTNPRGITV 1355

Dbb 1258 DTNTRRIYRPKSLTGAKDLTKNAEVVAGTGEQCLPFDEARCGDGGKAVEATLMSPKGMAY 1317

Qy 1356 DKFGLIYFVDGTMIRRIDONGIISTLLGSNDLTSARPLSCDSVMDISQVRLEWPTDLAIN 1415

Dbb 1318 DKNGLIYFVDGTMIRKVDQNGIISTLLGSNDLTSARPLTCDTSMHISQVRLEWPTDLAIN 1377

Qy 1416 PMDNSLYVLDDNNVLOIJSENHQVRIVAGRPMHCQVPGIDHFLLSKVAIHATLESATALAV 1475

Dbb 1378 PMDNSIYVLDDNNVLOITENRQVRIAAGRPMHCQVPGVE-YPVGKHAVQTILESATAIAV 1436

Qy 1476 SHNGVLYIAETDEKKINRIQVTTSGEISLVAGAPSGCDCKNDANCDCFSGDGKYAKDAK 1535

Dbb 1437 SYSGVLYIETDEKKINRIQVTTDGEISLVAGIPSEBCDCKNDANCDCYQSGDGYAKDAK 1496

Qy 1536 LNTPSSSLAVCADGELYVADLGNIRIRFIRKNKPFNTQNMVELSSPIDQELYLFDTTGKH 1595

Dbb 1497 LSAPSSLAASPDGTLTYADLGNIRIRAVSKNKPLLSNMNFYEVASPTDQELYIFDINGTH 1556

Qy 1596 LYTQSLPTGDYLYNFTYTGDDITLITDNNGMVMNVRRDSTGMPLWLVPDQGVYVWTMG 1655

Dbb 1557 QYTVSLVTGDYLYNFSYNDNDITAVTDSNGNTLRIRRDPNRMPPVRVVPSPDNQVIWLTIG 1616

Qy 1656 TNSALKSVTTQGHELAMMTYHGNSGLLATKSNENGWTTFFEYDVSFGRLLTNVTFPTGQVSS 1715

Dbb 1617 TNGCLKGMTAQGLELVLFTHYHGNSGLLATKSDETGTWTTFFDYDSEGRLLTNVTFPTGVVTN 1676

Qy 1716 FRSDTSSVHVQVETSSK-DDVTITTNLSASGAFYLLQDQVRNSYYIGADGSLRLLLAN 1774

Dbb 1677 LHGDMDKAITVDIESSSREEDVSITSNLSSIDSFTYMWQDLRNSYQIGYDGLRIIYAS 1736

Qy 1775 GMEVALQTEPHLLAGTVNPTVGKRNVTLPIDNGLNLVEWRQORKEAQGVTVFGRRLRVH 1834

Dbb 1737 GLDSHYQTEPHVLAGTANPTVAKRNMTLPGENGQNLVEWRFRKEAQAGKVNVEGRKL RVN 1796

Qy 1835 NRNLLSLDFDRVTRTEKIYDDHRKFTLRILYDQAGRPSLWSPSSRLNGVNVTVSPGGYIA 1894

Dbb 1797 GRNLLSVDFDRTTKTEKIYDDHRKFLRLRIAYDTSGHPTLWLPSKLMVNVTVSSTGQIA 1856

Qy 1895 GIORGIMSERMEYDQAGRITSRIFADGKTWSYTYLEKSMVLLHLSORQYIFEFDKNDRLS 1954

Dbb 1857 SIQRGTTSEKVDYDQGGRIVSRVFADGKTWSYTYLEKSMVLLHLSORQYIFEYDMWDRLS 1916

Qy 1955 SVTMPNVARQTLETIRSVGYYYRNIYOPPEGNASVIQDFTEDGHLHLHTFYLTGTRRRVIKY 2014

Dbb 1917 AITMPSVARHTMQTIRSIGYYRNIYNPPESNASIITDYNEEGLLLQTAFLTGTSRRVLFKY 1976

Qy 2015 GKLSKLAETLYDTTKVSFTYDETAGMLKTINLQNEGFTCTIRYRQIGPLIDRQIFRFTEE 2074

Dbb 1977 RRQTRLSEILYDSTRVSFTYDETAGVLKTVNLQSDGFICTIRYRQIGPLIDRQIFRSED 2036

Qy 2075 GMVNARFDYNDNSFRVTSMQAVINETPLPIDLYRYDDVSGKTEQFGKFGVIYYDINOII 2134

Dbb 2037 GMVNARFDYSYDNSFRVTSMQGVINETPLPIDLYQFDDISGKVEQFGKFGVIYYDINOII 2096

Qy 2135 TTAVMTHTKHFDAYGRMKEVQYEIFRSLMYWMTVQYDNMGRVVKKELKVGPYANTTRYSY 2194

Dbb 2097 STAVMTYTKHFDAGRIKEIQYEIFRSLMYWITIYQYDNMGRVTREIKIGPEFANTTKYAY 2156

Qy 2195 EYDADGQLQTVSINDKPLWRYSYDLNGLNHLLLSPGNSARLTPLRYDIRDRITRLGDVQYK 2254

Dbb 2157 EYDVGQLQTVYLNKIMWRNYNDLNGNHLNPSNSARLTPLRYDLRDRITRLGDVQYR 2216

Qy 2255 MDEDGFLRQGGDIFEYNSAGLLIKAYNRAGSWSVRYRYDGLGRRVSSKSSHHLQFFY 2314

Dbb 2217 LDEDGFLRQRGTEIFEYSSKGLLTRVYSKSGSGWTVIYRYDGLGRRVSSKTSLGQHLQFFY 2276

Qy 2315 ADLTNPTKVTHLYNHSSSEITSLYYDLQCHLPAMELSSGDEFYIACDNIGTPLAVFSGTG 2374

Dbb 2277 ADLTYPTRITHVYNHSSSEITSLYYDLQCHLPAMEISSGDEFYIASDNTGTPLAVFSSNG 2336

Qy 2375 LMIKOILYTAYGEIYMDTNPNFQIIIGYHGGLYDPLTKLVHMRDRDYDLAGRWTSPDHE 2434

Dbb 2337 LMLKQIQYTAYGEIYFDSNIDFQLVIGFHHGLYDPLTKLIHFGERDYDILAGRWTTPDIE 2396

Qy 2435 LWKHLSSSNVMPFNLYMFKNNNPISNSQDIKCFMTDVNSWLLTTFGQLHNVIPGYPKPDM 2494

Dbb 2397 IWKRI-GKDPAPFNLYMFRNNNPASKIHDVKDYITDVNSWLVTFGFHLHNAIPGFPVPKF 2455

Qy 2495 DAMEPSYELIHTQMKTOEWDNKSILGVQCEVQKQKAFVTLERFDQLYGSTITSCQQAP 2554

Dbb 2456 DLTEPSYELV----KSQQWDDIPPIFGVQQQVARQAKAFLSLGKMAEVQ----VSRRRAG 2507

Qy 2555 KTKK---FASSGSVFGKGVKFKALDGRVTTDIISVANEDGRRVAAILNHAHYLENLHFTI 2611

Dbb 2508 GAQSWLWFATVKSLIGKVM LAVSQGRVQTNVLNIANEDCIKVA AVLNNAFYLENLHFTI 2567

Qy 2612 DGVDTHYFVKPGPSEGDLAILGLSGRRFTLENGVNVTVSQINTVLNGRTRRYTDIQLQYG 2671

Dbb 2568 EGKOTHYFIKTTTPESDLGTLRLTSGRKALENGINVTVSQSTTVNNGRTRRFADVEMQFG 2627

Qy 2672 ALCLNTRYGTTLDDEEKARVLELARQRAVRQAWAREQQRLREGEGLRAWTEGEKQQVLST 2731

Dbb 2628 ALALHVRYGMTLDDEEKARILEQARQALARAWAREQQQRVRDGEGARLWTEGEKRQLLSA 2687

Qy 2732 GRVQGYDGGFFVISVEQYPELSDSANNIHFMRSQSEMGR 2769

Dbb 2688 GKVQGYDGYVLSVEQYPELADSANNIQFLRQSEIGRR 2725

RESULT 13

ADH41999

ID ADH41999 standard; protein; 2725 AA.

XX

AC ADH41999;

XX

DT 25-MAR-2004 (first entry)

XX

DE Novel human protein NOV40h #2.

XX

KW cardiovascular; antiarteriosclerotic; hypotensive; cytostatic; anorectic;





Db 369 -----DNGKLGFTQENNTIDSGELDIGRRAIQEIPIPGIFWRSQLFIDQPQLK 417

Qy 466 FNVSLGAALVGIYGRKGLPPSHT----QDFVELLDGRRLLTQEARSLSEGTQPSRGTV 521

Db 418 FNIISQKDALIGVYGRKKLPPSHTQSSPOYDFVELLDGSRLIAREQSSLLETERAGRQAR 477

Qy 522 PPSSETGFIQYLDSGIWHLAFYNDGKESSEVVSFLTTAIESVDNCPSCNGGDCISGTC 581

Db 478 SVSLHEAGFIQYLDSGIWHLAFYNDGKNAEQVSFNTIVIESVVECPRNCHNGECVSGTC 537

Qy 582 HCFLGFLGPDCCGRASCPVLCSGNGOYMKGRCLCHSGWKGAECDVPTNQCIDVACSNHGTC 641

Db 538 HCFPGFLGPDCCSRAACPVLCSGNGOYSKGRCLCFSGWKGTEDVPTTQCIDPQCGRGIC 597

Qy 642 ITGTCICNPGYKGESCEEVDCMDPTCSGRGVCVRGECCHCFVGWGGTNCETPRATCLDQCS 701

Db 598 IMGSCACSSGYKGESCEEADCIDPGCSNHGVCIHGECHCSPGWGGSNCEILKTMCPDQCS 657

Qy 702 GHGTFLPDTGLCSDPSWTGHDCSIIEICAADCGHGVCVGGTCRCEDGWMGAACDQACH 761

Db 658 GHGTYLQESGSCCTDNPWTGPDSCSNEICSVDCSGSHGVCMGGTCRCEEGWTGPACNQACH 717

Qy 762 PRCAEHGTCRDGKCECSPGWNGEHCTIAHYLDRVY-----KEGCPGLCNGNGRCTLDLN 815

Db 718 PRCAEHGTCDKGCECQGWNGEHCTIAHYLDKIVKDKIGYKEGCPGLCNSNGRCTLDQN 777

Qy 816 GWHCVCOLGWRGAGCDTSMETACGDSKDNDDGDLVDCMDPDCCIQPLCHINPLCLGSPNP 875

Db 778 GGHCVCQPGWRGAGCDVAMETLCTDSKDNEDGLIDCMDPDCCLOSSCQNPYCRGLPDP 837

Qy 876 LDIIQETQVPVSQQNLHSPYDRIKFLVGRDSTHIIIPGENPFDGGHACVIRGOVMTSDGTP 935

Db 838 QDIIISQLSQSPSQAAKSPYDRISFLIGSDSTHVIPGESPFNKSLASVIRGOVLTADGTP 897

Qy 936 LVGNWISFVNNPLFGYTIQRQDGSFDLVNTNGGISIILRFERAPFITQEHTLWLPWDRFFV 995

Db 898 LIGNVVSFFHYPEGYTITRQDGMFDLVANGGASLTIVFERSPFLTQYHTVWIPWNVYV 957

Qy 996 METIIMRHEENEIPSCDLSNFARPNPVWSPSPLTSPASSCAEKGPVPEIQALQEEISIS 1055

Db 958 MDTLVMEKEENDIPSCDLSGFVRPNPIIVSSPLSTFRSSPEDSPIIPETQVLHEETIP 1017

Qy 1056 GCKMRLSYLSSRTPGYKSVLRISLTHPTIPFNLMKVHLMVAVEGRLFRKWFAPAAPDLsY 1115

Db 1018 GTDLKLSYLSSRAAGYKSVLKITWTQSIIPFNLMKVHLMVAVVGRLLFQKWFEPASPNLAYT 1077

Qy 1116 FIWKTDDVYNQKVFGLSEAFVSVGYEYESCPDILWEKRTTVLQGYEIDASKLGGWSLDK 1175

Db 1078 FIWKTDAYNQKVGLSEAVVSVGYEYESCLDILTWEKRTAILQGYELDASNMGWTLDK 1137

Qy 1176 HHAJNIQSGILHKNGENQFVSQQPPVIGSIMNGRRRSISCPSCNGLADGNKLLAPVAL 1235

Db 1138 HHVLDVQNGILYKNGENQFISQQPPVSSIMNGRRRSISCPSCNGQADGNKLLAPVAL 1197

Qy 1236 TCGSDGSLYVGDFNYIRRIFPSPGNVTNILELRNKDFRSHSHSPAHHYYLATDPMGAVFLS 1295

Db 1198 ACGIDGSLYVGDFNYVRRIFPSPGNVTSVLELRNKDFRHSNPAHRYLLATDPVTGDLVVS 1257

Qy 1296 DSNRRRVFKIKSTVVVKDLVKNSEVAVGTGDQCLPFDDTRCGDGGKATEATLTNPRGITV 1355

Db 1258 DNTNRIYRPKSLTGAKDLTKNAEVAVGTGEQCLPFDEARCGDGGKAVEATLMSPKGMV 1317

Qy 1356 DKFGLIYFVDGTMIRRIDQNGIISTLLGSNDLTSARPLSCDSVMDISOVRLEWPTDLAIN 1415

Db 1318 DKNGLIYFVDGTMIRKVDQNGIISTLLGSNDLTSARPLTCDTSMHISOVRLEWPTDLAIN 1377

Qy 1416 PMDNSLYVLDDNNVVLQISENHQVRIVAGRPMHCQVPGIDHFLLSKVAIHATLESATALAV 1475

Db 1378 PMDNSIYVLDDNNVVLQITENQVRIVAAGRPMHCQVPGVE-YPVGKHAVQTTLLESATAIAV 1436

Qy 1476 SHNGVLYIAETDEKKINRIRQVTTSGEISLVAGAPSGCDCKNDANCDFCSGDDGYAKDAK 1535

Db 1437 SYSGLVYITETDEKKINRIRQVTTDGEISLVAGIPSECDCKNDANCDYQSGDGYAKDAK 1496

Qy 1536 LNTPSSLAVCADGELYVADLGNIRIRFIRKNKPFNTQNMYELSSPIDQELYLFDTTGKH 1595

Db 1497 LSAPSSLAASPDGTLYIADLGNIRIRAVSKNKPLLNSMNFYEASPTDQELYIFDINGTH 1556

Qy 1596 LYTQSLPTGDYLYNFYTYTGDGDITLITDNNGNMNVNRRDSTGMPLWLVPDGGQVYVWTMG 1655

Db 1557 QYTVSLVTGDYLYNFYSNDNDITAVTDSNGNTLRIRRDPNRMPVRVPSDPNQVWLITIG 1616

Qy 1656 TNSALKSVTTQCHELAMMTYHNGSGLLATKSNENGWTTTFYEYDSFGRLTNVTFTPTQVSS 1715

Db 1617 TNGCLKGMTAQGLELVLFYTHGNSGLLATKSDEGTWTTFFDYDSEGRLTNVTFTPTGVVN 1676

Qy 1716 FRSDTSSVHVQVETSSK-DDVTITTNLSASGAFYTLLODQVRNSYYIGADGSLRLLLAN 1774

Db 1677 LHGDMDKAITVDIESSSREEDVSITSNLSSIDSFYTMVQDQLRNSYQIGYDGSRLIYYAS 1736

Qy 1775 GMEVALQTEPHLLAGTVNPTVGKRNVTLPIDNGLNLVEWRQORKEAQGVTVFGRRLRVH 1834

Db 1737 GLDSHYQTEPHVLAGTANPTVAKRNMTLPGENGQNLVEWFRKEQAQGVNVFGRKLRVN 1796

Qy 1835 NRNLLSLDFDRVTRTEKIYDDHRKFTLRILYDQAGRPSLWSPSSRLNGVNVYTSPPGYIA 1894

Db 1797 GRNLLSVDFDRTTKTEKIYDDHRKFLRLRAYDTSGHPTLWLPSSKLMAVNVYTSSTGQIA 1856

Qy 1895 GIORGIMSERMEYDQAGRITSRIFADGKTWSYTYLEKSMVLLLLHSRQYIFEFDKNDRLS 1954

Db 1857 SIQRTTSEKVDYDGGQGRIVSRVFADGKTWSYTYLEKSMVLLLLHSRQYIFEYDMWDRLS 1916

Qy 1955 SVTMPNVAROTLETIRSVGYRNIYQPPEGNASVIODFTEGHLLHTFYLGTGRRVIYKY 2014

Db 1917 AITMPSVARHTMQTIRSIGYRNIYNPPESNASIITDYNEEGLLLQTAFLGTSRRVLFKY 1976

Qy 2015 GKLSKLAETLYDTTKVSFTYDETAGMLKTINLQNEGFTCTIRYRQIGPLIDRQIFRFTEE 2074

Db 1977 RRQTRLSEILYDSTRVSFTYDETAGVLKTVNLQSDGFICTIRYRQIGPLIDRQIFRFS 2036

Qy 2075 GMVNAREFNVYDNSFRVTSMQAVINETPLPIDLYRYDDVSGKTEQFGKFGVIYYDINQII 2134

Db 2037 GMVNAREFDYSYDNSFRVTSMQGVINETPLPIDLYQFDDISGKVEQFGKFGVIYYDINQII 2096

Qy 2135 TTAVMTHTKHFDAYGRMKEVQYEIFRSLMYMTVQYDNMGRVVKKELKVGPYANTTRYSY 2194

Db 2097 STAVMTYTKHFDAGRIKEIQYEIFRSLMWITIQYDNMGRVTKREIKIGFANTTKYAY 2156

Qy 2195 EYDADGQLQTVSINDKPLWRYSYDLNGLNHLSPGNSARLTPLRYDIRDRITRLGDVQYK 2254

Db 2157 EYDVDGQLQTVYVLEKIMWRNYDLNGLNHLNPSNSARLTPLRYDLDRITRLGDVQYR 2216

Qy 2255 MDEDGFLRQRGDIFEYNSAGLLIKAYNRAGSWVRYYDGLGRRVSSKSSHHLQFFY 2314

Db 2217 LDEDGFLRQRGTEIFEYSSKGLLTRVYSKSGWTVIYRYDGLGRRVSSKSLGQHLQFFY 2276

Qy 2315 ADLTNPTKVTHLYNHSSSEITSLYYDLQHLFAMELSSGDEFYIACDNIGTPLAVFSGTG 2374

Db 2277 ADLTYPTRITHVYNHSSSEITSLYYDLQHLFAMEISSGDEFYIASDNTGTPLAVFSSNG 2336

Qy 2375 LMIKQILYTAIGEIMDTNPNFQIIIGYHGGLYDPLTKLVHMGRRDYDVLAGRWTSPDHE 2434

Db 2337 LMLKQIQYTAIGEYFDSNIDFQLVGFHGGLYDPLTKLIHFGERDYDILAGRWTTPDIE 2396

Qy 2435 LWKHLSSSNVMPFNLYMFKNNPNISNQDIKCFMTDVNSWLLTFGFQLHNVTIPGYPKPDM 2494

Db 2397 IWKRI-GKDPAPFNLYMFRNNNPASKIHVDKDYITDVNSWLVTFGFHLHNAIPGFVPKF 2455

Qy 2495 DAMEPSYELIHTQMKTQEWDNKSILGVQCEVQKQLKAFVTLERFDLYGSTITSCQAP 2554

Db 2456 DLTEPSYELV----KSQQWDDIPPIFGVQQQVARQAKAFLSLGKMAEVQ----VSRRRAG 2507

Qy 2555 KTKK---FASSGSGVFGKGVKFALKDGRVTTDIISVANEDGRRVAAILNHAHYLENLHFTI 2611

Db 2508 GAQSWLWFATVKSLIGKVMIAVSOGRVQTVNLINIANEDCIKVAAVLNNAFYLENLHFTI 2567





Db 61 NRVKDLVHREADEFTROGNFTLRQLGVCEPATRRGLAFCAEMGLPHRGYSISAGSDADT 120

Qy 118 EADTVLSPEHPVRLWGRSTRSGRSSCLSSRANSNLTLTDEHEN---TETDHPGGLQNH 174

Db 121 ENEAVMSPEHAMRLWGRGVSGRSSCLSSRSNSALTTLTDEHENKSDSENEQPASNQGS 180

Qy 175 RLRTPPPLSHAHTPNQHAASINSLNRGNFTRSPNPPAPT DHSLSGEPAGGAQ---- 230

Db 181 TLQPLPP--SHKQHSQHH-PSITSLNRNSLTRNRQSPAP-----PAALPAELQTT 229

Qy 231 -EPAHAQENWLLNSNIPLETRNLGKQPFGLTQDNLIEMDILGASRHDGAYS DGHFLFKP 289

Db 230 PESVLQDSWVLGNSVPLESR-----HFLFKT 256

Qy 290 G-GTSPLFCTTSPGYPLTSSVYSPPPRPLPRSTFARPAFNLKKPSKYCNWKCAALSAIV 348

Db 257 GTGTTPLFSTATPGYTMASGSVYSPPTRPLPRNTLSRSAPFKKSSKYCSWKCTALCAVG 316

Qy 349 ISATLVI LLAYFVAMHLEGLNWHLQPMEGQMYE---ITEDTASSWPVPTDVSLYPSGGTG 405

Db 317 VSVLLAILLSYFIAMHLEGLNWLQQTENDTTFENGKNSDT-----MPTNTVSLPSG--- 368

Qy 406 LETPDRKGKGTTEGKPSFPFEDSFIDSGEIDVGRASQKIPPGTFWRSQVFI DHPVHLK 465

Db 369 -----DNGKLGGTQENNTIDSGELDIGRRAIQEI PPGIFWRSQLFIDQPQFLK 417

Qy 466 FNVSLGKAALVGIYGRKGLPPSHT-----QFDFVELLDGRRLLTQEARSL EGTFRQSRGTV 521

Db 418 FNISLQKDALIGVYGRKKLPPSHTQSSPOYDFVELLDGSRLLIAREQSRLL ETERAGQAR 477

Qy 522 PPSSHETGFIQYLDSGIWHLAFYNDGKESVVSFLTAIESVDNCPSN CYNGDCISGTC 581

Db 478 SVSLHEAGFIQYLDSGIWHLAFYNDGKNAEQVSFNTIVIESVVECPRNCHGN GECVSGTC 537

Qy 582 HCFGLGLGPDCCGRASCPVLCSGNGQYMKGRCLCHSGWKGAEC DVPTNQCIDVACSNHGTC 641

Db 538 HCFPGFLGPDCSRACAPVLCSGNGQYSGRCLCFSGWKGT ECDVPTTQCIDPQCGGRGIC 597

Qy 642 ITGTICINPGYKGESCEEYDCMDPTCSGRGVCVRGECHCFV GGGTNCETPRATCLDQCS 701

Db 598 IMGSCACSSGYKGESCEEADCIDPGCSNHGVCIHGECHCS PGWGSNCEILLKTMCPDQCS 657

Qy 702 GHGTFLPDTGLCSCDPSWTGHDCSIEICAADCGGHGVCVGGTCR CEDGWMGAACDQACH 761

Db 658 GHGTYLQESGSCTCDPNWTGPDCSNEICSVDCGSHGVC MGGTCCRCEE GWTPACNQORACH 717

Qy 762 PRCAEHGTCRDGKCECSPGNGEHCTIAHYLDRVV-----KEGCPGLCNGN GRCTLDLN 815

Db 718 PRCAEHGTC DKGKCECSQWNGEHCTIAHYLDKIVKD KIGYKEGCPGLCNSNGRCTLDQN 777

Qy 816 GWHCVQLGWRGAGCDTSMETACGDSKDN DGLVDCMDPDCC LQPLCHINPLCLGSPNP 875

Db 778 GGHCVCPGWRGAGCDVAMETLCTDSK DNEGDGLIDCMDPDCC LQSSCQNQPYCRGLPDP 837

Qy 876 LDIQETQVPVSQONLHSFYDRIKFLVGRDSTHII PGENPFDGGHACVIRGQVMTSDGTP 935

Db 838 QDIISQSLQSPSQAAKSFYDRISFLIGSDSTHVIPGESPFNKSLASVIRGQVLTADGTP 897

Qy 936 LVGVNISFVNPNPLFGYTIISRQDGSFDLVTNGGII IILPFERAPFITOEHTLWLPWDRFFV 995

Db 898 LIGVNVSFHYPEYGYTTITRQDGMFDLVANGGASLT LVFERSPFLTQYHTVWIPWNVFYV 957

Qy 996 METIIMRHEENEIPSCDLSNFARPNPVVSPSLTSF ASSCAEKGPVPEIQALQBEISIS 1055

Db 958 MDTLWMEKEENDIPSCDLSGFRPNPIIVSSPLSTFRSSPEDSPIIPETQVLHEETTIP 1017

Qy 1056 GCKMRLSYLSSRTPGYKSVLRISLTHPTIPFNLMKVHLMVA VEGRLFRKWFAAAPDLSYY 1115

Db 1018 GTDLKLSYLSSRAAGYKSVLKITMTQSIIPFNLMKVHLMVA VVGRLLFQKWFASPENLAYT 1077

Qy 1116 FIWDKTDVYNQKVFGLSEAFVSVGYEYESCPDLILWEKRTTV LQGYEIDASKLGWSLDK 1175

Db 1078 FIWDKTDAYNQKVGLSEAVVSVGYEYESCLDLTLWEKRTAIL QGYELDASNMGWTLDK 1137

Qy 1176 HHALNIQSILHKNGENQFVSQQPPVIGSIMGNRRRSISCPSCNGLADGNKLLAPVAL 1235

Db 1138 HVLDVQNGILYKNGENQFISQQPPVSSIMGNRRRSISCPSCNGQADGNKLLAPVAL 1197

Qy 1236 TCGSDGSLYVGDENYIRRIFPSGNVTNILELRNKDFRHSHPAHKYKYLATDPMSGAVFLS 1295

Db 1198 ACGIDGSLYVGDENYVRRIFPSGNVTSVLELRNKDFRHSNPAHRYLYLATDPVTGDLVYS 1257

Qy 1296 DSNRRRVFKIKSTVVVKDLVKNSEVVAGTGDQCCLPFDDTRCGDGGKATEATLTNPRGITV 1355

Db 1258 DYNTRRIYRPKSLTGAKDLTKNAE VVAGTGEQCCLPFDEARCGDGGKAVEATLMSPKGMAY 1317

Qy 1356 DKFGLIYFVDGTMIRRIDQNGIISTLLGSNDLTSARPLSCDSVMDISQVRLEWPTDLAIN 1415

Db 1318 DKNGLIYFVDGTMIRKVDQNGIISTLLGSNDLTSARPLTCDTSMHISQVRLEWPTDLAIN 1377

Qy 1416 PMDNSLYVLDNNVVLQISENHQVRIVAGRPMHCQVPGIDHFLLSKVAIHATLESATALAV 1475

Db 1378 PMDNSIYVLDNNVVLQITENRQVRIAAGRPMHCQVPGVE-YPVGKHAVQTLESATAIAV 1436

Qy 1476 SHNGVLYIAETDEKKINRIQVTTSGEISIVAGAPSGCDCKNDANCD CFSGDDGYAKDAK 1535

Db 1437 SYSGVLYITETDEKKINRIQVTTDGEISIVAGIPSECDCKNDANCD CYQSGDGYAKDAK 1496

Qy 1536 LNTPSSLAVCADGELYVADLGNIRIRIRKVKPFNTQNM YELSSPIDQELYLFDTTGKH 1595

Db 1497 LSAPSSLAASPDCTLYIADLGNIRIRAVSKVKP LLNSMNFYEVASPTDOELYIFDINGTH 1556

Qy 1596 LYTQSLPTGDYLYNFTYTGDGDTLITDNNGNMNVNRRDSTGMPLWLVPDQGVYVVTMG 1655

Db 1557 QYTVSLVTGDYLYNFYSNDNDITAVTDSNGNTLRIRRDPNRMPVRVVS PDNQVIWLTIG 1616

Qy 1656 TNSALKSVTTQGHELAMMTYHNSGLLATKNSNENGWTTTFEYDSFGRLTNVTFPTGQVSS 1715

Db 1617 TNGCLKGMTAQGLELVLFYTHGNSGLLATKSDETGWTTFDYDSEGR LTNVTFPTGVVTN 1676

Qy 1716 FRSDTSSVHVQVETSSK-DDVTITTNLSASGAFYTL LQDQVRNSYIIGADGSLRLLAN 1774

Db 1677 LHGDMDKAITVDIESSSREEDVSITSNLSSIDSFYTMVQDLRNSYQ IGYDGLRIIYAS 1736

Qy 1775 GMEVALQTEPHLLAGTVNPTVGKRNVTLPIDNGLNLVEWRQRKEQARGOVTVFGRRLRVH 1834

Db 1737 GLDSHYQTEPHVLAGTANPTVAKRNM TLPGENGQNLVEWFRKEQAQGVN VFGKRLVN 1796

Qy 1835 NRNLLSLDFDRVTRTEKIYDDHRKFLLRIAYDTSGHPTLWLPSSKLM AVNVTYSSTGOIA 1856

Db 1797 GRNLLSVDFDRTTKTEKIYDDHRKFLLRIAYDTSGHPTLWLPSSKLM AVNVTYSSTGOIA 1856

Qy 1895 GIQRGIMSERMEYDQAGRITSRIFADGKTWSYTYLEKSMVLL LHSQRQYIFEFDKNDRLS 1954

Db 1857 SIQRGTTSEKVDYDQGRIVSRVFADGKTWSYTYLEKSMVLL LHSQRQYIFEYDMWDRLS 1916

Qy 1955 SVTMPNVARQTLTETIRSVGYARNIYQPPEGNASVIQDFTEDGHLLHTF YLGTGRRVIKY 2014

Db 1917 AITMPSVARHTMQTIRSIGYARNIYNPPESNASIITDYN EEGLLLTQATAFLGTSRRVLFKY 1976

Qy 2015 GKLSKLAETLYDTTKVSFTYDETAGMLKTINLQNEGFTCTIRYRQ IGPLIDRQIFRPTEE 2074

Db 1977 RRQTRLSEILYDSTRVSFTYDETAGVLKTVNLQSDGFICTIRYRQ IGPLIDRQIFRSED 2036

Qy 2075 GMVNARFDYNDSPRVTSMQAVINETPLIDLYRYDDVSGKTEQFGKFGVIYYDINQII 2134

Db 2037 GMVNARFDYSYDNSPRVTSMQGVINETPLIDLYYQFDDISGKVEQFGKFGVIYYDINQII 2096

Qy 2135 TTAVMTHTKHFDAYGRMKEVQYEIFRSLMYWMTVQYDNMGRVVKELKVGPYANTTRYSY 2194

Db 2097 STAVMTYTKHFDAHGRIKEIQEYEIFRSLMYWITIQYDNMGRVTKREIKIGPFANTTKYAY 2156

Qy 2195 EYDADGLOQTVSINDKPLWRSYDLNGLNHLSPGNSARLTPLRYDIRDRITRLGDVQYK 2254

Db 2157 EYDVGLOQTIVYLNKIMWRNYDNLGNLHLLNPSNSARLTPLRYDLRDRITRLGDVQYR 2216







Qy	1895	GIORGIMSERMEYDQAGRITSRIFADGKTWSYTYLEKSMVLLLSHQRYTIFEDKNDRLS	1955
Db	1857	SIORGTTSKVDYDQGRIVSRVFADGKTWSYTYLEKSMVLLLSHQRYTIFEDKNDRLS	1916
Qy	1955	SVTMPNVARQTLETIRSVGYRNIYQPPGASVIQDFTEDGHLHHTFYLGTGRRVIYKY	2014
Db	1917	AITMPSVARHTMOTIRSIGYRNIYNPPESNASIITDYNEEGLLLQTAFLGTSRRVLFKY	1976
Qy	2015	GKLSKLAETLYDTTKVSFTYDETAGMLKTIINLQNEGFTCTIRYRQIGPLIDRQIFRTEE	2074
Db	1977	RQOTRLSEILYDSTRVSFTYDETAGVLKTVNLQSDGFICTIRYRQIGPLIDRQIFRSED	2036
Qy	2075	GMVNARFDYNDNSFRVTSMAVINETPLPIDLYRYDDVSGKTEQFGKFGVIYYDINOII	2134
Db	2037	GMVNAREDISYDNSFRVTSMQGVINETPLPIDLYQFDDISGKVEQFGKFGVIYYDINOII	2096
Qy	2135	TTAVMTHTKHFDAYGRMKEVQYEIFRSLMYMTVQYDNMGRVVKELKVGPYANTTRYSY	2194
Db	2097	STAVMTYTKHFDAGHRIKEIQYEIFRSLMYWITIYQYDNMGRVTKREIKIGPEANTTKYAY	2156
Qy	2195	EYDADGQLQTVSINDKPLWRYSYDLNGLHLLSPGNSARLTPLRYDIRDRITRLGDVQYK	2254
Db	2157	EYDVDGQLQTVYLNKIMWRNYDLNGLHLLNPSNSARLTPLRYDLRDRITRLGDVQYR	2216
Qy	2255	MDEGFLRQGGDIFEYNSAGLLIKAYNRAGSWRYRYDGLGRRVSSKSSHHLQFFY	2314
Db	2217	LDEGFLRQRGTEIFEYSSKGLLTRVYSKSGSWTVIYRYDGLGRRVSSKSLGHLQFFY	2276
Qy	2315	ADLTNPTKVTTHLYNHSSEITSLYYDLQHLFAMELSSGDEFYIACDNIGTPLAVFSGTG	2374
Db	2277	ADLTYPTRITHVYNHSSEITSLYYDLQHLFAMEISSGDEFYIASDNTGTPLAVFSSNG	2336
Qy	2375	LMIKQILYTAIGEYMDTNPNFQIIIGYHGGLYDPLTKLVHMGRDDYDLVLAGRWTSPDHE	2434
Db	2337	LMLKQIQYTAIGEYFDSNIDFQLVIGFHGGLYDPLTKLIHGERDYDILAGRWTTPDIE	2396
Qy	2435	LWKHLSSSNVMPENLYMFKNNPNISNSQDIKCFMTDVSNSWLLTFEGQLHNVPDGYPKPDM	2494
Db	2397	IWKRI-GKDPAPENLYMERNNPNASKIHVDKDYITDVSNSWLVTFGFHLNHAIPGFVPKPF	2455
Qy	2495	DAMEPSYELIHTQMKTQEWDNKSILGVQCEVQKQLKAFVTLERFDQLYGSTITSCQQAP	2554
Db	2456	DLTEPSYELV---KSQWDDDIPPIFGVQQQVARQAKAFLSLGKMAEVQ---VSRRRAG	2507
Qy	2555	KTKK---FASSGSVFGKGVKFALKDGRVTTDIISVANEDGRRVAAILNHAHYLENLHFTI	2611
Db	2508	GAQSWLWFATVKSILGKGVMLAVSQGRVQTVNLNLIANEDCIKVA AVLNNAFYLENLHFTI	2567
Qy	2612	DGVDTHYFVKPGPSEGLLAILGLSGRRRTLENGVNVTVVSQINTVLNGRTRRYTDIQLQYG	2671
Db	2568	EKGDTHYFIKTTTPESDLGTLRLTSGRKALENGINVTVSQSTTVNGRTRRRFADVEMQFG	2627
Qy	2672	ALCLNTRYGTTLDEEKARVLELARQAVRQAWAREQORLREGEGLRAWTEGKQQVLST	2731
Db	2628	ALALHVRYGMTLDEKARILEQARQALARAWAREQQORVDRDEEGARLWTEGKQQLLSA	2687
Qy	2732	GRVQYDGFVTVSVEQYPELSDSANNIHFMRQSEMGRR	2769
Db	2688	GKVQGYDGYVVLSEVQYPELADSANNIQFLRQSEIGRR	2725

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OM protein - protein search, using sw model

Run on: December 10, 2005, 17:39:23 ; Search time 41 Seconds  
(without alignments)  
6498.152 Million cell updates/sec

Title: US-10-029-020-14  
Perfect score: 14887  
Sequence: 1 MDVKERKPYRSLRRRDAER.....ELSDSANNIHFMRQSEMGR 2769

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues  
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 80:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	14269	95.8	2825	2	T14271	Doc4 protein, stre
2	3804.5	25.6	2515	2	S47008	tenascin-like prot
3	3515.5	23.6	2406	2	A54148	odz protein - frui
4	3111.5	20.9	849	2	T46253	hypothetical prote
5	2109	14.2	2531	2	T16743	hypothetical prote
6	1175.5	7.9	782	2	A61625	tenascin-like prot
7	943	6.3	184	2	T12457	hypothetical prote
8	659.5	4.4	2019	1	JQ1322	tenascin precursor
9	652	4.4	1746	1	S19694	tenascin precursor
10	649.5	4.4	2201	2	A32160	tenascin-C - human
11	641	4.3	1810	1	A32230	tenascin precursor
12	626	4.2	4006	2	T09070	probable tenascin
13	592	4.0	3566	1	A40701	tenascin-X precurs
14	577.5	3.9	647	2	A43902	tenascin - eastern
15	572.5	3.8	4135	2	T42629	tenascin-X - bovin
16	438.5	2.9	2703	1	A24420	notch protein - fr
17	429	2.9	2524	2	A35844	xotch protein - Af
18	428.5	2.9	2555	2	A40043	notch protein homo
19	427.5	2.9	2531	2	A46019	notch-1 protein -
20	424	2.8	1203	2	A49175	Notch B protein -
21	423.5	2.8	1064	2	A40136	fibropellin Ia - s
22	422.5	2.8	2531	2	S18188	notch protein homo
23	422	2.8	1620	2	T27283	hypothetical prote
24	420	2.8	2471	2	A49128	cell-fate determin
25	419.5	2.8	1220	2	A56136	jagged protein pre
26	413	2.8	2437	2	S42612	transmembrane prot
27	410	2.8	3191	2	T22945	hypothetical prote
28	400.5	2.7	1295	2	A32901	glp1 protein precu
29	399	2.7	2531	2	T31070	notch homolog - se

30	392.5	2.6	1353	1	JH0675	restrictin precurs
31	392.5	2.6	2321	2	S78549	notch3 protein - h
32	388	2.6	1574	2	T13954	MEGF6 protein - ra
33	387.5	2.6	1722	2	E89753	protein FllC7.4 [i
34	387.5	2.6	1964	2	T09059	notch4 - mouse
35	385.5	2.6	1356	2	A45445	janusin precursor,
36	384	2.6	2318	2	S45306	notch 3 protein -
37	383	2.6	1408	2	S16148	gene serrate prote
38	382.5	2.6	2139	2	A35672	crumbs protein - f
39	382	2.6	2352	2	T30201	Notch homolog prot
40	381	2.6	861	2	A48825	Notch homolog Motc
41	373.5	2.5	833	2	S19087	gene Delta protein
42	372.5	2.5	832	2	A31246	neurogenic protein
43	372.5	2.5	880	2	S00670	neurogenic repetit
44	369.5	2.5	1111	2	T26972	hypothetical prote
45	356.5	2.4	473	2	A56175	adhesive plaque pr

ALIGNMENTS

RESULT 1

T14271

Doc4 protein, stress-induced - mouse

N;Alternate names: odz protein homolog

C;Species: Mus musculus (house mouse)

C;Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 09-Jul-2004

C;Accession: T14271

R;Wang, X.Z.; Kuroda, M.; Sok, J.; Batchvarova, N.; Kimmel, R.; Chung, P.; Zinszner, H.

EMBO J. 17, 3619-3630, 1998

A;Title: Identification of novel stress-induced genes downstream of chop.

A;Reference number: Z17951; MUID:98315054; PMID:9649432

A;Accession: T14271

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-2825 <WAN>

A;Cross-references: UNIPROT:O70465; UNIPARC:UPI00000294B0; EMBL:AF059485; NID:g3170614;

C;Genetics:

A;Gene: Doc4

Query Match 95.8%; Score 14269; DB 2; Length 2825;  
Best Local Similarity 93.4%; Pred. No. 0;  
Matches 2654; Conservative 47; Mismatches 52; Indels 88; Gaps 4;

QY	1	MDVKERKPYRSLRRRDAERRY	SSADSEEGKAPOKSYSSSETLKAYDQDARLAYGSRV	60
DB	1	MDVKERKPYRSLRRRDAERRY	SSADSEEGKGPQKSYSSSETLKAYDQDARLAYGSRV	60
QY	61	KDIVPQEAEEFCRTGANFTL	RELGLEEVTPPHGTLVRTDIGLPQCGYSMGAGSDADMEAD	120
DB	61	KDMVPQEAEEFCRTGNTFTL	RELGLGEMTPPHGTLVRTDIGLPHCGYSMGASSDADLEAD	120
QY	121	TVLSPHPVRLWGRSTRSGRSS	CLSSRANSNLTLTDTTEHENTET-----	164
DB	121	TVLSPHPVRLWGRSTRSGRSS	CLSSRANSNLTLTDTTEHENTETGAPLHCSSASSTPIEQ	180
QY	165	-----	-----DHPGGL	170
DB	181	SPSPPPPPANESQRRLGNGVA	QPTPDSDEEEFVPSFLVKSGSASLGVAAANDHPSSL	240
QY	171	QNHARLRTPPPLSHAHTPNQ	HHAASINSLNRGNFTPRSNPSPAPTDHLSLGEPPAGGAQ	230
DB	241	QNHRLRTPPPLPHAHTPNQ	HHAASINSLNRGNFTPRSNPSPAPTDHLSLGEPPAGSAQ	300
QY	231	EPAHAQENWLLNSNIPLET	RNLGKQPFGLTQDNLIEMDILGASRHDGAYSDGHFLFKPG	290
DB	301	EPHAQDNWVLSKIPVETRN	LKGQPFGLGTWQDNLIEMDIFASRRDGAYSDGHFFFKPG	360
QY	291	GTSPFLCTTSPGYPLTSS	TVSYSPPPRPLPRSTFARPAFNLKKPSKYNWKCAALSAIVIS	350
DB	361	GTSPFLCTTSPGYPLTSS	TVSYSPPPRPLPRSTFARPAFNLKKPSKYNWKCAALSAILIS	420
QY	351	ATLVILLAYFVAMHLFGL	NWHLQPMEG--QMYEITEDTASSWPVPTDVSLYPSGGTGLET	408

Db	421	ATLVILLAYFVAMHLFGLNWLHPMEGQMOMYEITEDTASSWPVPTDVSLYPSGGTGLET	480
Qy	409	PDRKGKTTEGKPSFFPEDSFIDSGEIDVGRRASQKIPPGTFWRSQVFIIDHPVHLKFNV	468
Db	481	PDRKGAAEGKPSLFPEDSFIDSGEIDVGRRASQKIPPGTFWRSQVFIIDHPVHLKFNV	540
Qy	469	SLGKAALVGIYGRKGLPPSHTQDFVELLDGRRLLTQEARSLLEGTPRQSRGTVPSPSHET	528
Db	541	SLGKAALVGIYGRKGLPPSHTQLDFVELLDGRRLLTQEARSLLEGTPRQSRGPVPPSHET	600
Qy	529	GFIQYLDSGIWHLAFYNDGKESEVVSFLTТАIESVDNCPNSCYGNGDCISGTCCHFGL	588
Db	601	GFIQYLDSGIWHLAFYNDGKESEVVSFLTТАIESVDNCPNSCYGNGDCISGTCCHFGL	660
Qy	589	GPDCGRASCPVLCSENGQYMKGRCLCHSGWKGAECDVPTNOCIDVACSNHGTCTITGTCIC	648
Db	661	GPDCGRASCPVLCSENGQYMKGRCLCHSGWKGAECDVPTNOCIDVACSSHGTCTIMGTCIC	720
Qy	649	NPGYKGESCEEVDCMDPTCSEGRGVCVRGEGCHCFVGWGGTNCETPRATCLDQCSGHGTFLP	708
Db	721	NPGYKGESCEEVDCMDPTCSESRGVCVRGEGCHCSVGWGGTNCETPRATCLDQCSGHGTFLP	780
Qy	709	DTGLCSDPSSWTGHDCSIIEICAADCGGHGVCVGGTCRCEDGWMGAACDQACHPRCAEHG	768
Db	781	DTGLCNDPSSWTGHDCSIIEICAADCGGHGVCVGGTCRCEDGWMGAACDQACHPRCAEHG	840
Qy	769	TCRDGKBCECSPGWNGEHTIAHYLDRVVKEGCPGLCNGNGRCFTLDLNGWHCVQCQLGWRGA	828
Db	841	TCRDGKCECTPGWNGEHTI-----EGCPGLCNGNGRCFTLDLNGWHCVQCQLGWRGT	891
Qy	829	GCDTSMETACGDSKONDGDLVDCMDPDCCLQPLCHINPLCLGSPNPLDIIQETQVPVSQ	888
Db	892	GCDTSMETCGDGKONDGDLVDCMDPDCCLQPLCHVNPLCLGSPDPLDIIQETQAPVSQ	951
Qy	889	QNLHSFYDRIKFLVGRDSTHIIIPGENPFDGGHACVIRGOVMTSDGTPLVGNISFVNNPL	948
Db	952	QNLNSFYDRIKFLVGRDSTHSIIPGENPFDGGHACVIRGOVMTSDGTPLVGNISFINNPL	1011
Qy	949	FGYTIISROQGSFDLVNTGGISIIILRPERAPPITQEHLLWL PWD RFFVME TIIMRHEENEI	1008
Db	1012	FGYTIISROQGSFDLVNTGGISIIILRPERAPPITQEHLLWL PWD RFFVME TIIMRHEENEI	1071
Qy	1009	PSCDLSNFARPNPVWSPSPLTSFASCAEKGPVPEIQALQOEIISISGCKMRLSYLSRT	1068
Db	1072	PSRDLSNFARPNPVWSPSPLTSFASCAEKGPVPEIQALQOEIIVIA GCKMRLSYLSRT	1131
Qy	1069	PGYKSVLRISLTHPTIPFNLMKVLMVAVEGRLFRKWFAAAPDL SYFIWDKTDVYNQKV	1128
Db	1132	PGYKSVVRISLTHPTIPFNLMKVLMVAVEGRLFRKWFAAAPDL SYFIWDKTDVYNQKV	1191
Qy	1129	FGLSEAFVSVGVEYESCPDLILWEKRTVLQGYEIDASKLGGWSLDKHHALNIQSGILHK	1188
Db	1192	FGLSEAFVSVGVEYESCPDLILWEKRTAVLQGYEIDASKLGGWSLDKHHALNIQSGILHK	1251
Qy	1189	NGENQFVSQQPPVIGSIMGNRRRSISCPSCNGLADGNKLLAPVALTCGSDGSLYVGDF	1248
Db	1252	NGENQFVSQQPPVIGSIMGNRRRSISCPSCNGLADGNKLLAPVALTCGSDGSLYVGDF	1311
Qy	1249	NYIRRIFFSGNVTNILELRNKDFRHSHPAHKYLLATDPM SGAVFLSDSNSRRVFEIKST	1308
Db	1312	NYIRRIFFSGNVTNILEM-----SHSHPAHKYLLATDPM SGAVFLSDTNSRRVFEIKST	1364
Qy	1309	VVVKDLVKNSEVAGTDQCLPFDDTRCGDGGKATEATLTNPRGTVDKFGLIYFVDGTM	1368
Db	1365	TVVKDLVKNSEVAGTDQCLPFDDTRCGDGGKATEATLTNPRGTVDKFGLIYFVDGTM	1424
Qy	1369	IRRIDQNGIISTLLGSNDLTSARPLSCDSVMDISQVRLEWPTDLAINPMDNSLYVLDDNV	1428
Db	1425	IRRVQDNGIISTLLGSNDLTSARPLSCDSVMEISQVRLEWPTDLAINPMDNSLYVLDDNV	1484
Qy	1429	VLQISENHQVRIVAGRPMHCQVPGIDHFLLSKVAIHATLESATALAVSHNGVLVIAETDE	1488

Db	1485	VLQISENHQVRIVAGRPMHCQVPGIDQFLLSKVAIHATLESATALAVSHNGVLVIAETDE	1544
Qy	1489	KKINRIRQVTTSGEISLVAGAPSGCDCKNDANCDCFSGDDGYAKDAKLNTPSSSLAVCADG	1548
Db	1545	KKINRIRQVTTSGEISLVAGAPSGCDCKNDANCDCFSGDDGYAKDAKLNTPSSSLAVCADG	1604
Qy	1549	ELYVADLGNIRIRFIRKKNKPFNLNTQNM YELSSPIDQELYLFDTTGKHLYTQSLPTGDYLY	1608
Db	1605	ELYVADLGNIRIRFIRKKNKPFNLNTQNM YELSSPIDQELYLFDTSKGHLYTQSLPTGDYLY	1664
Qy	1609	NFTYTGDGDI TLITDNNGNMNVRRDSTGMPLWL VYPDGQVYVVTMGTNSALKSVTTQGH	1668
Db	1665	NFTYTGDGDI THITDNNGNMNVRRDSTGMPLWL VYPDGQVYVVTMGTNSALRSVTTQGH	1724
Qy	1669	ELAMMTYHGNSGLLATKSNENGTWTFEYEDSFGRLTNVTFTPTQVSSFRSDTDSSVHVQV	1728
Db	1725	ELAMMTYHGNSGLLATKSNENGTWTFEYEDSFGRLTNVTFTPTQVSSFRSDTDSSVHVQV	1784
Qy	1729	ETSSKDDVTITTNLSASGAFYTLLODQVRNSYYIGADGSLRLLLLANGMEVALQTEPHLLA	1788
Db	1785	ETSSKDDVTITTHLSGSGAFYTLLODQVRNSYYIGADGSLRLLLLANGMEVALQTEPHLLA	1844
Qy	1789	GTVNPTVGKRNVTLPIDNGLNLVWRQKEARGQVTVFGRRLRVHNRNLLSLDFDRVTR	1848
Db	1845	GTVNPTVGKRNVTLPIDNGLNLVWRQKEARGQVTVFGPRLRVHNRNLLSLDFDRVTR	1904
Qy	1849	TEKIYDDHRKFTLRILYDQAGRPSLWSPSSRLNGVNVYSPGGYIAGIQRGIMSERMEYD	1908
Db	1905	TEKIYDDHRKFTLRILYDQAGRPSFWSPSSRLNGVNVYSPGGHIAGIQRGIMSERMEYD	1964
Qy	1909	QAGRITSRIFADGKTWSYTYLEKSMVLLHLSQRQYIFEFDKNDRLSSVTMPNVARQTLET	1968
Db	1965	QAGRITSRIFADGKMWSYTYLEKSMVLHLHSQRQYIFEFDKNDRLSSVTMPNVARQTLET	2024
Qy	1969	IRSVGYRNIYQOPPEGNASVIODFTEDGHLLHTFVLGTGRRVIYKYGKLSKLAETLYD TT	2028
Db	2025	IRSVGYRNIYQOPPEGNASVIODFTEDGHLLHTFVLGTGRRVIYKYGKLSKLAETLYD TT	2084
Qy	2029	KVSFTYDETAGMLKTNLQNEGFTCTIRYRQIGPLIDRQIFRFTTEGMVNARFDVYD NS	2088
Db	2085	KVSFTYDETAGMLKTNLQNEGFTCTIRYRQIGPLIDRQIFRFTTEGMVNARFDVYD NS	2144
Qy	2089	FRVTSMQAVINETPLPIDLYRYDDVSGKTEQFGKFGVYIYDINQIITTA VMTHTKHFDAY	2148
Db	2145	FRVTSMQAVINETPLPIDLYRYDDVSGKTEQFGKFGVYIYDINQIITTA VMTHSKHFDAY	2204
Qy	2149	GRMKEVQYEI FRSLMYWMTVQYDNMGRVVKELKVGYPYANTTRYSEYDADGQLQTVSIN	2208
Db	2205	GRMKEVQYETFRSLMYWMTVQYDNMGRVVKELKVGYPYANTTRYSEYDADGQLQTVSIN	2264
Qy	2209	DKPLWRYSYDLNGNLHLLSPGNSARLTPLRYDIRDRI TRLDGVQYKMDDEGFLRQRGGDI	2268
Db	2265	DKPLWRYSYDLNGNLHLLSPGNSARLTPLRYDLDRITRLDGVQYKMDDEGSLRQRGGDV	2324
Qy	2269	FEYNSAGLLIKAYNRAGSWSVRYRYDGLRRRVSSKSSHHLQFFYADLTNPTKVTHLYN	2328
Db	2325	FEYNSAGLLIKAYNRAGSWSVRYRYDGLRRRVSSKSSHHLQFFYADLTNPTKVTHLYS	2384
Qy	2329	HSSSEITSLYDLQGHLFAMELSSGDEFYIACDNIGTPLAVFSGTGLMIKQILLYTAYGEI	2388
Db	2385	HSSSEITSLYDLQGHLFAMELSSGDEFYIACDNIGTPLAVFSGTGLMIKQILLYTAYGEI	2444
Qy	2389	YMDTNPNFQIIIGYHGGLYDPLTKLVHMGRDDYDLVLAGRWTS PDHELWKHLSSSNVMPFN	2448
Db	2445	YMDTNPNFQIIIGYHGGLYDPLTKLVHMGRDDYDLVLAGRWTS PDHELWKRLSSNSIVPEH	2504
Qy	2449	LYMFKNNNPISNSQDIKCFMTDVNSWLLTFGFQLHNVIPGYPKPDMDAMEPSYELIHTQM	2508
Db	2505	LYMFKNNNPISNSQDIKCFMTDVNSWLLTFGFQLHNVIPGYPKPDMDAMEPSYELVHTQM	2564
Qy	2509	KTQEWDNKSILGVQCEVQKQKAFVTLERFDQLYGSTITSCQQA PKTKKFASSSGSVFGK	2568
Db	2565	KTQEWDNKSILGVQCEVQKQKAFVTLERFDQLYGSTITSCQQA PETKKFASSSGSIFGK	2624





QY	1903	ERMEYDQAGRITSRIFADCKTWSYTYLEK--SMVLLLSQRQ--YIFEDKNDRLSSVTM	1958
Db	1642	EAYSFDRNGRLNEIKYGDGSTMVYAFKDMFGSLPLKVTTPRRSDYLQYDDAGALQSLTT	1701
QY	1959	P--NVARQTLETIRSGVYRNIIQPPEGNASVIQDFTEDGHLLHTFYLGTRRRVIYKYGK	2016
Db	1702	PRGHIHAFSLQT--SLGPFKYQYYSPINRHHPFEILYNDEGQILAKIHQSGKVAFVHDT	1759
QY	2017	LSKLAETLYDTTKVSFTYDETAGMLKTINLQNEGFTCTIRYRQIGPLIDRQIFRE-TEEG	2075
Db	1760	AGRLETILAGLSSHTYTYQDTTSLVKSVEVQPGFELRREFKYHAGILKDEKLRFGSKNS	1819
QY	2076	MVNARFDYNYDNSFRVTSMQAVINETPLPIDLYRYDDVSGKTEQFGKFGVIYYDI----	2131
Db	1820	LASARYKYAYDGNARLSGIEMAIIDDKELPTTRYKYSQNLGQLE-----VVQDLKITRN	1872
QY	2132	QIITAVMTHTKHF-----DAYGRMKEVQYEIFRSLMYWMTVQYDNMGRVVKELKVGP	2185
Db	1873	AFNRTVIODSAQOFFAIVDYDQHGRVKSULMVNKNIDVFRLELDYDLNRNIKSKQTTFG-	1931
QY	2186	YANTTRYSEYEDADQ-QQ-LQTVSINDKPLWRYSYDLNGN-LHLLSPGNSARLTPLRYDIRD	2243
Db	1932	-RSTAFDKINYNADGHVVEVLGTNN---WKLYFDENGNTVGVDQGEKFN---LGYDIGD	1984
QY	2244	RITRLGDVOY-KMDEDGFLRQGGDIFEYNSAGLLIKAYNRA--GSWSVRYRYDGLGRV	2300
Db	1985	RVIKVGDFEFNNYDARGFVVKRGEQKYRYNNRGLIHSFERERFSW---YYYDDRSRLV	2041
QY	2301	SSKSSHHLQFFYADLTNPTKVTHLYNHSSEITSLYYDLQGHLPAMELSSGDEFYIAC	2360
Db	2042	AWHDNKGNTTQYYANPRTPHLVTHVHPKISRTMKLFYDDRDMLIALE-HEDQRYYYAT	2100
QY	2361	DNIGTPLAVFSGTGLMIKQILYTAUGEIYMDTNPNFQIIIGVHGGLYDPLTKLVHMGRRD	2420
Db	2101	DQNGSPLAFFDQNGSIVKEMKRTPFGRITKDTKPEFFVPIDFHGGLIDPHTKLVYTEQRQ	2160
QY	2421	YDVLAGRWTSPDHELKHLSSSNVMPFN--LYMFKNNNPISNQDIKCFMTDVNSWLLTF	2478
Db	2161	YDPHVQWMTMTP---LWETLATEMSHPFDVFIYRYHNNDPI-NPNKPQNYMIDLDSWLQLF	2216
QY	2479	GFQLHNVIPGPKPDMDAMEPSYELIHTQMKTOEWDNSKS-----ILGVQCEVQKQLK	2531
Db	2217	GYDLNN-----MQSSRYTKLAQYTPQASIKSNTLAPDFGVISGLECIVEK----	2261
QY	2532	AFVTLERFDOLYGSTITSCQQAPKTKKFASGS-----VFGKGVKPAKDKGRVTTDIISVA	2587
Db	2262	---TSEKESDFDFVPKPLLKTEPKMRNLLPRVSYRRGVFGEVLLSRIGGRALVSVDGS	2318
QY	2588	N---EDGRRVAAILNHAHYLENLHFTIDGVDTHYFVKPGPSEGDLAJLGLSGGRFTLENG	2644
Db	2319	NSVVQD--VVSSVFNNSYFLD-LHFSIHDQDVYFVK----DNVLKLRDDNEELRLGGM	2371
QY	2645	VNVTVSQINTVLNGRTRRYTDIQLQYGALCLNTRYGTTLDDEEKARVLELARQAVRQAWA	2704
Db	2372	FNISTHEISDHGSSAAK---ELRLHGPDAVVIKYGVDPEQERHRIKHAHKAVERAWE	2428
QY	2705	REQQRLREGEEGLRAWTEGEKQQQVLSTGRVQGYDGGFFVLSVEQYPELSDSANNTHFMQRS	2764
Db	2429	LEKQLVAAGFQGRGDWTEEEKELVQHGDVDGWNNGIDHSIHKYPQLADDPGNVAFQORDA	2488
QY	2765	EMGRR	2769
Db	2489	KRKRR	2493

RESULT 3  
A54148  
odz protein - fruit fly (Drosophila sp.)  
C;Species: Drosophila sp.  
C;Date: 02-Aug-1994 #sequence\_revision 02-Aug-1994 #text\_change 21-Jul-2003  
C;Accession: A54148  
R;Levine, A.; Bashan-Ahrend, A.; Budai-Hadrian, O.; Gartenberg, D.; Menasherow, S.; Wide

Cell 77, 587-598, 1994  
A;Title: odd Oz: a novel Drosophila pair rule gene.  
A;Reference number: A54148; MUID:94243925; PMID:7514504  
A;Accession: A54148  
A;Status: preliminary; not compared with conceptual translation  
A;Molecule type: mRNA  
A;Residues: 1-2406 <LEV>  
A;Cross-references: UNIPARC:UPI0000017A1AC  
C;Genetics:  
A;Gene: FlyBase:Ten-m  
A;Cross-references: FlyBase:FBgn0004449  
F;514-540/Domain: EGF homology <EGF>  
F;610-637/Domain: EGF homology <EGF1>

Query Match 23.6%; Score 3515.5; DB 2; Length 2406;  
Best Local Similarity 34.0%; Pred. No. 9.6e-188;  
Matches 724; Conservative 433; Mismatches 843; Indels 130; Gaps 42;

QY	384	EDTASSWPVPTDVSLYPGGTGLETPDRKGKGTTEGKPSFFPEDSFIDSGEIDVGRRAS	443
Db	347	EATSSAATSSSQSLTPSLSSSLANANNGGARTF---PARSFPDPG-TTFGQITLGQKLT	402
QY	444	QKIPPGTFWRSQVFIIDHPVHLKFNVS LGKAALVGIYGRKGLPPSHTQDFVELLDGRRLL	503
Db	403	KEIQPYSYWNMQFYQSEPAYVKFDYTIIPRGASIGVYGRRNALPTHTQYHFKEVLSGFSAS	462
QY	504	TQEARS--LEGTPROSRGTVPSPSHETGFTQYLDSGIWHLAFYN-DGKESEVVSFLTITAI	560
Db	463	TRTARAAHLSITREVTR-----YMEPGHWFVSLYNDNDGDVQELTFYAAVAE	508
QY	561	ESVDNCPSNCYNGNDCISGTCHCFLGFLGPDGCRASCPLCSGNGQYMKGRCLCHSGWK	620
Db	509	DMTQNCNPGCSGNGQCLLGHQCQNPFGGDDCSESVCPVLCSEQHGEYTNGEICINPGWK	568
QY	621	AECDVPTNQCIDVACSNHGTCTITGTCICNPGYKGESCEEVDCMDPTCSGRGVCVRGECHC	680
Db	569	KECSLRHDECEVADCSGHGHCVSGKCQCVRGYKGFCEEVDCHPHNCSGHGFCADGTIC	628
QY	681	FVWGWTNCET--PRATCLDQCSGHGTFPLPDTGLCSCDPSWTGHDCSIEICAADCGGHG	737
Db	629	KKGWKGPDCATMDQDALQCLPDCSGHGTFDLDTQTCTCEAKWSGDDCSKELCDLDCGQH	688
QY	738	VCVGGTCRCEDGWMGAACDQACHPRCAEHGTCRDGKCECSPGNWGEHCTIAHYLDRVVK	797
Db	689	RCEGDACACDPEWGGEYCNTRLCDVRCNEHGQCKNGTCLCVTGWNGKHCTI-----	739
QY	798	EGCPGLCNGNRCCTLDLNG-WHCVCOLGWRGAGCDTSMETACGDSKDNDDGLVDCMDPD	856
Db	740	EGCPNSCAGHCQCRVSGEGQWECECYEGWDGPDGCGIALELNCGDSKDNDDGLVDCEDPE	799
QY	857	CCLQPLCHINPLCLGSPNPLDIITQETQVPVSQQNLHSFYDRIKFLVGRDSTHIIPGENPF	916
Db	800	CCASHVCKTSQLCVSAPKPIDVLRKKQPPAITA---SFFERMKFLIDESSLQNYAKLET	856
QY	917	DGGHACVIRGQVMTSDGTPLVGNISFVNNPLFGYTIISRQDGSFDLVNNGGISIILRFER	976
Db	857	NEPSAVIRGRVVTSLGMLVGVRS-TTTLLEGFTLTRDDGWFDMVNGGGAVTLQFGR	915
QY	977	APFITQEHTLWLPWDRFFVMEIIMRHEENE-----IPSCDLSNFARPNPVWSPSPLTS	1030
Db	916	APFRPQSRIVQVPWNEVVIIDLVMWSMSEKGLAVTTTHTCFADYDLMKPVVLASWKHG	975
QY	1031	FASSCAEKGPIVPEIQALQEEISISGCKMRLSYLSSRTPGYKSVLRISLTHPTIPFNLMK	1090
Db	976	FQACPDPSAILAESQVIESQIIPGTGLNLVYHSSRAAGVLSIKLQLTDPDVIPTSLHL	1035
QY	1091	VHLMVAVEGRLFRKWFAAAPDLSYFYFIWDKTDVYNQKVFGLSEAFVSVGYESPCPDJIL	1150
Db	1036	IHLRITIEGILFERIFEADPGIKFTYAWNRLNIYRQRYVGVTTAVVKVGYQYTDCTD-IV	1094
QY	1151	WEKRTTVLQGYEIDASKLGWSLDKQHALNIQSILHKNGENQFVSQQPPVIGSIMNG	1210
Db	1095	WDIQTKLSGHDMSISEVGGWNLDIHHRYNFHEGILQKGDGSGNIYLRNKPRIILTTMGDG	1154





Db	481	QMVI GFHGGLYDPLTKLVHFTQRDYDVLGRWTSPTYTMWKNVGEPA-PFNLYMFKSNN	539
Qy	2457	PISNSQDIKCFMTDVNSWLLTFFGQLHNVIPGYPKPDMDAMEPSYELIHTQMKTQEWDNS	2516
Db	540	PLSSELDLKNVYTDVKSWLMFEGQLSNIIPGFPRAKMYFVPPPYELSESQAS-----ENG	595
Qy	2517	KSILGVQCEVQQLKAFVTLERFDQLYGSTTITSQQAPKTK-----FASSGSVFGKGKVF	2572
Db	596	QLITGVQQTTERHNQAFMALE-----GQVITKKLHASIREKAGHWFATTTPIIGKIMF	649
Qy	2573	ALKDGRVTTDIISVANEDGRRVAAILNHAHYLENLHFTIDGVDTHYFVKPGPSEGD LAIL	2632
Db	650	AIKEGRVTTGVSSIASEDSRKVASVLNNAYLDKMHSIEGKDTHYFVKIGSADGDLVTL	709
Qy	2633	GLSGGRRTLENGVNVTVSQINTVLNGRTRTRYTDIQLQYGALCLNTRYG---TTLDEEKAR	2689
Db	710	GTTIGRKVLESGVNVTVSQPTLLVNGRTRRFTNIEFQYSTLLLSIRYGLTPD TTLDEEKAR	769
Qy	2690	VLELARQAVROAWAREQQRLREGEEGLAWTEGEKQQVLSTGRVQGYDGFVISVEQYP	2749
Db	770	VLDQARQALGTAWAKEQQKARDREGSRLWTEGEKQQLLSTGRVQGYEGYYVLPVEQYP	829
Qy	2750	ELSDSANNIHFMRQSEMGR	2769
Db	830	ELADSSSNIQFLRQNE MGKR	849
RESULT 5			
T16743			
hypothe tical protein R13F6.4 - Caenorhabditis elegans			
C;Species: Caenorhabditis elegans			
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004			
C;Accession: T16743			
R;Miller, N.			
submitted to the EMBL Data Library, April 1994			
A;Description: The sequence of C. elegans cosmid R13F6.			
A;Reference number: Z18570			
A;Accession: T16743			
A;Status: preliminary; translated from GB/EMBL/DBDJ			
A;Molecule type: DNA			
A;Residues: 1-2531 <MIL>			
A;Cross-references: UNIPROT:Q21980; UNIPARC:UPI000017A1A8; EMBL:U00046; NID:g470358; PID			
A;Experimental source: strain Bristol N2; clone R13F6			
C;Genetics:			
A;Gene: CESP:R13F6.4			
A;Map position: 3			
A;Introns: 52/2; 113/1; 170/2; 594/1; 1009/1; 1181/1; 1547/3; 1672/3; 1890/1; 2278/1; 24			
Query Match			
Best Local Similarity 14.2%; Score 2109; DB 2; Length 2531;			
Matches 674; Conservative 444; Mismatches 1064; Indels 568; Gaps 96;			
Qy	290	GGTSPLF---CTTSPGYPLTSSVTYSPPPRPLPRSTFARP-----AFNLKK-----	332
Db	25	GAPNPTYSDASTLLKYP LAAGTNQNRRRQQVGTMNNGDPVAGGPMALSKKKKFFDDSD	84
Qy	333	-----PSKYCNWKCAALS AIVISATLVILLAYFVAMHLFGLNWHLQPMEGQMYEITETA	387
Db	85	TCSRWPSK---WNILLAAALLVALFVICILLFRAPNYVY-----TQPAP-----SSDAT	130
Qy	388	SSWPVPTDVSLYPSGGTGLETPDRKGKGTTEGKPSFFBEDSFIDSGEIDVGRASQKIP	447
Db	131	SS--AAAAASRYQDLGLRALPP-----AISLGERVDVEFF	163
Qy	448	PGTFWRSQVFI DHPVHLKFNVSIGKAALVGIYGRKGLPPSHTQDFVELLDGRLLL---	503
Db	164	PKSMATTELTVTKPSRIREFNATVGSQAQLVLLMSAGVHPSLSLHDALFP I RADIRDSKS	223
Qy	504	-----TQEARSLGTPRQSRGTVPPSSHETGFIQLVDSGIWHLAFYNDGKESEVVS	554
Db	224	PTHIVEFGSRRRSLGASSSRHRNIEILSPRSATFEQVLEGRHYLTFINERSRVEPIS	283
Qy	555	FLTTAIE-----SVDNCPSNCYNGNGDCISGTCHCFLGLGPD C	592

Db	284	FVAEELQRPTTPPKTSSSGTSGAKEHPLASVLVCESNCNQRGECVHGKCHCAPGFTGRTC	343
Qy	593	GRASCPVLCSGNGQYMKGRCLCHSGWKGAECVDPTNQCIDVACSNHGTCIT-GTCICNPG	651
Db	344	DEAVCPVVCSGNGVFGGICVCKSGFKGKECEMRHNWCEVADCNGRGRCDTDGRCRCNPG	403
Qy	652	YKGESCEEVDCMDPTCSGRGVCVRGECHCFVGWGGTNCE-----	690
Db	404	WTGEACELRACPHASCHDRGVCVNGTCYCMDGWRGNDCSVFADAIHVHPQAQSPRRGOE	463
Qy	691	-----TPRATCLDQ-----	715
Db	464	PTESSKTRKAQVKPTPTSEKKKESRELQKPIIATVQVPTESSHPCSAHGQLIDD--ICQC	521
Qy	716	DPSWTGHDCSI EICAADCGGHGVCV-GGTCRCEDGWMGAACDQ RACHPRCAEHGTC-RDG	773
Db	522	ESGWDSDVCSQQAC--QC-VNGDCLDDGSCQCWKWGRGSNCTDKKCAIGCEDRGKCADSG	578
Qy	774	KCECSPGWNGEHCTIAHYLDRVVKEGCPGLCNGNCRCTLDLNG--WHCVQCQLGWRGAGCD	831
Db	579	SKCSSGWNGENCAI-----DGC PNQCSGKGECGM DRRSRSEWSCRCQAGSTGVDCS	629
Qy	832	TSMETACGDSKNDGDLVDCMDPDCCQLPLCHINPLCLGSPNPLDIIQETQVPVVSQQNL	891
Db	630	VSVEMHCDGDLNDSGLIDCDDPECCSSSSCSSESVCSTAASPIEVLMR-MPPIFNAN-	687
Qy	892	HSFYDRIKFLVGRDSTHIIIPGENPFDGGHACVIRGQVM-----TSDGTPL	936
Db	688	--FAQRVGFLIMEKSVQSYTSSQFNENLISVIRGRVMWGGSP TSGDDDLSTYSNKSTVPL	745
Qy	937	VGVNISFVNNPLFGYTISRQDGSFDLVNTNGGISIILRFERAPFITQEHILMLPWRFFVM	996
Db	746	VGVRVSDAAHPLYGFTLTREDGYFDLTVNGARSVTQLFLRTQFQSVKKSVPVSPRQIIHI	805
Qy	997	ETIIMRHEENEIPSCDLSNFARPNPVPSPLTSFASSCAEKG P-----	1040
Db	806	DDIVLYRQSGGSP-----PAISMAPARAKCSPTLRRIPDVVLISNWQYTS DGIE	854
Qy	1041	-----IVPEIQALQEEI S IGCKMRISYLS SRTPGYKSVLRISLTHPTIPFNLMKV	1091
Db	855	TDETS DSSRI VVDSRSIFESLP IQGTDVRLVYDSARSAPA PSTMLIGL L YDRVDKELRKV	914
Qy	1092	HLMVAVEGR LFRKWF AAAADLSY YFIWDKTDVYNQKV FGLSEAFVS VGYEYESCPDLI--	1149
Db	915	HINIRIAGRRFRDRVLAPRTNLTYVFAWDMKNAYRQSESGLVPTVTRVGYEYQGCDRTSER	974
Qy	1150	LWEKRTTVLQGEIDASKLGG--WSLDKXHALNIQSGILHKNGENQFVSQQPPVIGSIM	1207
Db	975	VWQTRRSQMMG--ATARKMIGTMTWLTDIHHLDIVNNVEMGNGGYRLITESEPRVSTFA	1032
Qy	1208	G-NGRRRSISCPSCNGLADGNKLLAPVALTCGDSGLYVGDFNYIRRIFFPSGNVTNILEL	1266
Db	1033	GLDGVKRDVECLKCEGKVDSISLFRPTTVVYAQDGS LII GDHNMI RRVSQDGVSTILT L	1092
Qy	1267	RNKDFRHSHPAHKYYLATDPM SGAVELSDSNRRRVFKIKSTVVVKDLVKNSEVWAGTD	1326
Db	1093	GLADTSHS-----YYIAVSPVDGTIAISLPLHKQVWRI-SSLEPQDSRNNYDVLAGDGT	1145
Qy	1327	QCLPFDDTRCGDGGKATEATLTNPRGITVDKFG LIYFVDGTMIRRIDQNGIISTLLGSND	1386
Db	1146	VCASAVDS-CGDGALAQNAQLIFPKGISFDMKGNLYLADSRRI RVIDTTGHIRSI--GET	1202
Qy	1387	LTSARPL-SCDSVMDISQVRLEWPTDLAINPMDNSLYLDNNVVLQISENHQVRIVA-GR	1444
Db	1203	TPDQHPIRTCAQITKLVDLQMEWPTSLTIDPTG SVLVLDTNVVVEIDVWHDVVVTIALGS	1262
Qy	1445	PMHCQVPGIDHFLLSKVAIHA--TLESATALAVSHNGVLYIAETDEKKINRIRQVTT S-G	1501
Db	1263	PTTCDLANATSSASAKSLDHRRHLLIONARDITVGT DGAIVYVESDGRRLNQVRKLS SDRS	1322
Qy	1502	EISLVAGAPSGCDCKNDANCDC---FSGDDGYAKDAKLNT PSSLAVCADGELYVADLGNI	1558

Db 1323 TFSILTGGKSPCSC-DVAACGDDAVSLRDVAASQAHLSSSPYAVCVSPSGDVIADSGNS 1381

Qy 1559 RIRFI-RKNKPFLNTQNMYELSSPIDQELYLFDTTGKHLYTQSLPTGDLYLNFTYTGDD 1617

Db 1382 KIKKVSARMAKYDGRSRTYEVTDAAERQEKYTFNRHGQHSSTVSLITGRTFFNFSYQVDS 1441

Qy 1618 ITLITDNNGMVNVRRDSTGMLWLVPDGVVYWTMGTSALKSVTTQGHE--LAMMTY 1675

Db 1442 ISMISE-----IRAAS-----GVVLRVLKRNDSLFDLETTLQRTTLTMSAY 1483

Qy 1676 HG-----NSGLLATKSNENGTTFYEYDSFGRLTNVTFPTQVS 1714

Db 1484 DGTLEQVSKRDSATSRDATKLFYKKGLL-TSRIDVATAVGFEYDEYGRAIGL----- 1534

Qy 1715 SFRSDTDSSVHVQVETSSKDDVTITTNLSASGAFYTLLOQOVVNSYYIGADGSLRLLLAN 1774

Db 1535 --KRDRE-YWRLGEETISMG--SVNTEVLLNGQRF-----QQVR----LG-EGNLAVHSTN 1580

Qy 1775 GME---VALQTEPHLLAGTV-NPTVGKRNVTLPIDNGLNLVEWRQKEQA-----RGQVT 1825

Db 1581 GATRLISLRNEGYSLASPLGTSTLYDKSSIPDSNGEPLISRRRTKVPAIGNPQRRELT 1640

Qy 1826 V-----FGRRL-----RVHNRNLLSLDFDRVTRTEKI-----YDDH 1856

Db 1641 TRWDWRHVARRGDDSDGSLGRKVAEVRFRPRINGVNMFSMEYDVKSNQDTLRLGSTTDD 1700

Qy 1857 RKFTLRILYDQAGRPSLWS--PSSRLNGVNVVTSYSGGYIAGIQRGIMSERMEYDQAGRIT 1914

Db 1701 AQALLFIDYTSSGRIRRIASAPEDSQMAEMNITWDGAGRKSEVTWGSWKIRLTYDNSNRLT 1760

Qy 1915 SRIFADGK---TWSYTYLEKSMVLLLSHQROYIFEFDKNDRLSSVTMPNVARQTLETIR 1970

Db 1761 EHAI-DGARVPIKMSYAGASRRPNEIQHDGAKWNIQVDNYDRIKEVISKSEATSFSSI- 1818

Qy 1971 SVGYRNIYQPPEGNASVIOBFTEDGHLHTFYLGTGRVVIYKYGKLSKLAETLYDTTKV 2030

Db 1819 ALG-----GDEWVLKRTS-----LNSKPSLV----RLSREGKVLSESTTPD 1855

Qy 2031 SPTY----DETAGMLKTINLQNEGFTCTIRYRQIGPLIDRQIFRFTTEGMVNARFDYNY 2085

Db 1856 ENHYWLERKDPITG--RTTEILNDEETTVVTCWS-----PEEPSITSSFTYEV 1901

Qy 2086 DNSFRVTSMAQVINETPLPIDLYRYDDVSGKTEQFGKFGVIYYDINQIITTAVMTHTKHF 2145

Db 1902 DDMLRVTTIQPVIEQSVLESIQLSYDERRGHVAAINGF-----KWADASTSRC 1950

Qy 2146 DAYCRMKEV-----QYEIFRSLMW-----MTVOYDNNGRVVKELKV---GPYANTTR 2191

Db 1951 QGHGLMYETSKANDHRQVVERKLIFGDARASIKIIRDKAGRASESHLEISSSGTQRN-QK 2009

Qy 2192 YSYEYDADGQLQTVSINDKP-----LWRYSYDLNGLNHLSPGNSARLTPLRYDIRDRITR 2247

Db 2010 ITRTFDAAGRVASVEQNDEPVRIIW-----NSDARVE----KINDRVVE 2050

Qy 2248 -----LGDVQYKMDDEGFLRQGG-DIFEYNSAGLLIKAYNRAGSWSVRYRYDGLG 2297

Db 2051 WNRGGALKTFQDISYQVDSIGVWVKRDNTTVFGYDGKGRLVSA--RSSQLRINIFYDRED 2108

Qy 2298 RRVSSKSSHSHLQFFYADLTNPTKVTHLYNHSSEITSILYYDLQGLHFAMELSSGDEFY 2357

Db 2109 RVVQIQNS-KDFIHFYGYIDTPKLVSHF--SKNGKISITLIFYDDDSVPFAMQSDDGTRYA 2165

Qy 2358 IACDNIGTPLAVFSGTGLMIKQILYTAYGEIYMTNPNQII-IGYHGGL-YDPLTKLVH 2415

Db 2166 LLTDETSTIKAI--GDSNVLRIDRSVFGALLPSSSSSHFFLPiGYLGIEISEISVSIL 2224

Qy 2416 MGRDYDVLAGRWTSPDHLMKHLSSSNVMPFNLYMFKNNPISNSQDIKCF----- 2467

Db 2225 NNGRPLDLYSERYS-----ISPEAVVRLELNKFKFSIDLMALEIDRQPFR 2271

Qy 2468 ----MTDVNSWLLTFGFQLHNVIP---GYPKPDMAMEPSYELIHTQMKTQEWDNKSI 2519

Db 2272 VENVPEDFETWFSLAGLS-PNLLPSAHLGLP-----ASSAIVHRLSS----- 2313

Qy 2520 LGVQCEVQQLKAFVTLERFDQLYGSTITSQQA-----PKTKKFASSGSVFGKGVKF 2572

Db 2314 -----FPRKLRPLTHL-----TTVLPTRLASDISLTSPTSETSWSIDDVGFSNLLI 2359

Qy 2573 ALKD---GRVTTDIISVANEDGRRVAAIILNHAHYLENLHFTIDG-VDTHYFVKPGPSEGD 2628

Db 2360 LNE DATTTGEVMVEMLSDLKSEEREVISKLPDG--VKSLDFATWGLVPTRHLWRAPNSKLE 2417

Qy 2629 LAILGLSGRRTRLENGVNVTVSQINTVLNGRTRRYTDIQLQYGALCLNTRYGTTLDEKA 2688

Db 2418 LS-----STFSHFMTAVN-----KOSVELRNGKSKIIVVHFSENKAEIVK 2457

Qy 2689 RVLELARQRAVRQAWAREQQRLREGEEGLRAWTEGEKQQVLSTGRVQGYD 2738

Db 2458 KIVEELKTRENIAVMRAERKRAEAGEKTWRQWSDRETRELTSKGSVSGYD 2507

RESULT 6

A61625

tenascin-like protein precursor - fruit fly (Drosophila melanogaster)

C;Species: Drosophila melanogaster

C;Date: 21-Jul-1995 #sequence\_revision 28-Jul-1995 #text\_change 09-Jul-2004

C;Accession: A61625; S28463

R;Baumgartner, S.; Chiquet-Ehrismann, R.

Mech. Dev. 40, 165-176, 1993

A;Title: Ten(a), a Drosophila gene related to tenascin, shows selective loca

A;Reference number: A61625; MUID:93264270; PMID:7684246

A;Accession: A61625

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-782 <BAU>

A;Cross-references: UNIPROT:Q24550; UNIPARC:UPI000017A1AB; EMBL:X68794

C;Genetics:

A;Gene: ten-a

A;Cross-references: FlyBase:FBgn0004446

C;Keywords: tandem repeat

F;1-62/Domain: signal sequence #status predicted <SIG>

F;63-782/Product: tenascin-like protein #status predicted <MAT>

F;497-524/Domain: EGF homology <EGF>

Query Match 7.9%; Score 1175.5; DB 2; Length 782;  
Best Local Similarity 31.4%; Pred. No. 1.2e-57;  
Matches 243; Conservative 101; Mismatches 240; Indels 191; Gaps 17;

Qy 301 PGYPLTSS-TVYSPPRPLPRSTFARPAFNLKPKSKY-CNWKCAALSAIVISATLVILLA 358

Db 2 PGFPLRNSHAAPHYSP-----YSPSRFHIDKRCQHCWSWKLSIALIFVSVVLTAMLA 56

Qy 359 YFVAMHLFGLNMH-----LQPMEGQMYEI-----TEDTASSWP----VPTDVSLYP 400

Db 57 YFAAVSSMKPNMDSTNCILVDVKSQPHDLHGGLAKSNEKGVATAFPTESIQTSTSDHG 116

Qy 401 SGGTGLETPDRKKGTTGEG-----KPSFFPPEDSFID----- 432

Db 117 QNGHGLMNPSSAGSGGNSGIIQQQLLVQQQQPHSINQPLTPLDATNTHLQDHHQLTYGGAL 176

Qy 433 -----SGEIDVG-----RRASQ----- 444

Db 177 PGVGGIGMSGGMNGLGGGLGGLMQQPQGGGLNGHHQALQPOLGGVVVELKEFNEAY 236

Qy 445 --KIPPGTFRSQVFIIDHPVHLKFNVS LGKALVGIYGRKGLPPSHTQDFVELLDGRRLL 502

Db 237 HATIPAYQFWTLEFRNKHPAFIRENFTLPWGAHFAVYSRRNVAPSVTQHDFVEFIKGGRLL 296

Qy 503 LT--QEARSLGTPRQSR----- 518

Db 297 DSHLRHRRSSANPPQLKIWSCIARTRTRVRNRLRIRTRNRTRVAVSIPANRTMRHPSI 356

Qy 519 -----GTVPPSSH-----ETGFIQYLDSGIWHLAFYNDGKES 550

Db 357 RPNSICNGLASPKVHVWNKRSAGDGLPALDVDAMTVNVSLQLYLDTGLWFIISVYNDELVA 416

QY 551 EVVSFLTAIESVD-NCPNSNCYNGDCISGTCCHCFLGFLGPDCCGRASCPVLCSGNGQYMK 609  
Db 417 HVSVLLAEAEAGVSTTCPNDCSGRGSCYLKGKDCIDIGQGVDCSKSVCPVLCSAHGHYGG 476  
QY 610 GRCLCHSGWKAECVPTNQCIDVACNSHGTCTITGTCINPGYKGESCEEVDICMDPTCSG 669  
Db 477 GVCHCEGWKAECDIPVGECEVPNCSHGRGCIIEGECHEGWKGPYCDQHDCLDPLCSG 536  
QY 670 RGVCVRGECHCFVWGVTNCTET---PRATCLDQCSHGHTFLPDTGLSCDPSWTGHDCSI 726  
Db 537 HGTCVAGQCYCKAGWQGEDCGTIDQQVYQCLPLGCSHGTYDLETGQCVCERHWTGPDSCQ 596  
QY 727 EICAADCGGHGVCVGGTCRCEDGWMGAACDQRACHPRCAEHGTCRDGKCEGSPGWNGEHC 786  
Db 597 AVCSLDCGRNGVCESGKCRCSGWTGNLCDQLPCDSRCSEHGQCKNGTCVCSQGWNGRHC 656  
QY 787 TTAHYLDRVVKEGCPGLCNGNGRCTLDLNGWHVCQLGWRGAGCDTSMETACGDSKDNHG 846  
Db 657 TL-----PGCENGCSRHGQCTLENGEYRCDCTEGWAGSDCSIALELNCKDNIDNDG 707  
QY 847 DGLVDCMDPDCCQLPLCHINPLCLGSPNPLDIIQETQVPVVSQQNLHSHFYDRIKFL 901  
Db 708 DGMTDCSDSECCSHPACSEHIMCLSSNDPVEVLLRKQPP---SVTASFQVRVKFL 759  
RESULT 7  
T12457  
hypothetical protein DKFZp564O0423.1 - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 23-Jul-1999 #sequence\_revision 23-Jul-1999 #text\_change 09-Jul-2004  
C:Accession: T12457  
R;Wambutt, R.; Heubner, D.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.  
submitted to the Protein Sequence Database, June 1999  
A:Reference number: Z17524  
A:Accession: T12457  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-184 <WAM>  
A:Cross-references: UNIPROT:Q9Y4S2; UNIPARC:UPI000007075D; EMBL:AL080120  
A:Experimental source: fetal brain; clone DKFZp564O0423  
C:Genetics:  
A:Note: DKFZp564O0423.1

Query Match 6.3%; Score 943; DB 2; Length 184;  
Best Local Similarity 99.5%; Pred. No. 1.1e-45;  
Matches 182; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 2587 ANEDGRRVAAILNHAHYLENLHFTIDGVDTHYFVKPGPSEGLAILGLSGRRRTLENGVN 2646  
Db 2 ANEDGRRVAAILDHAHYLENLHFTIDGVDTHYFVKPGPSEGLAILGLSGRRRTLENGVN 61  
QY 2647 VTVSQINTVLNGRTRRYTDIQLQYGALCLNTRYGTTLDEEKARVLELARQAVRQAWARE 2706  
Db 62 VTVSQINTVLNGRTRRYTDIQLQYGALCLNTRYGTTLDEEKARVLELARQAVRQAWARE 121  
QY 2707 QQRLREGEEGLRAWTEGEKQQVLSGTRVQGYDGFVISVEQYPELSDSANNIHFMRQSEM 2766  
Db 122 QQRLREGEEGLRAWTEGEKQQVLSGTRVQGYDGFVISVEQYPELSDSANNIHFMRQSEM 181  
QY 2767 GRR 2769  
Db 182 GRR 184

RESULT 8  
JQ1322  
tenascin precursor - mouse  
N;Alternate names: contactin; hexabrachion  
C:Species: Mus musculus (house mouse)  
C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 31-Dec-2004  
C:Accession: JQ1322; A37936; B37936; S14571; S50209  
R;Saga, Y.; Tsukamoto, T.; Jing, N.; Kusakabe, M.; Sakakura, T.  
Gene 104, 177-185, 1991

A:Title: Murine tenascin: cDNA cloning, structure and temporal expression of isoforms.  
A:Reference number: JQ1322; MUID:92009211; PMID:1717349  
A:Accession: JQ1322  
A:Status: nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 1-2019 <SAG>  
A:Cross-references: UNIPROT:Q64706; UNIPARC:UPI000005D89C; GB:D90343; NID:g220609; PIDN  
A:Experimental source: cell line 2H6GR  
A:Note: the authors translated the codon ATG for residue 60 as Trp  
R;Weller, A.; Beck, S.; Ekblom, P.  
J. Cell Biol. 112, 355-362, 1991  
A:Title: Amino acid sequence of mouse tenascin and differential expression of two tenascin  
A:Reference number: A37936; MUID:91107734; PMID:1703162  
A:Accession: A37936  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-201,'E',203-317,'S',319-620,622-1010,'N',1012-1018,'S',1020-1024,'H',1026-  
A:Cross-references: UNIPARC:UPI0000174346; GB:X56304  
A:Accession: B37936  
A:Status: preliminary; nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 1-201,'E',203-317,'S',319-620,622-1010,'N',1012-1018,'S',1020-1024,'H',1026-  
A:Cross-references: UNIPARC:UPI0000174347; GB:X56304  
R;Weller, A.; Beck, S.; Ekblom, P.  
submitted to the EMBL Data Library, August 1990  
A:Description: Aminoacid sequence of mouse tenascin and differential expression of two t  
A:Reference number: S14571  
A:Accession: S14571  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-201,'E',203-317,'S',319-1018,'S',1020-1024,'H',1026-1305,'S',1307-2019 <WE  
A:Cross-references: UNIPARC:UPI000002A093; EMBL:X56304; NID:g54768; PIDN:CAA39751.1; PID  
R;Glumoff, V.; Savontaus, M.; Vehanen, J.; Vuorio, E.  
Biochim. Biophys. Acta 1219, 613-622, 1994  
A:Title: Analysis of aggrecan and tenascin gene expression in mouse skeletal tissues by  
A:Reference number: S50206; MUID:95035091; PMID:7524681  
A:Accession: S50209  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: mRNA  
A:Residues: 46-146 <GLU>  
A:Cross-references: UNIPARC:UPI0000174348; EMBL:X80281  
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1994  
C:Superfamily: EGF homology; fibrinogen beta/gamma homology; fibronectin type III repeat  
C:Keywords: alternative splicing; calcium binding; cell adhesion; duplication; extracell  
F;1-22/Domain: signal sequence #status predicted <SIG>  
F;23-2019/Product: tenascin, long splice form #status predicted <MAT>  
F;23-1071,1527-2019/Product: tenascin, short splice form #status predicted <MAT2>  
F;408-434/Domain: EGF homology <EGF>  
F;622-703/Domain: fibronectin type III repeat homology <FN3A>  
F;711-793/Domain: fibronectin type III repeat homology <FN3B>  
F;802-884/Domain: fibronectin type III repeat homology <FN3C>  
F;892-976/Domain: fibronectin type III repeat homology <FN3D>  
F;984-1064/Domain: fibronectin type III repeat homology <FN3E>  
F;1073-1155/Domain: fibronectin type III repeat homology <FN3F>  
F;1346-1428/Domain: fibronectin type III repeat homology <FN3G>  
F;1437-1519/Domain: fibronectin type III repeat homology <FN3H>  
F;1527-1608/Domain: fibronectin type III repeat homology <FN3I>  
F;1616-1696/Domain: fibronectin type III repeat homology <FN3J>  
F;1704-1784/Domain: fibronectin type III repeat homology <FN3K>  
F;1799-2007/Domain: fibrinogen beta/gamma homology <FBG>  
F;38,166,184,327,788,1018,1079,1093,1119,1184,1210,1275,1301,1354,1364,1394,1627,1878,19

Query Match 4.4%; Score 659.5; DB 1; Length 2019;  
Best Local Similarity 19.5%; Pred. No. 4e-28;  
Matches 407; Conservative 273; Mismatches 714; Indels 689; Gaps 97;

QY 566 CPSNCGNGDCISGTCCHCFLGFLGPDCCGRASCPVLCSGNGQYMKGRCLCHSGWKAEC-- 623  
Db 315 CPNDCFDRGRCINGTCYCEEGFTGDCGELTCPNDCQGRGQCEEGQCVNCFGAGADCSE 374  
QY 624 -----DVPTNQCIDVACNSHGTCTITGTCINPGYKGES 656  
Db 375 KRCPADCHHRGRCLNGQCECDGDTGADCGDLQCPN-GCSGHRGVNGQVCDEGYTGED 433





A:Molecule type: mRNA

A:Residues: 1-1746 <NIS>

A:Cross-references: UNIPROT:Q29116; UNIPARC:UPI0000136BBB; EMBL:X61599; NID:g2124; PIDN:

C:Superfamily: tenascin; EGF homology; fibrinogen beta/gamma homology; fibronectin type

C:Keywords: alternative splicing; calcium binding; cell adhesion; duplication; extracell

F:1-22/Domain: signal sequence #status predicted <SIG>

F:23-1746/Product: tenascin #status predicted <MAT>

F:346-372/Domain: EGF homology <EGF>

F:377-403/Domain: EGF homology <EGF2>

F:622-703/Domain: fibronectin type III repeat homology <FN3A>

F:711-793/Domain: fibronectin type III repeat homology <FN3B>

F:802-884/Domain: fibronectin type III repeat homology <FN3C>

F:892-976/Domain: fibronectin type III repeat homology <FN3D>

F:984-1064/Domain: fibronectin type III repeat homology <FN3E>

F:1073-1155/Domain: fibronectin type III repeat homology <FN3F>

F:1164-1246/Domain: fibronectin type III repeat homology <FN3G>

F:1254-1335/Domain: fibronectin type III repeat homology <FN3H>

F:1343-1423/Domain: fibronectin type III repeat homology <FN3I>

F:1431-1511/Domain: fibronectin type III repeat homology <FN3J>

F:1526-1734/Domain: fibrinogen beta/gamma homology <FBG>

F:38,166,184,327,788,1034,1079,1121,1354/Binding site: carbohydrate (Asn) (covalent) #8

Query Match 4.4%; Score 652; DB 1; Length 1746;

Best Local Similarity 21.2%; Pred. No. 8.2e-28;

Matches 342; Conservative 204; Mismatches 558; Indels 512; Gaps 72;

QY	566	CPSN	CYNGDCISGTC	HCFLGFLGPD	CGRASC	PVLC	SGNGQYMKGR	CLCHSGWKGA	ECD- 624																															
Db	315	CPKC	DFDRGRCING	TCYCD	EGFEGED	CGRLAC	PHGCRGR	CEEGCQC	DEGFAGADCSE 374																															
QY	625	--VPT	NQCIDVAC	NHGT	CI	TGTC	ICNPGYK	GESCE	BEVDCMDPTCSGRGVCVRGECHCFV 682																															
Db	375	RRCP	SD-----	CHNR	GRCLDGR	CECD	GFEGED	CGELRC-	PGGCSGHGRVCVNGQCVCDE 427																															
QY	683	GWGT	NCETPRAT	CLDQCS	GHGTF	LPD	TGLCSD	PSWTG	HDCSIEICAAADCGHGVCVGG 742																															
Db	428	GRTG	EDCSQLR--	CPND	CHGR	GRCV--	QGR	CECEHGFQGYDC	SENSCPHDCHQHGRVCVNG 483																															
QY	743	TCRC	EDGWMGA	ACDQ	RACH	PRCA	EHGTCR	DGKCEC	SPGWNGEHC	CTIAHYLDRVVKEGCPG 802																														
Db	484	MCVC	DDGYTG	EDC	RELRC	PGDC	SQRGRC	VDGR	CVCEHGFAGPDC-----ADLACPS 534																															
QY	803	LCNG	NGRCTLD	LNG	WHCV	COLG	WRGAGC-----	D	TSMETACGDSK--DNDGDGLVDCM 853																															
Db	535	DCHG	RGRC---	VNG-Q	CV	CH	EGFTG	KDCG	QRRCPGDC	CHGQGR	CVDCVCH	EGFTGLDCG 590																												
QY	854	DPDC-----	CLQ	PLCH	INPL	CLG-----	SP	NPLDII	QETQ	VPVSQ	QNLSFYDR- 897																													
Db	591	QRSC	PNDCSN	WGCV	SGRC	CICNE	GYSGED	CSQVSP-P	KDLI---	VTE	TEETVNL	AWDNE 646																												
QY	898	---IK	FLVGRD	STH-----	I	IP	GENP	FDGG	HACVIR	GQVMT	SDGTPL	VGVN-----I 941																												
Db	647	MRV	TEYLIV	YTP	TH	EDG	LEM	QFRV	PGD-----	Q	TSTIRE	LEPGVEYFIRVF 693																												
QY	942	SFVN	NPLFGY	TISR	QDGS	FDL	VTNG	GISIL	LR	PERAP	FI	TOEHTL	WLWPDRFFV	METIIM 1001																										
Db	694	AILE	NKK-SIP	V	AR	VATY-L	P	T	PEG----	LK	FSIK-	ETS	VEV	WDPLDIAFET	WEIIF 746																									
QY	1002	RHE	NEIP	SCDLS	NFAR	PNPV	SP	PLTS	F	ASSCA	EKGPI	V	PEI	QALQ	EEISISGCKMRL 1061																									
Db	747	RNM	K	DEGE	ITK	SLRR	PE-----	T	YRQ	TGLAPG-----	Q	EY	EIS---	LHI 785																										
QY	1062	SYL	SSRTP	PGYK	SVLR	ISL	TH	PTIP	FN	LMKV	HLMV	A	VEGR	LF	FRKWF	AAAPDLSYFFI	WDKT 1121																							
Db	786	VKN	NTRG	PGLK	RV	TT	RLDAPS-----	Q	IEA	KD	VT	D	T	T	TALIT	WFKPL	AEID----- 831																							
QY	1122	DVYN	QKV	FGL	SEAF	SVSG	VEYES	CD	PLIL	WEK	RT	TV	LQ	GEI	D	ASKL	GW	SLDKH	HALNI 1181																					
Db	832	-----	GI	ELTY	G	IKD	VPG----	D	R	T	I	D	L	T	H	E	N	QYS	I	GNL	KP	DTE	VEV	SL 873																
QY	1182	QSG	ILH	K	NG	EN	QFVS	QQ	PP	VIG	S	IM	G	N	RR	RS	I	SC	P	SC	N	G	L	A	D	GN	K	L	L	A	P	V	A	L	T	C	G	S	D	G 1241
Db	874	IS-----	-----	RR-----	RR-----	-----	AD	M	S	S	N	P	A	K	E	T	F	T	T	G	L	D	A 895																	

QY	1242	SLYVGD	FNYIR	IFP	SGN	VNT	NI	EL	RN	KD	FR	HSH	S	PA	H	K	Y	Y	L	A	T	D	P	M	S	G	A	V	F	L	S	D	S	N	S	R	1301																								
Db	896	P-----	RNLRR	ISQ	T	D	N	S	I	T	L-----	EWR	N	G	K	A	A	A	D	T	Y	R	I	K	Y	A	P	I	S	G	-----	933																													
QY	1302	VFKIK	STVV	V	K	D	L	V	K	N	S	E	V	A	G	T	G	D	Q	C	L	P	F	D	D	T	R	C	G	D	G	K	A	T	E	A	T	L	N	P	R	G	I	T	V	D	K	F	G	L	I	1361									
Db	934	-----	DHAE	V	E	V	P	R	S	P	Q-----	TTT	K	A	T	L	T	G	L	R	P	G	T--	E	Y	G	I- 963																																		
QY	1362	YFVD	G	T	M	I	R	R	I	D	Q	N	G	I	I	S	T	L	G	S	N	D	L	T	S	A	R	P	L	S	C	D	S	V	M	D	I	S	Q	V	R	L	E	W	P	T	D	L	A-----	I	N	1415									
Db	964	---	G	V	S	A	V	K	G	D	K	E	S	D	P	A	T	I	N	A	A	T	D	L	D	P	P	K	D	F	R	V	S	E	L	K	E--	S	S	L	T	L	W	R	T	P	L	A	K	F	D	R	Y	R	L	N	1018				
QY	1416	-----	P	M	D	N	S	L	Y	V	L	D	N	N	V	L	Q	I	S	E	N	H	Q	V	R	I	V	A	G	R	P	M	H	C	V	P	G-----	1452																							
Db	1019	Y	G	L	P	S	G	Q	P	E	V	Q	L	P	R	N	A	T	S	I	L	R	G--	--	L	E	P	G	Q	E	Y	T	I	L	L	T	A	E	K	R	H	K	S	K	P	A	R	V	K	A	S	T	A	G	E	P	1075				
QY	1453	-----	I	D	H	F	L	L	S	K	V	A	I	H	A	T	L	E	S	A	T	A	L	A	V	S	H	N	G	V	L	Y	I	A	E	T	D	E	K	K	I	N	R	I--	R	Q	V	T	T	S	1500										
Db	1076	E	I	G	N	L	S	V	S	D	I	T	P	E	S	F	S	L	S	W	T	A	T	E	G	A	F	E	T	T	I	E	I	D	S	N	R	F	L--	E	T	M	E	Y	N	I	S	G	A	E	R	T	A	H	I	S	1132				
QY	1501	G-----	E	I	S	L	V	A	G	A	P	S	G	C	D	C	K	N	D	A	N	C	D	C	F	S	G	D	D	G	Y	A	K	A	D	A	K	N	T	P	S	S	L	A	V	C	A	D	G	E-----	1549										
Db	1133	G	L	R	P	G	N	D	F	I	V	L	S	G	L	A	P	G	I	Q	T	K-----	P	I	S	A	T	A	T	E	A	E	P	E	V	D	N 1170																								
QY	1550	L	Y	V	A	D	L	G	N	I	R	I	R	F	I	R	K	N	K	P	F	L	N	T	Q	N	M	Y	E	L	S	S	P	I	D	Q	E	L	Y-----	L	F	D	T	T	G	H	L	Y	T	Q	S	L	P	T	1603						
Db	1171	L	L	V	S	D	A-----	T	P	D	G	F	R	L	S	W	T	A	D	E	G	V	F	D	S	F	V	L	K	I	R	D	T	K-----	K	O	S	E	P	L 1209																					
QY	1604	G	D	Y	L	N	F	T	Y	T	G	D	I	T	L	I	T	D	N	G	N	M	V	N	R	D	S	T	G	M	P	L	W	L	V	V	P	D	G	O	V	Y	W	T	M	T	G	N	S	A	L	K	S	V	1663						
Db	1210	-----	E	I	T	L	L	A	S	E	R	T	R	D	I	T	G	L	R	E	A	T	E	Y	E	I-----	E	L	Y	G	I	S	S	G	K	R	S-----	1244																							
QY	1664	T	T	Q	H	E	L	A	M	T	Y	H	G	N	S	G	L	L	A	T	K	S	N	E	N	G	W	T	T	F	E	Y	D	S	F	G	R	L	T	N	V	T	F	P	T	G	O	V	S	S	F	R	S	D	T	D	S	1723			
Db	1245	-----	Q	P	V	S	A	I	A	T	T	A	M	G	S	P	K	E	I	T	F	S	D	I	T	E	N	S	A	T	V	S	W	M	V	P	T	A	Q	V	E	S	F	R-----	I 1287																
QY	1724	V	H	V	Q	E	T	S	S	K	D	D	V	T	I	T	N	L	S	A	S	A	F	Y	T	L	L	Q	D	V	R	N	S	Y	I	G	A	D	G	S	L	R	L	L	L	A	N	G	M	E	V	A	L	Q	T	E	1783				
Db	1288	T	Y	V	P	I	T	G	A	P	S	V	V	T	V	D	G	T	K	T	Q	T	R	L	L	R	L-----	P	G	V	E	Y	L	S	V	I	A	V	K	G	F	E---	E	S	E 1334																
QY	1784	P	H	L	L	A	G	T	V	N	P	T	V	G	K	R	N	V	T	L	P	I	D	N	G	L	N	L	V	E	W	R	Q	R	K	E	Q	A	R	G	Q	V	T	F	G	R	R	L	R	V	H	N	R	N	L	L	S	L	D	F	1843
Db	1335	P--	V	S	G	T-----	L	T	A	L	D	G	P	S	G	L	V	T-----	1352																																										
QY	1844	D	R	V	T	R	T	E	K	I	Y	D	D	H	R	K	F	T	L	R	I	L	Y	D	Q	A	G	R	P	S	L	W	S	P	S--	S	R	L	N	G	V	N	V	T	S	P	G	Y	I	A	G	I	Q	R	G	I	M	S	1902		
Db	1353	A	N	I	T	D	S	E	A	L-----	A	M	Q	P	A	I	A	P	D	V	H	Y	I	S	Y	T--	G	D	R	V	P	E	I	T	R	T	V	S	G 1392																						
QY	1903	E	R	M	E	Y-----	D	O	A	G	R	I	T	S	R	I	F	A	D--	G	K	T	W	S	Y	T	L	E	K	S	M	V	L	L	H	S	Q	R	Q	Y	I	F	E	F	D	K	N	D	R	L	S	S	V	1956							
Db	1393	N	T	V	E	A	L	T	N	L	E	P	A	T	E	Y	T	L	R	I	F	A	E	K	G	P	K	S	T	I	T	K-----	F	T	T	D	L--	D	S	P	R	D	L 1438																		
QY	1957	T	M	P	N	V	A	R	Q	T--	L	E	T	I	R-----	S	V	G	Y	R	N	I	Y	Q	P	P	E	G	N	A	S	V	I-----	Q	D	F	T	E	D	G	H	L	L	H	T	F	Y	L	G	2005											
Db	1439	T	A	T	E	Q	S	E	T	A	L	L	T	W	R	P	P	R	A	S	V	T	G	L	L	V	E	S	V	D	G	T	L	K	E	V	V	V	G	P	E	T	T	S	Y	S	L	S	G	L	S	P	S	T	H	Y	T	A	1498		
QY	2006	T	G	R	R	V	I	Y	K	G	K	L--	S	K	L	A	E	T	L	Y	D	T	T	K	V	S	F	TY-----	D	E	T	A	G	M	L	K	T	I	N	L	Q	N	E 2049																		
Db	1499	---	R	I	Q	A	L	N	G	P	L	R	S	K	N	S	Q	T	V	T	T	I	G	L	L	Y	P	F	P	R	D	C	S	O	A	M	L	N	G	D	T	T	S	G--	L	Y	T	I	Y	V	N	D	1550								

A;Accession: I38337  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-2201 <RES>  
A;Cross-references: UNIPROT:P24821; UNIPARC:UPI0000034A0E; EMBL:X78565; NID:G556844; PID:R;Gulcher, J.R.; Nies, D.E.; Marton, L.S.; Stefansson, K.  
Proc. Natl. Acad. Sci. U.S.A. 86, 1588-1592, 1989  
A;Title: An alternatively spliced region of the human hexabrachion contains a repeat of  
A;Reference number: A32160; MUID:89160821; PMID:2466295  
A;Accession: A32160  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 431-538, 'R', 540-1065, 'H', 1067-1599, 'LWLHPRASN', 1609-2054, 'L' <GUL>  
A;Cross-references: UNIPARC:UPI000016AAC6; GB:M24630; NID:G514363; PIDN:AAA52703.1; PID:R;Siri, A.; Carnemolla, B.; Saginati, M.; Leprini, A.; Casari, G.; Baralle, F.; Zardi, I  
Nucleic Acids Res. 19, 525-531, 1991  
A;Title: Human tenascin: primary structure, pre-mRNA splicing patterns and localization  
A;Reference number: S14015; MUID:91187670; PMID:1707164  
A;Accession: S14015  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-243,245-369, 'V', 371-679, 'R', 681-1676, 'I', 1678-2139, 'TR', 2142,2144-2201 <SI>  
A;Cross-references: UNIPARC:UPI0000155D15; EMBL:X56160; NID:G37226; PIDN:CAA39628.1; PID:R;Nies, D.E.; Hemesath, T.J.; Kim, J.H.; Gulcher, J.R.; Stefansson, K.  
J. Biol. Chem. 266, 2818-2823, 1991  
A;Title: The complete cDNA sequence of human hexabrachion (tenascin). A multidomain prob  
A;Reference number: S16166; MUID:91131572; PMID:1704365  
A;Accession: S16166  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-538, 'R', 540-1065, 'H', 1067-1599, 'LWLHPRASN', 1609-2054, 'LH', 2055-2201 <NIE>  
A;Cross-references: UNIPARC:UPI000016AAC5; EMBL:M55618; NID:G184483; PIDN:AAA88083.1; PID:R;Glumoff, V.; Savontaus, M.; Vehanen, J.; Vuorio, E.  
Biochim. Biophys. Acta 1219, 613-622, 1994  
A;Title: Analysis of aggrecan and tenascin gene expression in mouse skeletal tissues by  
A;Reference number: S50206; MUID:95035091; PMID:7524681  
A;Accession: S50208  
A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
A;Molecule type: mRNA  
A;Residues: 46-125 <GLU>  
A;Cross-references: UNIPARC:UPI0000177AF4; EMBL:X80280  
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1994  
C;Genetics:  
A;Gene: GDB:HXB  
A;Cross-references: GDB:120073; OMIM:187380  
A;Map position: 9q33-9q33  
C;Superfamily: tenascin; EGF homology; fibrinogen beta/gamma homology; fibronectin type  
C;Keywords: alternative splicing; extracellular matrix  
F;408-434/Domain: EGF homology <EGF>  
F;622-703/Domain: fibronectin type III repeat homology <FN3A>  
F;711-794/Domain: fibronectin type III repeat homology <FN3B>  
F;892-976/Domain: fibronectin type III repeat homology <FN3C>  
F;1437-1519/Domain: fibronectin type III repeat homology <FN3D>  
F;1619-1701/Domain: fibronectin type III repeat homology <FN3E>  
F;1709-1790/Domain: fibronectin type III repeat homology <FN3F>  
F;1798-1878/Domain: fibronectin type III repeat homology <FN3G>  
F;1886-1966/Domain: fibronectin type III repeat homology <FN3H>  
F;1981-2189/Domain: fibrinogen beta/gamma homology <FBG>

Query Match 4.4%; Score 649.5; DB 2; Length 2201;  
Best Local Similarity 22.3%; Pred. No. 1.7e-27;  
Matches 310; Conservative 166; Mismatches 492; Indels 423; Gaps 64;

Db 317 N-DCFDRGRRCINGTCYCEEGFTGEDCGKP--TCPHACHTQGRC--EEGQCVCDEGPAGLD 371  
Qy 724 CSIEICAADCGGHGVCVGGTCRCEDGWMGAACDQACHPRCAEHGTCRDGKCECSPGWNG 783  
Db 372 CSEKRCPADCHNRGRVCVDRCECDDGFTGADCGELKCPGCSHGRCVNGQCVCDEGYTG 431  
Qy 784 EHCT-----IAHYLDRVVKEG-----CPGLCNGNGRCTLDLNGWHCV 820  
Db 432 EDCSQLRCPNDCHSRGRCV-EGKVCCEQGFKGYDCSDMSPNDCHQHGRG---VNGM-CV 486  
Qy 821 CQLGWRGAGC-----DTSMETACGDSKNDGDGLV--DCMDPDC-----CL--Q 860  
Db 487 CDDGYTGEDCRDRQCPRDCSNRGLCVDGQVCEDGFTGPDCAELSCPNDCHGQGRCVNGQ 546  
Qy 861 PLCH---INPLCLGSPNPLDIIQETQVPVSQQNLHLSFYDRIKFLVGRDSTHIIPGENPFD 917  
Db 547 CVCHEGFMGKDCKEQRCPSDCHGQGRCVDGQCICHEGF-----TGLDC----- 589  
Qy 918 GGHAC-----VIRGQVMTSDGTPLVGVNISFVNNPLFGYTTISRQDGSFDLVNCGI 968  
Db 590 GQHSCPSDCNNLQCVCVSGRCICNEG--YSGEDCSEVSPK-----DLV----- 630  
Qy 969 SIILRFERAPFITQ--EHTLWLPWD-RFFVMEETIMRHEENEIPSCDLSNFARPNPVVSP 1025  
Db 631 -----VTEVTEETVNLAWDNEMRVTEYLV-----VYTP 658  
Qy 1026 SPLTSFASSCAEKGPVPEIQALQEEISISGCKMRLSYLSSRTPGYKSVLRLS---THP 1082  
Db 659 T-----HEGGLMQFRVPGDQTS-----TIQELPGVEYFIRVFAILNKK 700  
Qy 1083 TIPFNLMKVHLMVAVEGRLFRKWFAAAPDLSYYFIWDKTDV-----YNQKVFG- 1130  
Db 701 SIPVSARVATYLPAPGLKFK---SIKETSVEVEWDPDLIAFETWEIIFRNMNKEDEGE 756  
Qy 1131 -----LSEAFVSVGYEYESCPDLI-----LWEKRTTVLQG---YEI-----D 1164  
Db 757 ITKSLRRPETSyrQTGLAPGQEQEYELSHIVKNNTRGPGLKRVTTTRLDAPSQIEVKDVTD 816  
Qy 1165 ASKLGW--SLDKHHALNIQSGI-----LHKNGENQFVSQQPPVIGSIMNGRRR 1213  
Db 817 TTALITWFKPLAEIDGIELTYGIKDVPGDRTTIDLTEDENQY-----SIGNLKP-D-TEY 869  
Qy 1214 SISPCSCNGLADGNKLLAPVALTCGSDGSLYVGDFNYIRRIFFPSGNVTNILELRNKDPRH 1273  
Db 870 EVSLISRRGDMSSNP--AKETFTTGLDAP-----RNLRVVSQTDNSITL-----EWRN 915  
Qy 1274 SHSPAHHYYLATDPMGSAVFLSDSNSRRRVFKIKSTVVVKDLVKNSEVVAGTGDCQLPFDD 1333  
Db 916 GKAAIDSYRIKYAPISGG-----DHAEDVDPKSQLA----- 946  
Qy 1334 TRCGDGGKATEATLTNPRGITVDKFGLIYFVDGTMIRRIDQNGIISTLLGSNDLTSARPL 1393  
Db 947 -----TTKTTTLTGLRPGT--EYGI-----GVSAVKEDKESNPATINAATELDTPKDL 991  
Qy 1394 SCDSVMDISQVRLEWPTDLA-----IN-----PMDNSLYVLDNNVVQLQISE 1434  
Db 992 QVSETAETS-LTLLWKTPLAKFDRYRLNYSLPTGMVGVQLPRNTTSYVLRG---LEPGQ 1047  
Qy 1435 NHQVRIVAGRPMHC-----QVPGIDHFLLSKVAIHATLESATAL--AVSHNGVL 1481  
Db 1048 EYNVLLTAEKGRHKSPARVKASTEQAPELENLTIVTEGWDGLRLNWTAAADQAYEH---- 1103  
Qy 1482 VIAETDE-KKINRIRQVTTSGEISLVAGAPSGCDCKNNDANCDCFSGDDGYAKOAKLNTPS 1540  
Db 1104 FIIQVQEAANKVEAARNLTVPG--SLRAVDIPGLKAATPYTVSIYGIQY-----RTPV 1155  
Qy 1541 SLAVCADGELYVADLGNIRIRFIRKNKPFNTQNMVELSSPIDQELYLFDTTGKHLTYQS 1600  
Db 1156 LSABEASTGE--TPNLGEVVVAEVGWDALKLN-----WT 1186  
Qy 1601 LPTGDLYLNFTYTGDDITLITDNNNGNMVNVRDRDSTGMPLWLVPDQGVYVWTMTGNSAL 1660  
Db 1187 APEGAYEYFFIQVQEADTVEAAQN-----LTVPGGLRSTDLPLGLKAAT 1229





Qy	1341	KATEATLTNPRGITVDKFLIYFVDGTMIRRIDQNGIISTLLGSNDLTSARPLSCDSVMD	1400
Db	920	-TTRATLTGLRP-----GTEYGIGVTAVRQ-DRESAPATINAGTDLDNPKDLEVSDPTE	971
Qy	1401	ISQVRLEWPTDLA-----INPMDNSLYVLDDNNVVLQISENHQVRIV	1441
Db	972	-TTLSLRWRPRPAKFDRLRYLTVVSPGKKNEMEIPVDSTSFILRG---LDAGTEYTSILV	1027
Qy	1442	AGRPMHCQVP-----GIDHFLLSKVAIHATLESATALAVSHNGV	1480
Db	1028	AEKGRHKSPTTIKGSTEEPELGNLSVSETGWDGFQLTWTAAAGAYE-----NFV	1078
Qy	1481	LYIAETDEKKINRIRQVTTSGEISLVAGAPS---GCCKNDANCDCFSGDDGYAKDAKL	1536
Db	1079	IQVQQSDNPE-----ETWNITVPGGQHSVNVTTGLKANTPNVNTLYGVIRGYTKPLY	1130
Qy	1537	NTPSSLAVCADGELYVADL-----GNIRIRPIRKNK---PF-----L	1570
Db	1131	VETTTGAHPEVGELTVSDITPESFNLSWTTTNGDFDAFTIEIIDSNNLLEPMEFNISGNS	1190
Qy	1571	NTQNMVELSSPIDQELYLFDITGKHLV-----TQSLPTGDYLYNFTYTGDDITL	1620
Db	1191	RTAHISGLSPSTDFIVLYLGIS--HGFRTOAISAATTEAPEVDNLLVSDATPDGFRLT	1248
Qy	1621	ITDNG-----NMVNVRDRSTGMPLWLVP-----DGQVYVMTMGT	1656
Db	1249	WTADDDGVDFSFLVKIRDITKRKSD--PLELIVPGHERTHDITGLKEGTEYEIELYGVSSGR	1306
Qy	1657	NS-ALKSVTTQCHELAMTMTHGN-SGLLATKSNEN----GWTTFFEYDSFGRLTNTVTPPT	1710
Db	1307	RSQPINSVAT-----TVVGSPPKGISFSDITENSARVSWTP-----PR	1343
Qy	1711	GOVSSFRSDTDSSVHVQVETSSKDDVTITTNLSASGAFYTLLODQVRNSYYIGADGSLRL	1770
Db	1344	SRVDSYRVS-----YVPITGGTFPNVTVVDSGSKTR-----TKLVKLVP-----GVDYNVNI	1388
Qy	1771	LLANGMEVALQTEPHLLAGTVNPTVGKRN--VTLPIDNGLNLVEWR-----QRK	1817
Db	1389	ISVKGFE---ESEP--ISGILKTALDSPSGLVVMNITDSEALATWQPAIAAVDNYIVSYS	1443
Qy	1818	EQARGQVT--VFGRRLRVHNRNLLSLDFDRVTRTEKIYDDHRKFTLRILYDQA--GRPSL	1873
Db	1444	SEDEPEVTQMVSGNTVE-YDLNGLRPATEYTLRVHAVKDAQKSETLSTQFTTGLDAPKDL	1502
Qy	1874	WSPSSRLGNVNTYSPGGYIAGIQRGIMSERMEYDQAGRITSRIFADGKTWSYTYLEKSM	1933
Db	1503	SATEVQSETAVITWRPP-----RAPVTDYLLTYESIDGRVKEVILDPETTSYLTLE---	1553
Qy	1934	VLLHLSQRQYIFEFDKNDRLSSVTMPNVARQTLTIRSVGYRYNIYQPPEGNASVIQDFT	1993
Db	1554	---LSPSTQYTVKLOALSR-----SMRSKMIQTVFTTTGLLY-----PYPKDCSQALLNCEV	1602
Qy	1994	EDGHLLHTFYLGTR	2008
Db	1603	TSG--LYTIYLNQDR	1615
RESULT 12			
T09070			
probable tenascin X - mouse			
C;Species: Mus musculus (house mouse)			
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004			
C;Accession: T09070			
R;Rowen, L.; Mahairas, G.; Qin, S.; Ahearn, M.E.; Dankers, C.; Lasky, S.; Loretz, C.; Submitted to the EMBL Data Library, October 1997			
A;Description: Sequence of the mouse major histocompatibility locus class III region.			
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A;Accession: T09070			
A;Status: preliminary; translated from GB/EMBL/DBJ			
A;Molecule type: DNA			
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A;Gene: TNX			
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F;3789-3997/Domain: fibrinogen beta/gamma homology <FBG>			
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Qy	566	CPSNCYGNGDCISGTCFCFLGFLGPDCCGRASCPVLCSGNGQYMKGRCLCHSGWKGAECDV	625
Db	422	CPRDCRGRGCEDGVCVCHAGYSGEDCGVRSFGDCRGRGNCESGRCVCWPGYTGRDCG-	480
Qy	626	PTNQCIDVACSNHGTCTGTCTICINPGYKGESCEVD CMDPTCSGRGVCVRGECHECFVGMG	685
Db	481	-TRAC-PGDCRGRGRCVDGRVCVNPFTGTGEDCGSRRC-PGDCRGHGHCENGVCVCAVGYS	537
Qy	686	GTNCETPRATCLDQCSGHGTFLPDTGLCSCDPSWTHDCSIEICAADCGGHGVCVGGTCR	745
Db	538	GDDCST--RSCPSDCRGRGQL--NGLCECEGYSGEDCGIRRCPRDCSQHGVQODGLCM	593
Qy	746	CEDGWMGAACDQACHPRCAEHGTCRDGKCECSPGWNGEHCTIAHYLDRVVKEGCPGLCN	805
Db	594	CHAGYAGEDCSIRTCPADCRRRRCEDGRCVCNPGYTGPA-----AATRCPADCR	644
Qy	806	GNGRCTLDLNGWHVCVQLGWRGAGCDTSMETA-----CGDSKDNDDGLVDCMD---	855
Db	645	GRGRCVQGV---CMGVGYSGEDCGQEEPPASACPGGCG-PRELCRAGQCVCVEGFRGP	699
Qy	856	DCCLQPL---CHINPLCL-----P	872
Db	700	DCAIQTCPGDCRSRGECIQRCVCQEGYAGDDCGEEIPAIONMRMHLEETTVRTETRA	759
Qy	873	PNPLDIIQETQVPVSOQNLHSFYDRIKFLVGR-DSTHIIIPGENPFDGGHACVIRQVMTS	931
Db	760	PGPVDAEYEQIFPMTGVSPPFTARVPSSASAYDQRLAPGD-----YQVTVRALRGTS	814
Qy	932	DGTPLVGVNISFVNPLFGYTISRQDGSFDLVNNGGISIILRERAPFITQEHTLWLPW-	990
Db	815	WGPPASKTITTIMDGP-----QDLRVAVT-----PTTLDLSWL	848
Qy	991	-----DRFFVMTIIMRHEEN-EIPSCDLSNFARPNPVVSPSPLTSF-----	1031
Db	849	RPQAEVDRFVVSYSAGNQRVRLEVP-----PEADRTQLTDLMPGEYVVTVTA	897
Qy	1032	-----ASSCAEKGPVPEIQALQEEIISISGCKMRLSYLSRTPGYKSVLRISLTHP	1082
Db	898	ERGHAVSYPASIRANTGSLPSGLLEATDEPPPSG-----PSTTQGAQAAPILLEHH-	948
Qy	1083	TIPFNLMKVHLMVAVEGRLLFRKKWFAAAPDLSYVF-----IWDKTDV-----	1123
Db	949	--PLGELKV-LGRDKAGRLSVAW-TAQPDPSFAHFQLRMQVAEGPWAHEELPGDVQOALV	1004
Qy	1124	-----YNQKVFGLSE-AFVSVGYEYESCPDLLILWEKRTTVLQGYEIDASKLGWGLD	1174
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Qy	1175	KHALNIQSGILHKNGENQFVS-----QQPPVIGSIMGNRRRSISCPSCNGLADGN	1227
Db	1059	---GLTSDSLLLHWTVPGEFDFSFLIQYKDKDGPQAISVEGPPQRSTPIS-----GLEPGR	1110
Qy	1228	K-----LLAPVALTCGSD-----GSLYVGD-----FNVIRR	1253
Db	1111	KYKFILYGLIGKKRHGFLMAEAKILIQSDPDGSPRLGELWVTDPTPHSLHLSWTVLGG	1170
Qy	1254	IFPSGNVTNILELRNKDFR-----HSHSPAHHYY-----LA	1284
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QY	1285	TDPMSGAVFLSDSNS-RRVEKIKSTVVVKDLVKNSEVVA-GTGD-----QCL	1329
Db	1227	ADGTTAAETKEESSEPPRLGELTVGTPTDSLRLSWTVARGPFDSEVILYKDAQGPQSV	1286
QY	1330	PEDTRCGDGGKATEATLTNPRGITVDKFGLIYFVDGTMIRRIDQNGIISTLLGSNDLTS	1389
Db	1287	P1E-----GDENEVTVPGLESNRKYYKMNLVGL-----RGRQRVGPVSVV-----AKT	1328
QY	1390	ARPLSCDSVMDISQVRLEWPTDLAINPMDNSLYVLD---NNVLQ--ISENH-----QV	1438
Db	1329	APPDVVDQPLSPPEPSTEAP-EPPEKPLLRELIIVTDTPNSLSLSWTVSEGQDFQFVIQY	1387
QY	1439	RIVAGRPMHCQVPG-----IDH-FLLSKVAIHATLESATALAVSHNGVLYIAET	1486
Db	1388	KNGDGQPKVVRVPGHEDQVTISGLEPDHKYKMNLVGIH-----SGQRVGPVSVVGVTAA	1441
QY	1487	DEKKINRIRQVTTs-----GEISLVAGAPSGCDCKNDANCDFS-----GD-DG	1529
Db	1442	EEPPSPTEPSTEAPTEEPTEPLLGEALTVTGSSP-----DSLRLSWTVPQGD FDS	1490
QY	1530	YAKDAKLNTPSSLAVCADGELYVADLG---NIRIFIRKNKPFLLNTQNMVELS-----S	1580
Db	1491	FTVQYK-----SSDGRPQVMRVGGQREVIVRDLDPGHKY--KMNLYGLHEGHRVG	1539
QY	1581	PIDQELYLFDTTGKHLVYQSLPTGDYLYNFFVTGDDITLITDNNGMNVVRRDSTGMPL	1640
Db	1540	PVS-----TVGTTDKQ-PEEKPPLEPRLEELVTG-----VTPNS-----VSL	1576
QY	1641	WLVVPDGQ-----VVMVTMGNTSALKSVTTQGHELAM-----MTYHGNSG-----	1680
Db	1577	SWIVPEGQFDSFVVVQYQDRDQGPREVPLTAEQREVTVLDLDPARIYKMNIFYGLHRRRVG	1636
QY	1681	-----LLATKSNE-----NGWTTTFVEY--DSFGRLTNVTPFTGQVSSFR---SD	1719
Db	1637	PLSVSAMTAPAPATEASKLLPEPRLGELTVTDVTPDSVGLLW--TVPEGEFDSFTVQYKD	1694
QY	1720	TDSSVHVQVETSSKDDVTITNLSASGAFYTL---QDQVRNSYYIGADGSLRLLLANGM	1776
Db	1695	RDGQPHVSVVAADLREVTI-PGLEPSRKYKFLFGVQDGKRRSQV-----SV	1740
QY	1777	EVALQTEPHLLAGTVNPTVGKRNVTLPIDNGLNLVEWR-----QRKEAQARGQVT	1825
Db	1741	EAKTATHDDTSPG-APPRLGELWVTDPTTDSLRL-SWTVPEGHEDSFVVQFKDKSGPRVV	1798
QY	1826	VFGRRLRVHNRNLLSLDFDRVTRTEKIYDDHRKFETLRILYDQAGR	1870
Db	1799	PVKQER-----TATITALDAGRKYRF-LLYGLLGR	1828
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A40701			
tenascin-X precursor - human			
C;Species: Homo sapiens (man)			
C;Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 31-Dec-2004			
C;Accession: A40701; A33725; C42175			
R;Bristow, J.; Tee, M.K.; Gitelman, S.E.; Mellon, S.H.; Miller, W.L.			
J. Cell Biol. 122, 265-278, 1993			
A;Title: Tenascin-X: a novel extracellular matrix protein encoded by the human XB gene c			
A;Reference number: A40701; MUID:93300909; PMID:7686164			
A;Accession: A40701			
A;Status: preliminary			
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A;Cross-references: UNIPROT:P22105; UNIPROT:Q9UC11; UNIPARC:UPI0000174343; EMBL:X71937			
R;Morel, Y.; Bristow, J.; Gitelman, S.E.; Miller, W.L.			
Proc. Natl. Acad. Sci. U.S.A. 86, 6582-6586, 1989			
A;Title: Transcript encoded on the opposite strand of the human steroid 21-hydroxylase/c			
A;Reference number: A33725; MUID:89367293; PMID:2475872			
A;Accession: A33725			
A;Molecule type: mRNA			
A;Residues: 2748-3199,'V',3201-3298,'E',3299-3314,'G',3316-3566 <MOR>			
A;Cross-references: UNIPARC:UPI000016A98B; GB:M25813; NID:g183069; PIDN:AAA35884.1; PID:			

R;Matsumoto, K.; Arai, M.; Ishihara, N.; Ando, A.; Inoko, H.; Ikemura, T. Genomics 12, 485-491, 1992 A;Title: Cluster of fibronectin type III repeats found in the human major histocompatib enascin. A;Reference number: A42175; MUID:92217969; PMID:1373119 A;Accession: C42175 A;Molecule type: DNA A;Residues: 1849-1936 <MAT> A;Cross-references: UNIPARC:UPI000006F862 A;Experimental source: clone 3.9kF3-1 A;Note: sequence extracted from NCBI backbone (NCBIP:95694) C;Genetics: A;Gene: GDB:TNXA; D6S103E; TNX; XA; XB A;Cross-references: GDB:568487; OMIM:600261 A;Map position: 6p21.3-6p21.3 C;Superfamily: EGF homology; fibrinogen beta/gamma homology; fibronectin type III repeat C;Keywords: extracellular matrix; glycoprotein F;435-461/Domain: EGF homology <EGF> F;748-828/Domain: fibronectin type III repeat homology <3F1> F;829-856/Domain: fibronectin type III repeat homology #status atypical <3F2> F;873-953/Domain: fibronectin type III repeat homology <3F3> F;975-1055/Domain: fibronectin type III repeat homology <3F4> F;1078-1158/Domain: fibronectin type III repeat homology <3F5> F;1167-1247/Domain: fibronectin type III repeat homology <3F6> F;1248-1317/Domain: fibronectin type III repeat homology #status atypical <3F7> F;1323-1403/Domain: fibronectin type III repeat homology <3F8> F;1412-1492/Domain: fibronectin type III repeat homology <3F9> F;1510-1590/Domain: fibronectin type III repeat homology <3F10> F;1618-1676/Domain: fibronectin type III repeat homology #status atypical <3F11> F;1678-1749/Domain: fibronectin type III repeat homology #status atypical <3F12> F;1751-1831/Domain: fibronectin type III repeat homology <3F13> F;1849-1929/Domain: fibronectin type III repeat homology <3F14> F;1955-2035/Domain: fibronectin type III repeat homology <3F15> F;2061-2141/Domain: fibronectin type III repeat homology <3F16> F;2167-2246/Domain: fibronectin type III repeat homology <3F17> F;2274-2354/Domain: fibronectin type III repeat homology <3F18> F;2382-2462/Domain: fibronectin type III repeat homology <3F19> F;2488-2568/Domain: fibronectin type III repeat homology <3F20> F;2584-2664/Domain: fibronectin type III repeat homology <3F21> F;2677-2757/Domain: fibronectin type III repeat homology <3F22> F;2771-2851/Domain: fibronectin type III repeat homology <3F23> F;2878-2958/Domain: fibronectin type III repeat homology <3F24> F;2977-3067/Domain: fibronectin type III repeat homology #status atypical <3F25> F;3078-3159/Domain: fibronectin type III repeat homology <3F26> F;3167-3247/Domain: fibronectin type III repeat homology <3F27> F;3255-3334/Domain: fibronectin type III repeat homology <3F28> F;3349-3557/Domain: fibrinogen beta/gamma homology <FBG>  Query Match 4.0%; Score 592; DB 1; Length 3566; Best Local Similarity 21.4%; Pred. No. 5.9e-24; Matches 364; Conservative 182; Mismatches 549; Indels 606; Gaps 86;  QY 562 SVDNCPSNCYNGDCISGTCHCFLGPLPDCGRASCPVLCSNGQYMKGRCLCHSGWKGA 621 			
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Qy	878	IIQETQVPVSQQNLHSFYDRIKFLVGRD-STHIIIGE-----NPFDDGGHACVIRGQVMTS	931
Db	697	LCRAGQCVC-----VEGFRGPDCAIQTCPGDCRGRGECHDG--SCVCKDGYAGE	743
Qy	932	DGTPLVGVNISFVNNPLFGYTISRQDGSFDLVTNGGISIILRFERAPFITQEHILWLWP-	990
Db	744	DCGEVI-----DGPQDL-----RVVSVTPT-TLELGWL	770
Qy	991	-----DRFFVM-----ET-----IIMRHEENEIPSCDLS	1014
Db	771	RPQAEVDRFVSVYVSADNQVRLEVPVETDGTLLTDLMPGVEYVVTVAERGRAVSYPAS	830
Qy	1015	NFARPNPVVS-PSPLTSFASSCAEKGPIVPEIQALQEBISISGCKMRLS--YLSRTPGY	1071
Db	831	VRANTDPGRKYKFVLYGFVK-KRHGPLVAEAKILPQSDPSPGTPPRLGNLWVTDTPP--	887
Qy	1072	KSVLRISLTHPTIPFNLMKVHL-----MVAVEGRFLRFKWFAAAPDLSYFYFDKTDV	1123
Db	888	-DSLHLSWTVPEGQDFTFMVQYRDRDRGRPVVPVEGP-ERSFVVSLLDPDHKYRFTLFGI	945
Qy	1124	YNQKVFLSEAFVSVGYEYES-----CPD--LILWEKRTTVLQG	1160
Db	946	ANKKRYGPLTADGTTAPERKEBPPRPEFLEQPLLGLTGTGTVPDLSRLSW----TVAQG	1001
Qy	1161	-----YEIDAS-----KLGWSLDKHHAJNIQSGILHKNGBNQFVS	1197
Db	1002	PFDSPMWQYK-DAQQPQAVPVAGDENEVTVPLGDPDRKYKNLYGLRGRQVGPESWA	1060
Qy	1198	QPPVIGSIMGNRRRSISCPSCNGLADGNKLLAPVALTCGSDGSLYVGDFNYIRRIF--	1255
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Qy	1256	-PSGNVTNI-LELRNKDFR-----HSHSPAHKYYL-----	1283
Db	1101	VPOGSFDSFTVQYKDRDRPRAVRVGGKESEVTVGGLEPGHKYKWHLYGLHEGRVGPVS	1160
Qy	1284	-----ATDPMGAVFLSDSNSRRV-----FKIKSTVV-VKDLVKNSEVVAGTDQCL	1329
Db	1161	AVGLTALPRLGELTVTDITPDSVGLSWTVPEGEFDSFVVQYKORDGQPQVVPVAADQ--	1218
Qy	1330	PFDDTRCGDGGKATEATLTNPRGITVDKFLIYFVDG-----	1366
Db	1219	-----REVITPDLPESTKYKFLLFQIQDGKRSPSVSVEAKTAILSWTVPEAS	1265
Qy	1367	---TWIRRIDQNG-----IISTLLGSNDLTSARPLSCD-	1396
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Qy	1397	-----SVMDISQ--VRLEWPTDLAINPMDNSLYVLDDNNVVLQISENHQVRI--VAGR	1444
Db	1323	TSGEHSLQVTTVTQNSVGLSWTVPEG-----QFDSFVVQYKDRDGQPQVVPVEGS	1373
Qy	1445	PMHCQVPGID--HFLLSKVAIH--ATLESATALAVS-----HNGVLVYIAETDEKKINRIR	1495
Db	1374	LREVSVPGLDPAHRYKLLLYGLHGHKRVGPISAVAITAPEPHLGELTVVEEATSHTLH-LS	1432
Qy	1496	QVTTSGRISLVAGAPSGCDCKNANDCDFSGDDGYAKDAKLNTPSSLAVCADGELYVADL	1555
Db	1433	WMVTEGEFD-----SFEIQYTD-----RDGQLQMVRI	1459
Qy	1556	G---NIRIRFIRKNKPFNTQNMVELSSPIDQELYLFDTTGKH---LYTQSL---PTGD	1605
Db	1460	GGDRNDITLSGLESDHRYLVT-----LYGF-SDGHVGPVHVVEALTTEPPTA-	1504
Qy	1606	YLYNFTYTG-----GDITLITDNNGNMVNVRDSTGMPLVLVVPDQV-YVWTMGTN	1657
Db	1505	-----TPEPPIKPRLGELT-VTDATPDSLSSL-----W-TVPEGQFDHFLVQVRN	1547
Qy	1658	--SALKSVYTTQGHE-----LAMMTYHGNS-----GLLATKSNENGWT	1692

Db	1548	GDQPKAVRGPGHEEGVTISGLEPDHKYKNLYGFHGGQRMGPVSVVGVTAABEETPSPT	1607
Qy	1693	-----TFVEYDSFGRLT-----NVTFTQGVSSFR---SDTDSSVHV---Q	1727
Db	1608	EPSMEAPEPAEEPLLGLTGTGSSPDSLSTSWTVPQGRFDSFTVQYKDRDRGRPPQVVRVG	1667
Qy	1728	VETSSKD-----DVTITTNLAS-----GAF-YTLLQDQVRNSYYIGADGS	1767
Db	1668	PEEESPDAPLAKRLQGTMVRDIT-SDLSLSWTVPEGQDFHFLVQ-----FKNGDGO	1719
Qy	1768	LRLLLANGMEVALQTEPHLLAGTVNPTVGKRNVTLPIDNGLNLVWVRQRKEQARGQVTVF	1827
Db	1720	PKALRVPGHEDGAEFE-----TPSPTEPSMEAPEP-----PEEPLLGLTGT	1761
Qy	1828	GRRLRVHNRNLLSLDFDRVTRTEKIYDDHRKFTLRILYDQAGRPSLWSPSSRLNGVNVTY	1887
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C;Species: Notophthalmus viridescens, Triturus viridescens (eastern newt)			
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004			
C;Accession: A43902			
R;Onda, H.; Poulin, M.L.; Tassava, R.A.; Chiu, I.M.			
Dev. Biol. 148, 219-232, 1991			
A;Title: Characterization of a newt tenascin cDNA and localization of tenascin mRNA dur			
A;Reference number: A43902; MUID:92038434; PMID:1718799			
A;Accession: A43902			
A;Molecule type: mRNA			
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F;435-517/Domain: fibronectin type III repeat homology <FN2>			
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Qy	625	--VPTNQCIDVACSNHGTICITGTCICNPGYKGESCEVEDCMDPTCSGRGVCVRGECHCFV	682
Db	130	LRCPND-----CNDRGRCVNGKCVCKEGFMGEDCADLRCPN-DCNNRGRCVNGQCVCDE	182
Qy	683	GWGGTNCETPRATCLDQCSGHGTFLPDTGLCSCDPSWTGHDCSIIEICAADCGGHGVCVGG	742
Db	183	GFMGEDCSDLR--CPGDCNNRGRCV--NGQCVCDEGPRGEDCGELRCPDDCNRNRGVCVNG	238
Qy	743	TCRCEDGWMGAACDQACHPRCAEHGTCRDGKCECSPGWNGEHCTIAHYLDRVVKEGCPG	802
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Qy	803	LCNNGNRCRTLDLNGWHCVCLGWRGAGCDTSMETACGDSKNDGDGLVDCMDPCCLOPL	862
Db	290	DCNDRGRC---ING-QCVCAEGFTGENCDS--LAC-----LNNCNDRGLCVNGQ	332
Qy	863	CHINPLCLG-----SNPLDI-----IQE---TQVPVSQQNLHSF	894
Db	333	CVCEEGLGEDCSEVSP-PKDLTVTDVTTQSVNLEWANEMKYTEYLITYIPTSPGGL---	388
Qy	895	YDRIKFLVGRDST-----HIIPGENPFDGGHACVIRGQVMTSDGTPLVGVNISFVNNPLF	949

Db	389	--ELDFRVPGDQTATTATQEELEPGVEYFVRVFA-ILRNQ-----RSIPV-----	428
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Db	429	-----SARVATHLPTTDDLRFRSVK-ETSVEVEWDPLDISFTWDLIIRNTKEE--	476
Qy	1010	SCDLSNFARPNPVVSPS---PLTSFASSCAEKGPVPEIQALQEEISISGCKMRLSYLSS	1066
Db	477	-----NGEISTSLQRPVTSYVQTGLAPG-----ETYNFS---IHVVKNST	513
Qy	1067	RTPGYKSVLRISLTHPTIPFNLMKVHLMVAVEGRLFRKWF	1106
Db	514	RGPGLAKVTTTTRLDAPS-----QVEVRDVTDSMALVTWF	547
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T42629			
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C;Species: Bos primigenius taurus (cattle)			
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004			
C;Accession: T42629			
R;Elefteriou, F.; Exposito, J.Y.; Garrone, R.; Lethias, C.			
J. Biol. Chem. 272, 22866-22874, 1997			
A;Title: Characterization of the bovine tenascin-X.			
A;Reference number: Z22180; MUID:97426436; PMID:9278449			
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A;Gene: TN-X			
C;Superfamily: tenascin-X; EGF homology; fibrinogen beta/gamma homology; fibronectin typ			
C;Keywords: extracellular matrix; glycoprotein; heptad repeat			
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Best Local Similarity 33.6%; Pred. No. 9.3e-23;			
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Qy	623	CDV-----PTNQCI-----DVA-----CSNHGTCITGTICINPGYKG	654
Db	460	CGVRSCPGDCRRRGRCESGRCVWPVGYTGRDCGTRACPGDCRGRRCVDRGCVCNPGFAG	519
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Db	520	EDCGSRRC-PGDCRGRGRCGDGVCSVDVGYEGEDC--GKRSCPRGCQGRGQCL--EGRCV	574
Qy	715	CDPSWTGHDCSIICAADCGGHGVCVGGTCRCEDGWMGAACDORACHPRCAEHGTCRDGK	774
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Qy	775	CECSPGWNGEHCTIAHYLDRVVKEGCPGLCNGNGRCTLDLNGWHVCVQLGWRGAGCDTSM	834
Db	635	CVCDSGYTGPSC-----AATRTCPADCRGRGRCVQGV----CVCHVGYSGEDCCQEE	681
Qy	835	ETA-----CGDSKDNDDGLVDCMD-----PDCCLQ	860
Db	682	PPASACPGGCG-PRELCSAGQCVCVEGFRGPDCAIQ	716

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: December 9, 2005, 20:16:07 ; Search time 572 Seconds  
(without alignments)  
5460.108 Million cell updates/sec

Title: US-10-029-020-13  
Perfect score: 8354  
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Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 3392430 seqs, 186927314 residues

Total number of hits satisfying chosen parameters: 6784860

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications NA New:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	8354	100.0	8354	7	US-11-113-424-13
2	3542.2	42.4	8362	9	US-11-096-051-1
3	3502.2	41.9	8645	9	US-11-096-051-9
4	3473.8	41.6	8657	9	US-11-096-051-7
5	3396.4	40.7	7786	9	US-11-096-051-3
6	1560.4	18.7	3626	6	US-10-821-234-245
7	1151.6	13.8	2589	9	US-11-096-051-19
8	1151.2	13.8	2482	9	US-11-096-051-5
9	842.2	10.1	1833	9	US-11-096-051-13
10	390	4.7	783	9	US-11-096-051-11
11	390	4.7	891	9	US-11-096-051-17
12	168.2	2.0	768	9	US-11-096-051-15
13	144	1.7	2064	6	US-10-750-185-39327
14	101.6	1.2	972	6	US-10-750-185-39351
15	92.6	1.1	1835	6	US-10-750-185-28736
16	67.4	0.8	1068	6	US-10-750-185-33643
17	64.8	0.8	699	6	US-10-750-185-39288
18	64.4	0.8	110	6	US-10-909-125-169
19	45.4	0.5	1500	7	US-11-087-100-7
20	45.4	0.5	8730	7	US-11-087-100-1
21	43.8	0.5	1359	6	US-10-858-730-53
22	42.8	0.5	822	7	US-11-015-546A-36
23	42.8	0.5	1557	6	US-10-996-217A-6

C	24	42	0.5	191684	7	US-11-121-086-2	Sequence 2, Appli
	25	41.8	0.5	164810	7	US-11-121-086-4	Sequence 4, Appli
	26	41.4	0.5	5221	6	US-10-821-234-367	Sequence 367, App
C	27	41	0.5	1957	6	US-10-750-185-34207	Sequence 34207, A
	28	40.6	0.5	808	7	US-11-110-082-1	Sequence 1, Appli
C	29	40.2	0.5	150481	7	US-11-112-908-37	Sequence 37, Appl
C	30	40.2	0.5	171162	7	US-11-112-908-38	Sequence 38, Appl
C	31	40.2	0.5	179892	7	US-11-112-908-39	Sequence 39, Appl
	32	40	0.5	15720	7	US-11-108-172-1058	Sequence 1058, Ap
	33	39.8	0.5	3289	6	US-10-971-560-8	Sequence 8, Appli
	34	39.8	0.5	4158	6	US-10-971-560-3	Sequence 3, Appli
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	37	39.6	0.5	1506	6	US-10-971-560-9	Sequence 9, Appli
C	38	39.6	0.5	1647	7	US-11-137-465-14	Sequence 14, Appl
	39	39.6	0.5	153376	7	US-11-121-086-5	Sequence 5, Appli
	40	39	0.5	2319	6	US-10-858-730-148	Sequence 148, App
	41	38.8	0.5	1306	6	US-10-821-234-388	Sequence 388, App
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	43	38.4	0.5	1938	6	US-10-967-527A-29	Sequence 29, Appl
	44	38.4	0.5	1979	6	US-10-967-527A-31	Sequence 31, Appl
C	45	38.4	0.5	2673	6	US-10-750-185-43708	Sequence 43708, A

ALIGNMENTS

RESULT 1

US-11-113-424-13

; Sequence 13, Application US/11113424

; Publication No. US20050260713A1

; GENERAL INFORMATION:

; APPLICANT: Gangolli et al.

; TITLE OF INVENTION: Polypeptides and Nucleic Acids Encoding Same

; FILE REFERENCE: 21402-225

; CURRENT APPLICATION NUMBER: US/11/113,424

; CURRENT FILING DATE: 2005-04-21

; PRIOR APPLICATION NUMBER: 60/256,704

; PRIOR FILING DATE: 2000-12-19

; PRIOR APPLICATION NUMBER: 60/311,590

; PRIOR FILING DATE: 2001-08-10

; PRIOR APPLICATION NUMBER: 60/257,314

; PRIOR FILING DATE: 2000-12-20

; PRIOR APPLICATION NUMBER: 60/311,613

; PRIOR FILING DATE: 2001-08-10

; PRIOR APPLICATION NUMBER: 60/315,617

; PRIOR FILING DATE: 2001-08-29

; PRIOR APPLICATION NUMBER: 60/307,506

; PRIOR FILING DATE: 2001-07-24

; PRIOR APPLICATION NUMBER: 60/322,358

; PRIOR FILING DATE: 2001-09-14

; PRIOR APPLICATION NUMBER: 60/294,075

; PRIOR FILING DATE: 2001-05-29

; PRIOR APPLICATION NUMBER: 60/288,153

; PRIOR FILING DATE: 2001-05-02

; NUMBER OF SEQ ID NOS: 190

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 13

; LENGTH: 8354

; TYPE: DNA

; ORGANISM: Homo sapiens

US-11-113-424-13

Query Match 100.0%; Score 8354; DB 7; Length 8354;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 8354; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 181 CCAGGACGCCCGCTAGCCCTATGGCAGCCGCGTCAAGGACATTGTGCCGCGAGGCGCGA 240

Db 181 CCAGGACGCCCGCTAGCCCTATGGCAGCCGCGTCAAGGACATTGTGCCGCGAGGCGCGA 240

Qy 241 GGAATTTCTCCGCGACAGGTGCCAATTCAACCTCGCGGAGCTGGGCTGGAAGTAAC 300

Db 241 GGAATTTCTCCGCGACAGGTGCCAATTCAACCTCGCGGAGCTGGGCTGGAAGTAAC 300

Qy 301 GCCCCCTCACGGACCCCTGTACCGGACAGACATTGGCCCTGCCCAATCGGCTACTCCAT 360

Db 301 GCCCCCTCACGGACCCCTGTACCGGACAGACATTGGCCCTGCCCAATCGGCTACTCCAT 360

Qy 361 GGGGGCTGGCTCTGATGCCGACATGGAGCTGACCGGTGCTGTCCCTTGAGCACCCCGT 420

Db 361 GGGGGCTGGCTCTGATGCCGACATGGAGCTGACCGGTGCTGTCCCTTGAGCACCCCGT 420

Qy 421 GCGTCTGTGGSSCGGAGCACACGGTCAAGGCGCAGCTCCTGCTGTCCAGCCGGGCCAA 480

Db 421 GCGTCTGTGGSSCGGAGCACACGGTCAAGGCGCAGCTCCTGCTGTCCAGCCGGGCCAA 480

Qy 481 TTCCAATCTCACTCACCGACACCGAGCATGAAAACACTGAGACTGATCATCCGGCGG 540

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Db 1741 CTGCTATGGCAATGGTGACTGCATCTCTGGGACCTGCCACTGCTTCTCTGGGTTTCTCTGGG 1800

Qy 1801 CCCCAGCTGCGCAGAGCCCTCCTGCCCGCTGCTCTGTAGCGGAAATGGCCAATACATGAA 1860

Db 1801 CCCCAGCTGCGCAGAGCCCTCCTGCCCGCTGCTCTGTAGCGGAAATGGCCAATACATGAA 1860

Qy 1861 AGGCAGATGCTTGTGCCACAGTGGCTGGAAGGCGCTAGTGCATGTGCCCAACCA 1920

Db 1861 AGGCAGATGCTTGTGCCACAGTGGCTGGAAGGCGCTAGTGCATGTGCCCAACCA 1920

Qy 1921 GTGTATCGATGTGGCCTGCAGCAACCATGGCACCTGCATCACGGGCACCTGCATCTGCAA 1980

Db 1921 GTGTATCGATGTGGCCTGCAGCAACCATGGCACCTGCATCACGGGCACCTGCATCTGCAA 1980

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Qy	2821	GACATCAGATGGAACCCCTCGTGGTGGTGAACATCAGATTTGTCAATAACCTCTCTT	2880
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Qy	3061	CAGCTGTGACCTGAGCAATTTTGCCCGCCCCCAACCCAGTGGTCTCTCCATCCCCCACTGAC	3120
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Qy	3121	GTCCTTCGCCAGCTCCTGTGCAGAGAAAGGCCCCATTTGTGCCGGAATTCAGGCTTTGCA	3180
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Qy	3181	GGAGGAAATCTCTATCTCTGGCTGCAAGATGAGGCTGAGCTACCTGAGCAGCCGAGCCCC	3240
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Qy	3241	TGGCTACAAAATCTGTCTGTAGGATCAGCCTCACCCACCCGACCATCCCCCTTCAACCTCAT	3300
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Qy	3301	GAAGTGCACCTCATGGTAGCGGTGAGGGCCGCCCTCTTCAGGAAGTGGTTTCGCTGCAGC	3360
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Qy	3361	CCACAGCCTGTCCCTATTATTTTCATTTGGGACAAGACAGACGCTCTACAACCAAGGTGTT	3420
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Qy	3721	CCTGGCCCCAGTGGCCCTCACCTGTGGCTCTGACGGGAGCCTCTATGTGSGTGATTTCAA	3780
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Qy	3781	CTACATTAGAAAGGATCTTCCCCTCTGGAATGTCAACCAACATCCTAGAGCTGAGGAATAA	3840
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QY	4621	TTATGCCAAGGATGCAAAAGTTAAATACCCCATCTTCCTTGGCTGTGTGCTGATGGGGA	4680
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Db	5161	TACTGGCCAGGTGAGCAGTTTCCGAAGTGATACAGACAGTTTCAGTGCATGTCCAGGTAGA	5220
QY	5221	GACCTCCAGCAAGGATGATGTACCCATAACCAACCAACCTGTCTGCCTCAGGCGCCTTCTA	5280
Db	5221	GACCTCCAGCAAGGATGATGTACCCATAACCAACCAACCTGTCTGCCTCAGGCGCCTTCTA	5280
QY	5281	CACACTGCTGCAAGACCAAGTCCGGAACAGTACTACATCGGGGCCGATGGCTCCTTGCG	5340
Db	5281	CACACTGCTGCAAGACCAAGTCCGGAACAGTACTACATCGGGGCCGATGGCTCCTTGCG	5340
QY	5341	GCTGCTGTGGCCAAACGGCATGGAGTGGCGCTGCAGACTGAGCCCCACTTGCTGGCTGG	5400
Db	5341	GCTGCTGTGGCCAAACGGCATGGAGTGGCGCTGCAGACTGAGCCCCACTTGCTGGCTGG	5400
QY	5401	CACCGTCAACCCACCGTGGGCAAGAGGAATGTACCGTGTCCCATCGACAACGGCCTCAA	5460
Db	5401	CACCGTCAACCCACCGTGGGCAAGAGGAATGTACCGTGTCCCATCGACAACGGCCTCAA	5460
QY	5461	CCTGGTGGAGTGGCGCCAGCGCAAGAGCAGGCTCGGGGCCAGGTCACTGTCTTTGGGCG	5520
Db	5461	CCTGGTGGAGTGGCGCCAGCGCAAGAGCAGGCTCGGGGCCAGGTCACTGTCTTTGGGCG	5520
QY	5521	CCGGCTGCGGTGCACAAACCGAAATCTCCTATCTCTGGACTTTGATCGCGTAACACGCAC	5580
Db	5521	CCGGCTGCGGTGCACAAACCGAAATCTCCTATCTCTGGACTTTGATCGCGTAACACGCAC	5580

QY	5581	AGAGAAGATCTATGATGACCAACCGCAAAGTTCCACCCTTCGGATTCTGTACGACCAGGCGGG	5640
Db	5581		5640
QY	5641	GCGGCCCAGCCTCTGGTCACCCAGCAGCAGGCTGAATGGTGTCAACTGACATACTCCCC	5700
Db	5641		5700
QY	5701	TGGGGTTACATTGCTGGCATCCAGAGGGGCATCATGTCTGAAGAATGGAATACGACCA	5760
Db	5701		5760
QY	5761	GGCGGGCCGCATCACATCCAGGATCTTCGCTGATGGGAAGACATGGAGCTACACATACTT	5820
Db	5761		5820
QY	5821	AGAGAAGTCCAATGGTGTCTACTACACAGCCAGAGGCAGTATCTTTGAGTTCGACAA	5880
Db	5821		5880
QY	5881	GAATGACCGCCTCTTCTGTGACGATGCCAACGTTGGCGGCAGACACCTAGAGACCAT	5940
Db	5881		5940
QY	5941	CCGCTCAGTGGCTACTACAGAAAACATCTATCAGCCCCCTGAGGCAANTGCCTCAGTCAT	6000
Db	5941		6000
QY	6001	ACAGGACTTCACTGAGGATGGGCACCTCTTCAACCTTCTACCTGGGCACCTGGCCCGCAG	6060
Db	6001		6060
QY	6061	GGTGATATCAAGTATGGCAAACCTGTCAAAGCTGGCAGAGACGCTCTATGACACCACCAA	6120
Db	6061		6120
QY	6121	GGTCAGTTTCACTATGACGAGACGGCAGGCATGCTGAAGACCATCAACCTACAGAATGA	6180
Db	6121		6180
QY	6181	GGGCTTCACTGCAACCATCCGCTAACGTCAGATTGGGCCCTGATTGACCGACAGATCTT	6240
Db	6181		6240
QY	6241	CCGCTTCACTGAGGAAGGCATGGTCAACGCCCTTTTGACTACAACCTATGACAAACAGCTT	6300
Db	6241		6300
QY	6301	CCGGTGACAGCATGCAGGCTGTGATCAACGAGACCCCACTGCCCATTTGATCTCTATCG	6360
Db	6301		6360
QY	6361	CTATGATGATGTGTGAGCAAGACAGAGCAGTTTGGGAAGTTTGGTGCTATTACTATGA	6420
Db	6361		6420
QY	6421	CATTAAACGAGATCATCACCACAGCTGTATGATCTTCCGCTCGCTGATGTCATATGG	6480
Db	6421		6480
QY	6481	CAGGATGAAGGAAGTGCAATGATGATCTTCCGCTCGCTCATGTACTGGATGACCGTCCA	6540
Db	6481		6540
QY	6541	GTATGATAACATGGGGCGAGTAGTGAAGAAGGAGCTGAAGGTAGGACCCCTACGCCAATAC	6600
Db	6541		6600
QY	6601	CACTCGTACTCTCTATGAGTATGATGCTGACGGCCAGTGCAGACAGTCTCCATCAATGA	6660
Db	6601		6660



QY 6661 CAAGCCACTCTGGCGCTACAGCTACGACCTCAATGGGAACCTGCACTTACTAGAGCCCTGG 6720  
Db |||||  
6661 CAAGCCACTCTGGCGCTACAGCTACGACCTCAATGGGAACCTGCACTTACTAGAGCCCTGG 6720  
QY 6721 GAACAGTGACGGCTCACACCACCTACGGTATGACATCCGCGACCGCATCACTCGGCTGG 6780  
Db |||||  
6721 GAACAGTGACGGCTCACACCACCTACGGTATGACATCCGCGACCGCATCACTCGGCTGG 6780  
QY 6781 TGACGTGCAATACAAGATGGATGAGGATGGCTTCTGAGGCAGCGGGCGGTGATATCTT 6840  
Db |||||  
6781 TGACGTGCAATACAAGATGGATGAGGATGGCTTCTGAGGCAGCGGGCGGTGATATCTT 6840  
QY 6841 TGAGTAAACTCAGCTGGCCCTGCTCATCAAGGCCTACAACCGGGCTGGCAGCTGGAGTGT 6900  
Db |||||  
6841 TGAGTAAACTCAGCTGGCCCTGCTCATCAAGGCCTACAACCGGGCTGGCAGCTGGAGTGT 6900  
QY 6901 CAGGTACCGCTACGATGGCCCTGGGGCGGCGGTGTCAGCAAGAGCAGCCACAGCCACCA 6960  
Db |||||  
6901 CAGGTACCGCTACGATGGCCCTGGGGCGGCGGTGTCAGCAAGAGCAGCCACAGCCACCA 6960  
QY 6961 CCTGCAGTTCTTCTATGCGAGACCTGACCAACCCCAACCAAGGTCAACCCACCTGTACAACCA 7020  
Db |||||  
6961 CCTGCAGTTCTTCTATGCGAGACCTGACCAACCCCAACCAAGGTCAACCCACCTGTACAACCA 7020  
QY 7021 CTCCAGCTCTGAGATCACTCCCTCTACTACGACTTCAAGGACACCTCTTTGCCATGGA 7080  
Db |||||  
7021 CTCCAGCTCTGAGATCACTCCCTCTACTACGACTTCAAGGACACCTCTTTGCCATGGA 7080  
QY 7081 GCTGAGCAGTGGTGAGTTTTACATAGCTTTGTGACAAACATCGGGACCCCTCTTGCTGT 7140  
Db |||||  
7081 GCTGAGCAGTGGTGAGTTTTACATAGCTTTGTGACAAACATCGGGACCCCTCTTGCTGT 7140  
QY 7141 CTTTAGTGGAACAGGTTTGATGATCAAGCAAATCTGTACACAGCCTATGGGAGATCTA 7200  
Db |||||  
7141 CTTTAGTGGAACAGGTTTGATGATCAAGCAAATCTGTACACAGCCTATGGGAGATCTA 7200  
QY 7201 CATGGATACCAACCCCAACTTTAGATCATATAGGTACCATGGTGGCCTCTATGATCC 7260  
Db |||||  
7201 CATGGATACCAACCCCAACTTTAGATCATATAGGTACCATGGTGGCCTCTATGATCC 7260  
QY 7261 ACTCACCAGCTTGTCACATGGGCGGCGAGATTATGATGTGCTGGCCGACGCTGGAC 7320  
Db |||||  
7261 ACTCACCAGCTTGTCACATGGGCGGCGAGATTATGATGTGCTGGCCGACGCTGGAC 7320  
QY 7321 TAGCCCAGACCAAGCTGTGGAAGCACCTTAGTAGCAGCAACGTCATGCCTTTTAATCT 7380  
Db |||||  
7321 TAGCCCAGACCAAGCTGTGGAAGCACCTTAGTAGCAGCAACGTCATGCCTTTTAATCT 7380  
QY 7381 CTATATGTTCAAAAAACAACACCCCATCAGCAACTCCAGGACATCAAGTGCTTCATGAC 7440  
Db |||||  
7381 CTATATGTTCAAAAAACAACACCCCATCAGCAACTCCAGGACATCAAGTGCTTCATGAC 7440  
QY 7441 AGATGTTAACAGCTGGCTGCTCACCTTTGGATTCCAGCTACACAACGTCATCCCTGGTTA 7500  
Db |||||  
7441 AGATGTTAACAGCTGGCTGCTCACCTTTGGATTCCAGCTACACAACGTCATCCCTGGTTA 7500  
QY 7501 TCCCAAAACAGACATGGATGCCATGGAACCCCTCCTACGAGCTCATCCACACAGATGAA 7560  
Db |||||  
7501 TCCCAAAACAGACATGGATGCCATGGAACCCCTCCTACGAGCTCATCCACACAGATGAA 7560  
QY 7561 AACGCAGGAGTGGGACAAACGAAAGTCTATCCTCGGGGTACAGTGGAAGTACAGAAGCA 7620  
Db |||||  
7561 AACGCAGGAGTGGGACAAACGAAAGTCTATCCTCGGGGTACAGTGGAAGTACAGAAGCA 7620  
QY 7621 GCTCAAGGCCTTTGTACCTTAGAACGGTTTGACCAAGCTATGGCTCCACAATCACCAG 7680  
Db |||||  
7621 GCTCAAGGCCTTTGTACCTTAGAACGGTTTGACCAAGCTATGGCTCCACAATCACCAG 7680  
QY 7681 CTGCCAGCAGGCTCCAAAGACCAAGAAAGTTTGCATCCAGCGGCTCAGTCTTTGGCAAGGG 7740  
Db |||||  
7681 CTGCCAGCAGGCTCCAAAGACCAAGAAAGTTTGCATCCAGCGGCTCAGTCTTTGGCAAGGG 7740  
QY 7741 GGTCAAGTTTGCCTTGAAGGATGGCCGAGTGACCAACAGACATCATCAGTGTGGCCAATGA 7800

Db 7741 GGTCAAGTTTGCCTTGAAGGATGGCCGAGTGACCACAGACATCATCAGTGTGGCCAATGA 7800  
QY 7801 GGATGGCGAAAGGTTGCTGCCATCTTTGAACCATGCCCACTACCTAGAGAACCTGCACCT 7860  
Db 7801 GGATGGCGAAAGGTTGCTGCCATCTTTGAACCATGCCCACTACCTAGAGAACCTGCACCT 7860  
QY 7861 CACCATTGATGGGTGGATACCCATTACTTTGTGAAAACCAAGGACCTTCAGAAAGGTGACCT 7920  
Db 7861 CACCATTGATGGGTGGATACCCATTACTTTGTGAAAACCAAGGACCTTCAGAAAGGTGACCT 7920  
QY 7921 GGCCATCTGGGCCCTCAGTGGGGCGGCGAACCCCTGGAGAAATGGGGTCAACGTCACTGT 7980  
Db 7921 GGCCATCTGGGCCCTCAGTGGGGCGGCGAACCCCTGGAGAAATGGGGTCAACGTCACTGT 7980  
QY 7981 GTCCAGATCAACACAGTACTTTAATGGCAGGACTAGACGCTACACAGACATCCAGCTCCA 8040  
Db 7981 GTCCAGATCAACACAGTACTTTAATGGCAGGACTAGACGCTACACAGACATCCAGCTCCA 8040  
QY 8041 GTACGGGCACTGTGCTTTGAACACACGCTACGGGACAACGTTGGATGAGGAGGACG 8100  
Db 8101 GGTCTTGAGCTGGCCCGGCGAGAGAGCGGTGCGCCAAAGCTGGSCCGGAGCAGAG 8160  
QY 8101 GGTCTTGAGCTGGCCCGGCGAGAGAGCGGTGCGCCAAAGCTGGSCCGGAGCAGAG 8160  
Db 8101 GGTCTTGAGCTGGCCCGGCGAGAGAGCGGTGCGCCAAAGCTGGSCCGGAGCAGAG 8160  
QY 8161 ACTGCGGAAAGGGAGGAAGGCCCTGCGGGCCTGGACAGAGGGGGAGAAAGCAGGTGCT 8220  
Db 8161 ACTGCGGAAAGGGAGGAAGGCCCTGCGGGCCTGGACAGAGGGGGAGAAAGCAGGTGCT 8220  
QY 8221 GAGCACAGGGCGGTTGCAAGGCTACGAGGCTTTTTCGTGATCTCTGTCGAGCAGTACCC 8280  
Db 8221 GAGCACAGGGCGGTTGCAAGGCTACGAGGCTTTTTCGTGATCTCTGTCGAGCAGTACCC 8280  
QY 8281 AGAACTGTCAGACAGCGCCAAACATCCACTTCATGAGACAGAGCGAGATGGCCGGAG 8340  
Db 8281 AGAACTGTCAGACAGCGCCAAACATCCACTTCATGAGACAGAGCGAGATGGCCGGAG 8340  
QY 8341 GTGACAGAGAGGAC 8354  
Db 8341 GTGACAGAGAGGAC 8354

RESULT 2

US-11-096-051-1

; Sequence 1, Application US/11096051  
; Publication No. US2005024486A1  
; GENERAL INFORMATION:  
; APPLICANT: Kekuda, Ramesh  
; APPLICANT: MacLachlan, Timothy K  
; APPLICANT: Rastelli, Luca  
; APPLICANT: Vernet, Corine  
; APPLICANT: Ettenberg, Seth  
; TITLE OF INVENTION: Ten-M3 Polypeptides and Polynucleotides and their Methods of Use  
; FILE REFERENCE: Attorney Docket No. Cura 967  
; CURRENT APPLICATION NUMBER: US/11/096,051  
; PRIOR FILING DATE: 2005-03-30  
; PRIOR APPLICATION NUMBER: 10/038,854  
; PRIOR FILING DATE: 2001-12-31  
; PRIOR APPLICATION NUMBER: 10/455,772  
; PRIOR FILING DATE: 2003-06-04  
; PRIOR APPLICATION NUMBER: 60/557,978  
; PRIOR FILING DATE: 2004-03-30  
; NUMBER OF SEQ ID NOS: 38  
; SOFTWARE: CuraSeqList version 0.1  
; SEQ ID NO 1  
; LENGTH: 8362  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (71)..(8215)

US-11-096-051-1

Query Match		42.4%;	Score 3542.2;	DB 9;	Length 8362;
Best Local Similarity		65.5%;	Pred. No. 0;		
Matches 5458;		Conservative 0;	Mismatches 2683;	Indels 186;	Gaps 12;
QY	33	CCATGGACGTGAAGGAGAGGAAGCCCTTACCGCTCGCTGACCCGGCGC--	CGCGACGCCG	89	
Db	69	CCATGGATGTGAAGAAACGCAGGCCCTTACTGCTCCCTGACCAAGAGCAGACGAGAAGG	128		
QY	90	AGCGCCGCTACACCCAGCTCGTCCGGGACAGCGAGGAGGGCAAG--	CCCCGCAGAAAT	146	
Db	129	AACGGCGCTACACAAATTCTCCGCAGACAATGAGGAGTGCCGGGTACCCACACAGAAGT	188		
QY	147	CGTACAGCTCCAGCGAGACCCCTGAAGGCCCTACGACCAGGA--	CGCCCCCTAGCCTATG	203	
Db	189	CCTACAGTTCAGCGAGACATTGAAAGCTTTTGATCATGATTCTCTCGGGCTGCTTTACG	248		
QY	204	GCAGCCGCTCAAGGACATTGTGCCGAGGAGGCCGAGGAATTTCTGCCGCACAGGTGCCA	263		
Db	249	GCAACAGAGTGAGGATTGGTTTCACAGAGAAGCAGACGAGTTCACTAGACAAGGACAGA	308		
QY	264	ACTTCACCCCTGCGGAGCTGGGGCTGGAAGAAAGTAACGCCCCCTCACGGGACCCCTGTACC	323		
Db	309	ATTTTACCCTAAGCAGTTAGGAGTTTGTGAACCAGCAACTCGAAGAGGACTGGCATTTT	368		
QY	324	GGACAGACATTGGCCCTGCCCAATGCGGCTACTCCATGGGGGTGGCTCTGATGCCGACA	383		
Db	369	GTGCGGAAATGGGGCTCCCTCACAGAGGTTACTCTATCAGTGCAGGGTCAGATGCTGATA	428		
QY	384	TGGAGGCTGACACGGTGCTGTCCCCCTGAGCACCCCGTGCGTCTGTGGGGCCGGAGCACAC	443		
Db	429	CTGAAATGAAGCAGTGATGTCCCCAGAGCATGCCATGAGACTTTGGGGCAGGGGGTCA	488		
QY	444	GGTCAGGGCGCAGCTCCTGCCTGTCCAGCCGGGCCAAATTCCAATCTCACACTCACCGACA	503		
Db	489	AATCAGGCCGAGCTCCTGCCTGTCAAGTCGGTCCAACCTCAGCCCTCACCCCTGACAGATA	548		
QY	504	CCGAGCATGAAAAACACTGAGACTGATCATCCGGCGGCTTGAGAACCCACGCGCGGCTCC	563		
Db	549	CGGAGCACGAAAAACAAGTCCGACAGTGAGATGAGCAACCTGCAAGCAATCAAGGCCAGT	608		
QY	564	GGACGCCGCGCCGCGCTCTCGCACGCCCCACACCCCCCAACAGCACCCAGCGGCCCTCCA	623		
Db	609	CTACCTTGACGCCCTTGCCGCCTTCCCATAGCAGCACTCTGCACAGCATCATCCATCCA	668		
QY	624	TTAACTCCCTGAACCGGGGCAACTTCACGCCGAGGAGCAACCCACAGCCCGCCCCACAGG	683		
Db	669	TCACCTTCTCAACAGAAACTCCCTGACCAATAGAAGGAACACAGAGTCCGGCCCGCCCGG	728		
QY	684	ACCACCTGCTCTCCGGAGAGCCCCCTGCGGGCGGCCCGAGGAGCCTGCCCAACGCCCCAGG	743		
Db	729	CTGCTTTGCCCGCGAGCTGCAAAAC-----CACACCCGAGTCCGTCCAGTGCAGG	779		
QY	744	AGAACTGGTGTCTCAACAGCAACATCCCCCTGGAGACCAGGAACCTAGGCAAGCAGCCAT	803		
Db	780	ACAGCTGGGTCTTGGCAGTAATGTACCACCTGGAAGAGCAGGCATT-----	825		
QY	804	TCCTAGGGACATTGCAGGACAACTCATTTGAGATGGACATTTCTGGCGCCTTCCCGCCATG	863		
Db	826	-----	825		
QY	864	ATGGGGCTTACAGTGACGGGCACTTCTCTTCAAGCCTGGAGGCACCTCCCGCTCTTCT	923		
Db	826	-----CCTATTCAAAACAGGAACAGGTACAACGCCACTGTTCA	863		
QY	924	GCACACATCACCAGGGTACCACCTGACGTCCAGCACAGTGTACTCTCTCCGCCGCCGAC	983		
Db	864	GTACTGCAACCCAGGATACAAATGGCATCTGGCTCTGTTTATTTCACCACCTACTCGGC	923		
QY	984	CCCTGCCCGCAGCACCTTCGCCCGCGGCCCTTTAACTCAAGAAGCCCTCAAGAGCTCT	1043		
Db	924	CACCTACCTAGAAACACCCCTATCAAGAAGTGCTTTTAAATTCAGAAGTCTTCAAGTACT	983		

QY	1044	GTAACGTGAAGTGGCAGCCCTGAGCGCCATCGTCACTCTCAGCCACTCTGTGTCATCCTGC 1103			
Db	984	GTAGCTGGAATGCACTGCACTGTGTGCCGTAGGGGTCTCGGTCTCTTGCAATACTCC 1043			
QY	1104	TGGCATACTTTGTGGCCATGCACCTGTTTGGCCTAAACTGGCACCTGCAGCCGATGGAGG 1163			
Db	1044	TGTCTTATTTATAGCAATGCATCTCTTTGGCCTCAACTGGCAGCTACAGCAGACTGAAA 1103			
QY	1164	GGCAGATGTATGAGATCAGGAGGACACAGCCAGCAGTTGGCCTGTGCCAACCCGACGTCT 1223			
Db	1104	ATGACACATTTGAGA-----ATGGAAGAGTGAATTTCTGATACCATGCCAACAAACACTG 1157			
QY	1224	CCCTATACCCCTCAGGGGGCACTGGCTTAGAGACCCCTGACAGGAAAGCAAGGAACCA 1283			
Db	1158	TGTCATTACCTTCTGGAGACA----- 1178			
QY	1284	CAGAAAGGAAAGCCAGTAGTTTCTTTCCAGAGGACAGTTTTCATAGATTTCTGGAGAAATTG 1343			
Db	1179	---ATGGAATTAGGTGGATTTACGCAAGAAAAATAACCATAGATTTCCGGAGAACTTG 1235			
QY	1344	ATGTGGGAAGGCGAGCCTCCAGAAAGATTCTCTCTGGGAAAGGCAGCCCTGGTTG 1403			
Db	1236	ATATTGGCCGAAGAGCAATTCAAGAGATTCTCCCGGATCTTCTTGAGAGGATCACAGCTCT 1295			
QY	1404	TCATAGACCATCCTGTGCATCTGAAATTCAAATGTGTCTCTGGGAAAGGCAGCCCTGGTTG 1463			
Db	1296	TCATTGATCAGCCACAGTTTCTTAAATTCAAATATCTCTCTTCAGAAAGGATGCATTGATTG 1355			
QY	1464	GCATTTTATGGCAGAAAGGCCCTCCCTCCTTACATACACAGTTTGACTTTGTGGAGCTGC 1523			
Db	1356	GAGTATATGGCCGAAAGGCTTACCGCCTTCCCATACTCAGTATGACTTCGTGGAGCTCC 1415			
QY	1524	TGGATGGCAGGAGGCTCCTAACCCAGGAGCGCGGAGCCCTAGAGGGACCCCGCCAGT 1583			
Db	1416	TGGATGGCAGCAGGCTGATTGCCAGAGAGCAGCGGAGCCTGCTTGAGACGAGAGAGCCG 1475			
QY	1584	CTCGGGAACTGTGCCCCCTCCAGCCATGAGACAGGCTTCAATCCAGTATTTGGATTGAG 1643			
Db	1476	GGCGGACGCGAGATCCGTGAGCCTTCATGAGGCCGCTTATCCAGTACTTGGATTCTG 1535			
QY	1644	GAATCTGGCACTTGGCTTTTACAAATGACGGAAGGAGTCAAGAGTGGTTTCTCTTCTCA 1703			
Db	1536	GAATCTGGCATCTGGCTTTTATAATGATGGGAAAAATGCAGAGCAGGTGTCTTTTAATA 1595			
QY	1704	CCACTGCCATTGAGTCGGTGGATAACTGCCCCAGCAACTGCTATGGCAATGGTGACTGCA 1763			
Db	1596	CCATTGTTATAGAGTCTGTGGTGAATGTCCCCGAAATTGCCATGGAATGGAGAATGCG 1655			
QY	1764	TCTCTGGACCTGCCACTGCTTCTCTGGGTTTCTTGGSCCCCGACTGTGGCAGAGCCTCCT 1823			
Db	1656	TTTCTGGAACTTGCCATTGTTTTTCCAGGATTTCTGGGTCCGGATTGTTCAAGAGCCGCCT 1715			
QY	1824	GCCCCGTGCTCTGTAGCGGAAATGGCCAATACATGAAAGGCAGATGCTTGTGCCACAGTG 1883			
Db	1716	GTCCAGTGTATGTAGTGGCAACGGGCAGTACTCCAAGGGCCGCTGCCGTGTTTCAAGCG 1775			
QY	1884	GCTGAAAGGCGCTGAGTCGATGTGCCCAACCAACAGTGTATCGATGTGGCCTGCAGCA 1943			
Db	1776	GCTGAAAGGCGCACCGAGTGTGATGTGCCGACTACCCAGTGTATTGACCCACAGTGTGGG 1835			
QY	1944	ACCATGGCACCTGCATCACGGGACCTGCATCTGCAACCTGGCTACAAGGGCGAGAGCT 2003			
Db	1836	GTGTTGGGATTTGTATCATGGGCTCTTGTGCTTGCAACTCAGGATACAAAGGAGAAAGTT 1895			
QY	2004	GTGAGAAAGTGGACTGCATGGACCCCAATGTTTTCAGGCGGGGTGTCTCGTGTAGAGGG 2063			
Db	1896	GTGAAGAAAGCTGACTGTATAGACCCCTGGGTGTTCTAATCATGGTGTGTATCCACGGG 1955			
QY	2064	AATGCAATGCTTTGTGGATGGGAGGCACCAACTGCGAGACCCCCAGGGCCCATGCT 2123			
Db	1956	AATGCTACTGCAGTCCAGGATGGGAGGTAGCAATTGTGAAATACTGAAGACCATGTGTC 2015			



QY 2124 TAGACCAGTGTTCAGGCCACGGAACCTTCTCCGGACACCGGGCTTTGACGCTGTGACC 2183  
|||||  
Db 2016 CAGACCAGTGTCTCGGCCACGGAACGATATCTTCAAGAAAGTGGCTCCTGCACGTGTGACC 2075  
|||||  
QY 2184 CAAGCTGGACTGGACACGACTGTTCTATCGAGATCTGTGCTGCCGACTGTGGTGGCCATG 2243  
|||||  
Db 2076 CTAACCTGGACTGGCCACAGACTGCTCAAACGAAATATGTTCTGTGACTGTGGCTCACACG 2135  
|||||  
QY 2244 GCGTGTGCGTAGGGGGCACCTGCCGCTGCCGAGGATGGCTGGATGGGGGAGCCCTGCCACC 2303  
|||||  
Db 2136 GCGTTTGCAATGGGGGGACGTTGCTGCTGGAAGAGGCTGGACGGGCCACGCTGTAATC 2195  
|||||  
QY 2304 AGCGGGCCTGCCACCCGCGCTGTGCCGAGCATGGGACCTGCCGCGACGCGCAAGTCCGAGT 2363  
|||||  
Db 2196 AGAGAGCCTGCCACCCCGCTGTGCCGAGCACGGGACCTGCAAGGATGGCAAGTGTGAAT 2255  
|||||  
QY 2364 GCAGCCCTGGCTGGAATGGCGAAACACTGCACCATCGCTCACTATCTGGATAGGGTAGTTA 2423  
|||||  
Db 2256 GCAGCCAGGGCTGGAATGGAGAGCACTGCATATCGCTCACTATTTGGATAAGATAGTTA 2315  
|||||  
QY 2424 AAGAGGGTTCCTCGGTGTGCAATGGCAACGGCAGATGTACCTTAGACCTGAATGGTT 2483  
|||||  
Db 2316 AAGAGGGTGTCTGCTGTGCAACAGCAATGSAAGATGTACCTGGACCAAAATGGCT 2375  
|||||  
QY 2484 GGCACCTGCGTCTGCCAGCTGGGCTGGAGAGGAGTGGCTGTGACACTTCCATGGAGACTG 2543  
|||||  
Db 2376 GGCAATTGTGTGCCACGCTGGATGGAGAGGAGCAGGCTGTGACGTAGCCATGGAGACTC 2435  
|||||  
QY 2544 CCTGCGGTGACAGCAAGACAATGATGGAGATGGCCTGGTGGACTGCATGGACCCCTGACT 2603  
|||||  
Db 2436 TTTGCACAGATAGCAAGACAATGAAGGAGATGGACTCATTTGACTGCAATGGACCCCGATT 2495  
|||||  
QY 2604 GCTGCCCTCCAGCCCTGTGCCATATCAACCCGCTGTGCCCTTGGCTCCCTTAACCCCTCTGG 2663  
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Db 2496 GCTGCCCTACAGAGTTCCTGCCAGAATCAGCCCTTATGTGGGGACTGCCGGACCCCTCAGG 2555  
|||||  
QY 2664 ACATCATCCAGGAGACACAGGTCCCTGTGTACAGCAGAAACCTACACTCCTTCTATGACC 2723  
|||||  
Db 2556 ACATCATTAGCCAAAGCCTTCAATCGCCTTCTCAGCAAGCTGCCAAATCCTTTATGATC 2615  
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QY 2724 GCATCAAGTTCCTCGTGGCAGGGACAGCACGGCACATAATCCCCGGGGAGAACCCCTTTG 2783  
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Db 2616 GAATCAGTTTCCTTATAGGATCTGATAGCACCCCATGTTATACCTGGAGAAAGTCTTTCA 2675  
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QY 2784 ATGGAGGGCATGCTTGTGTTATTCTGTGGCCAAAGTATGACATCAGATGGAACCCCTGG 2843  
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Db 2676 ATAAGAGCCTTGCACTGTTCATCAGAGGCCAAAGTACTGACTGCTGTATGGAATCCACTTA 2735  
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QY 2844 TTGGTGTGAACATCAGTTTGTCAATAACCCCTCTCTTTGGATATACAATCAGCAGGCAAG 2903  
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Db 2736 TTGGAGTAAATGTCTCGTTCCTTCCATTACCCAGAAATGGAATATGATATCTATTACCGCCAGG 2795  
|||||  
QY 2904 ATGGCAGCTTTGACTTTGTGACAAATGGCGGCATCTCCATCATCTCGGTTGAGCGGG 2963  
|||||  
Db 2796 ACGGAATGTTGACTTTGGTGGCAAAATGGTGGGCTCTCTAACTTTGGTATTTGAAACGAT 2855  
|||||  
QY 2964 CACCTTTTCATCACACAGGAGCACACCCCTGTGGCTGCCATGGGATCGCTTCTTTGTGATGG 3023  
|||||  
Db 2856 CCCCATTCCTCACTCAGTATCATACTGTGTGGATTCCATGGAATGTCTTTTATGTGATGG 2915  
|||||  
QY 3024 AAACCATCATCATGAGACATGAGGAGAATGAGATTCAGCTGTGACCTGAGCAATTTTG 3083  
|||||  
Db 2916 ATACCCCTAGTCATGAAGAAAGAGAAATGATATTCACAGCTGTGATCTGATGGATTCG 2975  
|||||  
QY 3084 CCGGCCCAACCCAGTGTCTCTCCATCCCCACTGACGTCCTTCGCCAGCTCCTGTGCAG 3143  
|||||  
Db 2976 TGAGGCCAAATCCCATCATTTGTGTCAACCTTTATCCACCTTTTTCAGATCTTCTCCTG 3035  
|||||  
QY 3144 AGAAAGGCCCCCATTTGTGCCGGAATTCAGGCTTTGCAGGAGGAAATCTCTATCTCTGGCT 3203  
|||||  
Db 3036 AAGACAGTCCCATCATTTCCGAAACACAGGTACTCCAGGAGAACTACAATTCAGGAA 3095  
|||||  
QY 3204 GCAAGATGAGGCTGAGCTACTGAGCAGCGGACCCCTGGCTACAAATCTGTCTGTGAGGA 3263  
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Db 3096 CAGATTTGAAAACCTCTCCTACTTGTAGTTCAGAGCTGCAGGGTATAAGTCAGTTCTCAAGA 3155  
|||||  
QY 3264 TCAGCCTCACCCACCCGACCATCCCTTCAACCTCATGAAGGTGCACCTCATGGTAGCGG 3323  
|||||  
Db 3156 TCACCATGACCCAGTCTATTATTCCATTAAATTAATGAAGGTTCATCTTATGGTAGCTG 3215  
|||||  
QY 3324 TGGAGGGCCGCTCTTCAGGAAAGTGGTTCGCTGCAGCCCCCAGACCTGTCTCTATTATTCA 3383  
|||||  
Db 3216 TAGTAGGAAGACTCTTCCAAAAGTGGTTCCTGCCCTCACCAAACTTGGCCTATACTTTCA 3275  
|||||  
QY 3384 TTTGGGACAAAGACAGACGCTCTAACACCAGAAAGGTGTTTGGGCTTTCAGAAAGCCTTTGTTT 3443  
|||||  
Db 3276 TATGGGATAAAAACAGATGCATATAATCAGAAAGTCTATGGTCTATCTGAAGCTGTTGTGT 3335  
|||||  
QY 3444 CCGTGGTTATGAATATGAATCCTGCCCAGATCTAATCCTGTGGGAAAAAAGAACACAG 3503  
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Db 3336 CAGTTGGATATGAGTATGAGTCGTGTTTGGACCTGACTCTGTGGGAAAAGAGGACTGCCA 3395  
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QY 3504 TGCTGCAGGCTATGAAATTGACGCGTCCAAAGCTTGAGGATGGAGCTAGACAAAACATC 3563  
|||||  
Db 3396 TTCTGCAGGCTATGAATTGGATCGCTCCAAACATGGTGGCTGGACATTAGATAAAACATC 3455  
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QY 3564 ATGCCCTCAACATTCAAAGTGGTATCCTGCACAAAAGGGAATGGGGAGAACCAAGTTTGTGT 3623  
|||||  
Db 3456 ACGTGTGGATGTACAGAACGGTATACTGTACAAGGAAACCGGGGAAAACCAAGTTCATCT 3515  
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QY 3624 CTCAGCAGCCTCCTGTCAATTGGGAGCATCATGGGCAATGGGCGCCCGGAGAACGATCTCCT 3683  
|||||  
Db 3516 CCCAGCAGCCTCCAGTCGTGAGTAGCATCATGGGCAATGGGCGAAGGCGCAGCATTTCTT 3575  
|||||  
QY 3684 GCCCAGCTGCAACGGCCTTGCTGACGGCAACAAGCTCCTGGCCCCAGTGGCCCCCTCACCT 3743  
|||||  
Db 3576 GCCCCAGTTGCAATGGTCAAGCTGATGGTAAACAAGTTACTGTGGCCCCAGTGGCGCTAGCTT 3635  
|||||  
QY 3744 GTGGCTCTGACGGGAGCCTCTATGTGGTGAATTTCAACTACATTTAGAAGATCTTCCCCT 3803  
|||||  
Db 3636 GTGGGATCGATGGCAGTCTGTACGTAGGCGATTTCAACTATGTGCGGCGGATATTCCCTT 3695  
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QY 3804 CTGGAATGTCAACCAACATCCTAGAGCTGAGGAATAAAGATTTTCAGACATAGTCACAGTC 3863  
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Db 3696 CTGGAATGTAAACAAGTGTCTTAGAACTAAGAAATAAAGATTTTAGACATAGCAGCAACC 3755  
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QY 3864 CAGCACACAATACTACCTGGCCACAGACCCCATGAGTGGGGCCGCTCTTCTTTCTGACA 3923  
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Db 3756 CAGCTCATAGATACTACCTTGCAACCGGACCCAGTCACGGGAGATCTGTACGTTTCTGACA 3815  
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QY 3924 GCAACAGCCGGCGGTCTTTAAAAATCAAATCAAGTCCACTGTGGTGTGAAGACCTTGTCAAGA 3983  
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Db 3816 CAAACACCCGAGAAATTTATCGCCCAAAGTCACTTACGGGGGCAAAAGACTTGACTAAAA 3875  
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QY 3984 ACTCTGAGGTGTTGCGGGACAGGTGACAGTGCCTCCCTTTGATGACACTCGTGC 4043  
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Db 3876 ATGCAGAAGTCTGTCGAGGGACAGGGGAGCAATGCCCTCCGTTTACGAGGCGAGATGTG 3935  
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QY 4044 GGGATGGTGGBAAGGCCACAGAAAGCCACACTCACCAATCCCAGGGGTATTACAGTGGACA 4103  
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Db 3936 GGGATGGAGGGAAGGCCGTGGAAGCCCACTCATGAGTCCCAAAGGAATGSCAGTTGATA 3995  
|||||  
QY 4104 AGTTTGGGCTGATCTACTTCGTGGATGGCAACCATGATCAGACGCATCGATCAGAAATGGGA 4163  
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Db 3996 AGAATGGATTAAATCTACTTTGTTGATGGAAACCATGATTAGGAAAGTTGACCAAAATGGAA 4055  
|||||  
QY 4164 TCATCTCCACCCTGCTCGGCTCTAATGATCTCACATCAGCCCGGCCACTCAGCTGTGATT 4223  
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Db 4056 TCATATCAACTCTTCTGGGCTCTAACGAATTTGACTTCAGCCAGACCTTTTAACTTGTGACA 4115  
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QY 4224 CTGTCTATGGATATTTCCAGGTAAGACTGGAGTGGCCACACAGACTTAGCCATCAACCCAA 4283  
|||||  
Db 4116 CCAGCATGCACATCAGCCAGGTACGCTGTGAATGGCCCACTGACCTTAGCCATTAACCCCTA 4175  
|||||  
QY 4284 TGGACAACTCACTTTATGTCTCTCGACAAACAATGTGGTCTTGCAAAATCTCTGAAAAACCACC 4343  
|||||



Db 4176 TGGATAACTCCATTATGTCTGGATAAATAATGTAGTTTTACAGATCACTGAAATCGTC 4235

QY 4344 AGGTGCGATTGTGCGGGAGGCCCATGCACCTGCCAGTCCCTGGCATTTGACCACCTTCC 4403

Db 4236 AAGTTCGCATTGCTGCTGGACGCCCATGCACCTGTACAGTTCCTCGGAGTGG---AATATC 4292

QY 4404 TGCTAAGCAAGGTGGCCATCCACGCCAACCCCTGGAGTACAGCCACCCTTTGGCTGTTTCAC 4463

Db 4293 CTGTGGGAAGCACGCGGTGCAGACAACACTGGAATCAGCCACTGCCATTGCTGTGTCTT 4352

QY 4464 ACAATGGGTCTCTGTATATTGTGAGACTGATGAGAAAAAGATCAACCGCATCAGGCAGG 4523

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QY 4524 TCACCAC TAGTGAGAGATCTCACTCGTTGCTGGGGCCCCCAGTGGCTGTGACTGTAAAA 4583

Db 4413 TCACAACAGATGGAGAAATCTCCTTAGTGGCCGGAATACCTTCAGAGTGTGACTGCAAAA 4472

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Db 4593 ATATCCGGATACGGGCTGTGTCAAAGAATAAGCCTTTACTTAACTCTATGAACCTTCTATG 4652

QY 4764 AGCTGTCTTCACCAATTGACCAGGAGCTCTATCTGTTTGATACCAACCGGCAAGCACCTGT 4823

Db 4653 AAGTTGCGTCTCCAACTGATCAAGAACTCTACATCTTTTGACATCAATGGTACTCACCAAT 4712

QY 4824 ACACCCAAAGCCTGCCACAGGAGACTACCTGTACAACCTTCACCTACACTGGGGACGGCG 4883

Db 4713 ATACTGTAAGTTTAGTCACTGGTGATTACCTTTACAATTTTAGTACAGCAATGACAAATG 4772

QY 4884 ACATCACACTCATCACAGACAACAATGGCAACATGGTAATGTCCGCCGAGACTCTACTG 4943

Db 4773 ATATTACTGCTGTGACAGACAGCAATGGCAACACCCTTAGAAATTAGACGGGACCCAAATC 4832

QY 4944 GGATGCCCTCTGGCTGGTCCCAGATGGCCAGGTGTACTGGGTGACCATGGGCACCA 5003

Db 4833 GCATGCCAGTTCGAGTGGTGTCTCCTGATAACCAAGTGATATGGTTGACAAATAGGAACAA 4892

QY 5004 ACAGTGCACTCAAGAGTGTGACCACAAAGGACACGAGTTGGCCATGATGACATACCATG 5063

Db 4893 ATGGATGTTTGAAAAGCATGACTGCTCAAGGACTGGAATTAGTTTGTTTACTTACCATG 4952

QY 5064 GCAATTCGGCTTCTGGCAACCAAAAGCAATGAAAACGSGATGGACAAACATTTTATGAGT 5123

Db 4953 GCAATAGTGGCTTTTAGCCACTAAAAGTGATGAAACTGSGATGGACAACGTTTTTTGACT 5012

QY 5124 ACGACAGTTTGGCCGCTGACAAATGTGACCTTCCCTACTGGCCAGGTGAGCAGTTTCC 5183

Db 5013 ATGACAGTGAAGGTGCTCTGACAAATGTTACGTTTCCAACTGGAGTGGTCAAAACCTGC 5072

QY 5184 GAAGTGATACAGACAGTTTCAGTGCATGTCCAGGTAGAGACCTCCAGC---AAGGATGATG 5240

Db 5073 ATGGGACATGGACAAGGCTATCACAGTGGACATTGAGTCACTAGCCGAGAAGAAGATG 5132

QY 5241 TCACCATAACCAACCAACCTGCTGCTCAGGCGCCTTCTACACACTGCTGCAAGACCAAG 5300

Db 5133 TCAGCATCACTTCAAATCTGTCTCGATCGATTCTTCTACACCATTGTTCAAGATCAGT 5192

QY 5301 TCCGGAACAGCTACTACATCGGGCCGATGGCTCCTTGGCTGGCAGCTGCTGGCCAAACCGCA 5360

Db 5193 TAAGAAACAGCTACCAGATTGTTATGACGGCTCCCTCAGAAATTAATCTACGCCAGTGGCC 5252

QY 5361 TGGAGGTGGCGCTGCAGACTGAGCCCCCACTTGTGGCTGGCACCGTCAACCCCAACCGTGG 5420

Db 5253 TGGACTCACACTACCAAAACAGAGCCGACGTTCTGGCTGGCACCGCTAAATCCGACGGTTG 5312

QY 5421 GCAAGAGGAATGTACGCTGCCCCATCGACAACGGCCTCAACCTGGTGGAGTGGCGCCAGC 5480

Db 5313 CCAAAAGAAAACATGACTTTGCTTGGCGAGAACGGTCAAAACTTTGGTGAATGGAGATTCC 5372

QY 5481 GCAAAAGACAGGCTCGGGGCCAGGTCACTGTCTTTGGGCGCCGGCTGCGGTTGCACAACC 5540

Db 5373 GAAAAGAGCAAGCCCAAGGGAAGTCAATGTCTTTGGCCGAAGCTCAGGGTTAATGGCA 5432

QY 5541 GAAATCTCCTATCTCTGGAATTTTGATCGCGTAAACACGCACAGAGAAAGATCTATGATGACC 5600

Db 5433 GAAACCTCCTTTCAAGTTGACTTTTGATCGAACAACAAAGACAGAAAAGATCTATGACGACC 5492

QY 5601 ACCGCAAGTTTCAACCCTTCGGATTCTGTACGACAGCGGGCGGCCAGCCTCTGTTCTAC 5660

Db 5493 ACCGTAATTTCTACTGAGGATCGCCTACGACACGTTCTGGGCACCCGACTCTCTGGCTGC 5552

QY 5661 CCAGCAGCAGGCTGAATGGTGTCAACCGTGAATCTCCCTTGGGGTTTACATTTGCTGGCA 5720

Db 5553 CAAGCAGCAAGCTGATGGCCGTCAATGTCACTTATTCATCCACAGSTCAAAATGGCCAGCA 5612

QY 5721 TCCAGAGGGGCATCATGTCTGAAAGAAATGGAATACGACACGAGCGGCGCCGCATCACATCCA 5780

Db 5613 TCCAGCGAGGCACCACTAGCGAGAAAGTAGATTATGACGGACAGGGGAGGATCGTGTCTC 5672

QY 5781 GGATCTTCGCTGATGGGAAGACATGGAGCTACACATACCTTAGAGAAAGTCCATGGTGTGC 5840

Db 5673 GGGTCTTTGCTGATGGTAAACATGGAGTTACACATATTTAGAAAAGTCCATGGTTCTTC 5732

QY 5841 TACTACACAGCCAGAGGCGAGTATATCTTTGAGTTCGACAAGAAATGACCGCCTCTCTTCTG 5900

Db 5733 TGCTTCATAGCCAGCGGACGTACATCTTCGAATACGATATGTGGACCGCCTGTCTGCCA 5792

QY 5901 TGACGATGCCCAACGTTGGCGGGCAGACACTAGAGACCATCCGCTCAGTGGGCTACTACA 5960

Db 5793 TCACCATGCCAGTGTGGCTCGCCACACCATGCAGACCATCCGATCCATTTGGTACTACTACC 5852

QY 5961 GAAACATCTATCAGCCCCCTGAGGGCAATGCCTCAGTCAATACAGGACTTCACCTGAGGATG 6020

Db 5853 GCAACATATACAACCCCCCGGAAAGCAACGCCTCCATCATCACGGACTACAACGAGGAAG 5912

QY 6021 GGCACTCTCTCACACCTTCTACCTGGGCACTGGCCGACGGGTGATATACAAGTATGGCA 6080

Db 5913 GGCTGCTTCTACAAAACAGCTTCTTTGGGTACAAGTCGAGGGTCTTATTCAAATACAGAA 5972

QY 6081 AACTGTCAAAAGCTGGCAGAGACGCTCTATGACACCAACCAAGGTCAAGTTTCACTATGACG 6140

Db 5973 GGCAGACTAGGCTCTCAGAAAATTTATATATGATAGCACAAGAGTCAAGTTTACCTATGATG 6032

QY 6141 AGACGCGAGGCATGCTGAAGACCATCAACCTACAGAAATGAGGGCTTCACCTGCACCATCC 6200

Db 6033 AAACAGCAGGAGTCCCTAAAGACAGTAAACCTCCAGAGTATGAGTTTATTTGACCATTA 6092

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Db 6093 GATACAGGCAAAATTTGTTCCCTGATTGACAGGCAAGATTTTCCGCTTTAGTGAAGATGGGA 6152

QY 6261 TGGTCAACGCCCGTTTGTACTACAACATATGACAACAGCTTCCGGGTGACCAAGATGCAGG 6320

Db 6153 TGGTAAATGCAAGATTTGACTATAGCTATGACAACAGCTTTTCGAGTGACCATGCAGG 6212

QY 6321 CTGTGATCAACGAGACCCCACTGCCCATTTGATCTCTATCGCTATGATGATGTGTGAGGCA 6380

Db 6213 GTGTGATCAATGAACGCCCACTGCCTATTGATCTGTATCAGTTTGTATGACATTTCTGGCA 6272

QY 6381 AGACAGAGCAGTTTGGGAAGTTTGGTGTCAATTTACTATGACATTAACCAAGATCATCACCA 6440

Db 6273 AAGTTGAGCAGTTTGGAAAAGTTTGGAGTTATATATATATGATATTAACCAAGATCATTTCTA 6332

QY 6441 CAGCTGTCAATGACCCACACCAAGCATTTTGTATGCATATGGCAGGATGAAGGAAGTGCAGT 6500

Db 6333 CAGCTGTAATGACCTATACGAAGCACTTTGATGCTCATGGCCGTATCAAGGAGATTCAAT 6392





; SOFTWARE: CuraSeqList version 0.1									
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; LENGTH: 8645									
; TYPE: DNA									
; ORGANISM: Homo sapiens									
; FEATURE:									
; NAME/KEY: CDS									
; LOCATION: (151)..(8313)									
US-11-096-051-9									
Query Match 41.9%; Score 3502.2; DB 9; Length 8645;									
Best Local Similarity 65.3%; Pred. No. 0;									
Matches 5449; Conservative 0; Mismatches 2688; Indels 204; Gaps 13;									
QY	35	ATGGACGTGAAGGAGAGAACCTTACCGCTCGCTGACCCGGCGC---CGCGACGCCGAG	91						
Db	151	ATGGATGTGAAGAAGCAGCAGGCCTTACTGCTCCCTGACCAAGAGCAGACGAGAGAAGGAA	210						
QY	92	CGCCGCTACACGAGCTCGTCCGGGACAGCGAGGAGGGCAAG---CCCCGACAGAAATCG	148						
Db	211	CGGCGCTACACAAATTCCTCCGACAGCAATGAGGAGTGCCGGGTACCCACACAGAAGTCC	270						
QY	149	TACAGCTCCAGCGAGACCTGAAAGGCCTACGACCAGGA---CGCCGCTAGCCTATGCG	205						
Db	271	TACAGTTCCAGCGAGACATTGAAAGCTTTTGATCATGATTCCTCGCGGCTGCTTTACGGC	330						
QY	206	AGCCGCGTCAAGGACATTGTGCCGAGGAGGCCGAGGAATTCTGCCGCACAGGTGCCAAC	265						
Db	331	AACAGAGTGAAGGATTGGTTTCACAGAGAAGCAGCAGGTTCACTAGACAAGGACAGAAAT	390						
QY	266	TTACCCCTGCGGAGCTGGGGCTGGRAAGTAACGCCCCCTCACGGGACCTGTACCGG	325						
Db	391	TTTACCCTAAGCAGTTAGGAGTTTGTGAACCAAGCAACTCGAAGAGGACTGGCATTTTGT	450						
QY	326	ACAGACATTGGCCTGCCCCCAATGCGGCTACTCCATGGGGTGCGCTCTGATGCCGACATG	385						
Db	451	GCGGAAATGGGGTCCCTCACAGAGGTTACTCTATCAGTGCAGGGTCAGATGCTGATACT	510						
QY	386	GAGGCTGACACGGTGCTGTCCCTGAGCACCCCGTGCGGTCTGTGGGGCCGGAGCACACGG	445						
Db	511	GAAATGAAGCAGTGATGTCCCCAGAGCATGCCATGAGACTTTGGGGCAGGGGGGTCAAA	570						
QY	446	TCAGGGCGAGCTCTGCCCTGTCCAGCCGGGCCAAATCCAATCTCACACTCACCGACACC	505						
Db	571	TCAGGCGCAGCTCCTGCCGTGTCAAGTCGGTCCAACCTCAGCCCTCACCCCTGACAGATACG	630						
QY	506	GAGCATGAAAAACACTGAGACTGATCATCCGGCGGCTGCAGAACCCACGCGCGCTCCGG	565						
Db	631	GAGCACGAAAAACAAGTCCGACAGTGAGAATGAGCAACCTGCAAGCAATCAAGSCCAGTCT	690						
QY	566	ACGCCGCGCCGCGCTCTCGCACGCCCCACACCCCCCAACCCAGCACCAACGCGCGCTCCATT	625						
Db	691	ACCCTGCAGCCCTTGCCGCTTCCCATAAGCAGCACTTGCACAGCATCATCCATCCATC	750						
QY	626	AACTCCCTGAACCGGGCAACTTCACGCCGAGGAGGCAACCCCAAGCCCGCCCAAGGAC	685						
Db	751	ACTTCTCTCAACAGAAACTCCCTGACCAATAGAAGGAACCAAGATCCGGCCCGCCGGCT	810						
QY	686	CACTCGCTCTCCGGAGAGCCCCCTGCGGGCGGCCAGGAGCCTGCCCAAGCCCAAGGAG	745						
Db	811	GCTTTGCCCGCGAGCTGCAAC-----CACACCCGAGTCCGTCCAGTGCAGGAC	861						
QY	746	AACTGGCTGCTCAACAGCAACATCCCCCTGGAGACCAGGAACCTAGGCAAGCAGCCATT	805						
Db	862	AGCTGGTCTTGGCAGTAATGTACCACCTGGAAGGAGGAGGCAATT-----	905						
QY	806	CTAGGACATTGCAGGACAACCTCATTTGAGATGGACATTTCTCGGCGCCTCCGCGCATGAT	865						
Db	906	-----	905						
QY	866	GGGGCTTACAGTGACGGGCACCTTCTCTTCAAGCCTGGAGGCACCTCCCGCTCTTCTGCG	925						
Db	906	-----CCTATTCAAAACAGGAACAGGTACAAACGCCCACTGTTTCAGT	945						
QY	926	ACCACATCACCAAGGTACCCTACTGACGTCCAGCACAGTGTACTCTCTCCGCCCGACCC	985						
Db	946	ACTGCAACCCCGAGATACACAATGGCATCTGGCTCTGTTATTACCACTACTCTCGCCA	1005						
QY	986	CTGCCCCGCGACACCTTCGCCCGCGCCCTTTAACTCAAGAAGCCCTCCAAGTACTGT	1045						
Db	1006	CTACCTAGAAACACCTTATCAAGAAAGTGCTTTTAAATTCAGAAGCTTCAAAAGTACTGT	1065						
QY	1046	AACTGGAAGTGGCAGACCCCTGAGCGCCATCGTCATCTCAGCCACTCTGGTCATCCTGCTG	1105						
Db	1066	AGCTGGAATGCACTGCACTGTGTGCCGTAGGGGTCTCGGTGCTCTGGCAATACTCCTG	1125						
QY	1106	GCATACCTTTGTGGCCATGCACCTGTTTGGCTTAAACTGGCACTTGACCGCATGGAGGGG	1165						
Db	1126	TCTTATTTTATAGCAATGCATCTCTTTGGCTCAACTGGCAGCTACAGCAGACTGAAAT	1185						
QY	1166	CAGATGTATGAGATCACGGAGGACACAGCCAGCAGTTGGCCTGTGCCAACCGACGTCTCC	1225						
Db	1186	GACACATTTGAGA-----ATGGAAGTGAATTTCTGATACCATGCCAACAAACACTGTG	1239						
QY	1226	CTATACCCCTCAGGGGGCACTGGCTTAGAGACCCCTGACAGGAAAGGCAAAAGCAACACA	1285						
Db	1240	TCATTACCTTCTGGAGACA-----	1258						
QY	1286	GAAGGAAAGCCCAGTAGTTTCTTCCAGAGGACAGTTTTCATAGATTTCTGGAGAAATTGAT	1345						
Db	1259	-ATGGAATAATTAGGTGGATTTACGCAAGAAATAACACCATAGATTCGGGAACTTTGAT	1317						
QY	1346	GTGGGAAGCGAGCCCTCCAGAAAGATTCTCTCTGGGAAAGCAGCCCTGGTTGGC	1405						
Db	1318	ATTGCCGAAGAGCAATTCAAGAGATTCTCCCGGATCTTCTGGAGATCACAGCTCTTC	1377						
QY	1406	ATAGACCATCTGTGCATCTGAAATTCATATGTCTCTCTGGGAAAGCAGCCCTGGTTGGC	1465						
Db	1378	ATTGATCACCCACAGTTTCTTAAATTCATATCTCTCTTCAGAAGGATGCATTTGATTGA	1437						
QY	1466	ATTTATGGCAGAAAAGGCCTCCCTCTTCACATACACAGTTTGACTTTTGTGGAGCTGCTG	1525						
Db	1438	GTATATGGCCGGAAGGCTTACCGCTTCCCATACTCAGTATGACTTCGTGGAGCTCCTG	1497						
QY	1526	GATGGCAGAGGCTCTTAACCCAGAGGCGCGAGCCCTAGAGGGACCCCGCGCCAGTCT	1585						
Db	1498	GATGGCAGAGGCTGATTGCCAGAGAGCAGCGGAGCCTGCTTGAGACGGAGAGCCGGG	1557						
QY	1586	CGGGAACTGTGCCCCCTCCAGCCATGAGACAGGCTTCATCCAGTATTTGGATTGAGGA	1645						
Db	1558	CGGCAGCGAGATCCGTGAGCTTTCATGAGCCGCTTATCCAGTACTTTGGATTCTGGA	1617						
QY	1646	ATCTGGCACTTGGCTTTTACAAATGACGGAAGGAGTCAAGAGTGGTTTCTCTCTCACC	1705						
Db	1618	ATCTGSCATCTGGCTTTTATAATGATGGGAAAAATGCAGAGCAGGTGTCTTTTAATACC	1677						
QY	1706	ACTGCCATTGAGTCGGTGGATAACTGCCCCAGCAACTGCTATGGCAATGGTACTGCATC	1765						
Db	1678	ATTGTTATAGAGTCTGTGGTGGAAATGCCCCGAAATTGCCATGGAAATGGAGAATGCGTT	1737						
QY	1766	TCTGGACCTGCCACTGCTTCTGGGTTTCTGGGCCCGACTGTGGCAGAGCCTCCTGC	1825						
Db	1738	TCAGAACTTGCCATTGTTTCCAGGATTTCTGGGTCCGATTTGTTCAAGAGCCCGCTGT	1797						
QY	1826	CCGTGCTCTGTAGCGGAAATGGCCAATACATGAAGGCAGATGCTTGTGCCACAGTGGC	1885						
Db	1798	CCAGTTTATGTAGTGGCAACGGGCAGTACTCCAAGGCCGCTGCCTGTGTTTCAGCGGC	1857						
QY	1886	TGAAAGGCGCTGAGTGCATGTGCCCAACCAACCAAGTGTATCGATGTGGCTGCAGCAAC	1945						
Db	1858	TGAAAGGCGCACCGAGTGTGATGTCCCGACTACCCAGTGTATTGACCCACAGTGTGGGGT	1917						
QY	1946	CATGGCACCTGCATCACGGGCACCTGCATCTGCAACCCCTGGCTACAAGGCGGAGAGCTGT	2005						
Db	1918	CGTGGATTGTATCATGGGCTCCTGTGCTTTCAGCTCAGGATACAAAGGAGAAAGTTGT	1977						





Db 4138 GTTGACCAAAATGGAATCATATCAACTCTTCTGGGCTCTAACGATTTGACTTCAGCCAGA 4197

QY 4208 CCACTCAGCTGTGATTCTGTCAATGGATATTTCCAGGTAAGACTGGAGTGGCCACAGAC 4267

Db 4198 CTTTAACTTGTGACACCAGCATGCACATCAGCCAGGTACGTCCTGGAATGGCCACCTGAC 4257

QY 4268 TTAGCCATCAACCCAAATGGACAACTCACTTTATGTCTCTGACAAACAATGTGGTCTTGCAA 4327

Db 4258 CTAGCCATTAAACCTTATGGATAACTCCATTATGTCTCTGGATAAATAGTTTACAG 4317

QY 4328 ATCTCTGAATAACCAACAGGTGCGCATTTGTCCGGAGGCCCATCCACGCAACCTTGGAGTCAGCCACC 4387

Db 4318 ATCACTGAAAAATCGTCAAAGTTCGCAATTGCTGTGGACGGCCCATGCACGTGTCAAGGTTCCC 4377

QY 4388 GGCATTGACCACTTCCTGTCTAAGCAAGGTGGCCATCCACGCAACCTTGGAGTCAGCCACC 4447

Db 4378 GGAGTGG---AATATCCTGTGGGAAGCACGCGGTGCAGACAACACTTGAATCAGCCACT 4434

QY 4448 GCTTTGGCTGTTTACACAAATGGGGTCTGTATATTGCTGAGACTGATGAGAAAAAGATC 4507

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QY 4508 AACCGCATCAGGCAGGTCAACCACCTAGTGGAGAGATCTCACTCGTTGCTGGGGCCCCCAGT 4567

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QY 4568 GGCTGTGACTGTAAAAATGATGCCAACTGTGATTGTTTCTGGAGACGATGGTTATGCC 4627

Db 4555 GAGTGTGACTGCAAAAATGATGCCAACTGTGACTGTTACCAGAGTGGAGATGGCTACGCC 4614

QY 4628 AAGGATGCAAAAGTTAAATACCCCATCTTCTTGGCTGTGTGCTGATGGGAGCTCTAC 4687

Db 4615 AAGGATGCCAAACTCAGTGCCCCCATCTCCTGGCTGTCTCCAGATGGTACACTGTAT 4674

QY 4688 GTGGCCGACCTTGGGAACATCCGAATTCGGTTTATCCGGAAGAACAAAGCCTTTCCTCAAC 4747

Db 4675 ATTGCAGATCTAGGGAAATATCCGGATCCGGGCTGTGTCAAAGAAATAAGCCTTTACTTAAC 4734

QY 4748 ACCCAGAACATGTATGAGCTGTCTTACCAATTTGACCAGGAGCTCTATCTGTTTGATACC 4807

Db 4735 TCTATGAACCTTCTATGAAGTTGCGTCTCCAACCTGATCAAGAACCTTACATCTTTGACATC 4794

QY 4808 ACCGGCAAGCACCTGTACACCCAAAGCCTGCCACAGSAGACTACCTGTACAACTTCACC 4867

Db 4795 AATGGTACTCACCAATATACTGTAAAGTTTAGTCACTGSGTATTACCTTTACAAATTTAGC 4854

QY 4868 TACACTGGGACGGCGACATCACTCATCACAGACACAAATGGCAACATGGTAAATGTC 4927

Db 4855 TACAGCAATGACAATGATATTACTGTCTGTGACAGACAGCAATGGCAACCCCTTAGAATT 4914

QY 4928 CGCCGAGACTCTACTGGGATGCCCTCTGGCTGGTGGTCCCAGATGGCCAGGTGTACTGG 4987

Db 4915 AGACGGGACCCAAATCGCATGCCAGTTCGAGTGGTGTCTCCTGTATAACCAAGTATATGG 4974

QY 4988 GTGACCATGGGCACCAACAGTGCACTCAAGAGTGTGACCACACAAGGACACGAGTTGGCC 5047

Db 4975 TTGACAAATAGGAACAAATGGATGTTTGAAGGCAATGACTGCTCAAGGACTTGAATTAGTT 5034

QY 5048 ATGATGACATACCATGGCAATTCGGCCTTCTGGCAACCAAAAGCAATGAAAACGGATGG 5107

Db 5035 TTGTTTACTTACCATGGCAATAGTGGCCTTTTAGCCACTAAAAGTGTAGAACTGGATGG 5094

QY 5108 ACAACATTTTATGAGTACGACAGCTTTGGCCGCTGACAAATGTGACCTTCCCTACTGGC 5167

Db 5095 ACAACGTTTTTTGACTATGACAGTGAAGGTGCTGTGACAAATGTTACGTTTCCAACCTGA 5154

QY 5168 CAGGTGAGCAGTTTCCGAAGTGATACAGACAGTTTCAGTGCATGTCCAGGTAGAGACCTCC 5227

Db 5155 GTGGTCACAAACCTGCATGGGACATGGACAAGGCTATCAAGTGGACATGAGTCATCT 5214

QY 5228 AGC--AAGGATGATGTCAACCAATACCAACCAACCTGTCTGCCTCAGGGCCCTTCTACACA 5284

Db 5215 AGCCGAGAAGAAGATGTGAGCATCACTTCAATCTGTCTCGATCGATTCTTCTACACC 5274

QY 5285 CTGCTGCAAGACCAAGTCCGGAAACAGCTACTATACATCGGGCCGATGGCTCCTTGGGCTG 5344

Db 5275 ATGGTTCAAGATCAGTTAAGAAACAGCTACAGATTGGTTATGACGGCTCCCTCAGAATT 5334

QY 5345 CTGCTGGCCAAACGSCATGGAGGTGGCGCTGCAGACTGAGCCCCACTTGTGGCTGGCACC 5404

Db 5335 ATCTACGCCAGTGGCTGGACTCACACTACCAAAACAGAGCCGCACGTTCTGGCTGGCACC 5394

QY 5405 GTCAACCCCAACCGTGGGCAAGAGGAATGTACGCTGCCCATCGACAACGGCCTCAACCTG 5464

Db 5395 GCTAATCCGACCGTTGCCAAAAGAAACATGACTTTGCCCTGGCGAGAACGGTCAAAACTTG 5454

QY 5465 GTGGAGTGGCCAGCGCAAGAGAGAGGCTCGGGGCCAGGTCACTGTCTTTTGGGCGCCGG 5524

Db 5455 GTGGAATGGAGATTCCGAAAAGAGCAAGCCCAAGGGAAAGTCAATGTCTTTGGCCGCAAG 5514

QY 5525 CTGCGGTTGCAAAACCGAAATCTCCTATCTCTGGACTTTTGATCGGTFAAACACGACAGAG 5584

Db 5515 CTCAGGGTTAATGGCAGAAACCTCCTTTCAGTTGACTTTGATCGAAACAACAAAGACAGAA 5574

QY 5585 AAGATCTATGATGACCAACCGCAAGTTTCAACCTTTCGGATTCTGTACACAGCGGGGCGG 5644

Db 5575 AAGATCTATGACGACCAACCGTAAATTTCTACTGAGGATCGCCTACGACACGCTCTGGGCAC 5634

QY 5645 CCCAGCCTCTGGTCAACCCAGCAGCAGSGCTGAATGGTGTCAACGTTGACATACTCCCCCTGG 5704

Db 5635 CCGACTCTCTGGCTGCCAAGCAGCAAGCTGATGGCCGTCAATGTACCTATTCTATCCACA 5694

QY 5705 GGTTACATTGCTGGCATCCAGAGGGGSCATCATGTCTGAAAGAATGGAATACGACCAGGCG 5764

Db 5695 GGTCAAATTGCCAGCATCCAGCGAGGCAACCACTAGCGAGAAAAGTAGATTATGACGGACAG 5754

QY 5765 GGCCGCATCACATCCAGGATCTTCGCTGATGGGAAGACATGGAGCTACACATACTTAGAG 5824

Db 5755 GGGAGGATCGTGTCTCGGGTCTTTGCTGATGGTAAAAACATGGAGTTACACATATTTAGAA 5814

QY 5825 AAGTCCATGGTGTCTACTACACAGCCAGAGGCAGTATATCTTTGAGTTTCGACAAAGAT 5884

Db 5815 AAGTCCATGGTCTTCTGCTTCATAGCCAGCGGCAGTACATCTTCGAATACGATATGTGG 5874

QY 5885 GACCGCCTCTCTTCTGTGACGATGCCAAACGTGGCGCGGACACACTAGAGACCATCCGC 5944

Db 5875 GACCGCCTGTCTGCCATCACCATGCCAGTGTGGCTCGCCACACCATGCAGACCATCCGA 5934

QY 5945 TCAGTGGGCTACTACAGAAACATCTATCAGCCCCCTGAGGGCAATGCCCTCAGTCATACAG 6004

Db 5935 TCCATTGGCTACTACCGCAACATATACAACCCCGGAAAGCAACGCTTCCATCATCACG 5994

QY 6005 GACTTCACTGAGGATGGGCACCTCTCTTACACCTTCTACCTGGGCACGTGGCCGAGGGTG 6064

Db 5995 GACTACAACGAGGAAGGGCTGCTTCTACAACACAGCTTTCTTGGGTACAAGTCGAGGGGTC 6054

QY 6065 ATATACAAGTATGGCAAACCTGTCAAAGCTGGCAGAGACGCTCTATGACACCACCAAGTTC 6124

Db 6055 TTATTCAAATACAGAAAGGCAGACTAGGCTCTCAGAAATTTTATATGATAGCACAAGATC 6114

QY 6125 AGTTTCACTTATGACGAGACGGCAGGCATGCTGAAGACCACTAACCTACAGAATGAGGGC 6184

Db 6115 AGTTTACCTATGATGAACACAGCAGGAGTCTTAAAGACAGTAAACCTCCAGAGTGTGGT 6174

QY 6185 TTCACCTGCACCATCCGCTACCGTCAGATTGGGCCCCCTGATTTGACCGACAGATCTTCCGC 6244

Db 6175 TTTATTTGCACCATTAGATACAGGCAAAATGGTCCCCCTGATTTGACAGGAGATTTTCCGC 6234

QY 6245 TTCACTGAGGAAGGCATGGTCAACGCGCCCGTTTTTGACTACAACATATGACAACAGCTTCCG 6304

Db 6235 TTTAGTGAAGATGGGATGGTAAATGCAAGATTTGACTATAGCTATGACAACAGCTTTTCCA 6294

QY 6305 GTGACAGCATGCAGGCTGTGATCAACGAGACCCCACTGCCCCATTGATCTCTATCGCTAT 6364

Db 6295 GTGACCAGCATGCAGGGTGTGATCAATGAAACGCGCACTGCCATTGATCTGTATCAGTTT 6354



Qy	6365	GATGATGTGTCAAGGCAAGACAGAGCAGTTTGGAAAGTTTGGTGTCTATTTACTATGACATT	6424
Db	6355	GATGACATTTCTGGCAAAAGTTGAGCAGTTTGGAAAGTTTGGAGTTATATATATATGATATT	6414
Qy	6425	AACCAGATCATCACACAGCTGTCTATGACCCACACCAAGCATTTTGTATGCATATGGCAGG	6484
Db	6415	AACCAGATCATTTCTACAGCTGTAATGACCTTATACGAAGCACTTTGTATGCTCATGGCCGT	6474
Qy	6485	ATGAAGGAAGTCAGTATGAGATCTTCCGCTCGCTCATGTACTGGATGACCGTCCAGTAT	6544
Db	6475	ATCAAGGAGATTCAATATGAGATATTTCAGGTCTGCTCATGTACTGGATTACAAATTCAGTAT	6534
Qy	6545	GATAACATGGGCGAGTAGTGAAGAAAGGAGCTGAAGGTAGGACCTTACGCCAATACCACT	6604
Db	6535	GATAACATGGGTGGGTAAACCAAGAGAGAGATTAAAAATAGGGCCCTTTTGCCAACACCACC	6594
Qy	6605	CGCTACTCTATGAGTATGATGCTGACGGCCAGCTGCAGACAGTCTCCATCAATGACAAG	6664
Db	6595	AAATATGCTTATGAATATGATGTTGATGGACAGCTCCAAACAGTTTACCTCAATGAAAAG	6654
Qy	6665	CCACTCTGGCGCTACAGCTACGACCTCAATGGGAACCTGCACCTTACTGAGCCCTGGGAAC	6724
Db	6655	ATAATGTGGCGGTACAACCTACGATCTGAATGGAAACCTCCATTTACTGAACCCAAAGTAAC	6714
Qy	6725	AGTGACGGGTACACACCACTACCGTATGACATCCGGACCGCATCACTCGGCTGGGTGAC	6784
Db	6715	AGTGCGGTCTGACACCCCTTCGCTATGACCTGCGAGACAGAAATCACTCGACTGGGTGAT	6774
Qy	6785	GTGCAATACAAAGATGGATGAGGATGGCTTCTGAGGCAGCGGGCGGTGATATCTTTGAG	6844
Db	6775	GTTCAATATCGGTGGATGAAGATGGTTTCTTACGTCAAAGGGGCACGGAATCTTTGAA	6834
Qy	6845	TACAACTCAGCTGGCCTGCTCATCAAGGCCTCAACCGGGCTGGCAGCTGGAGTGTCAAG	6904
Db	6835	TATAGCTCCAAGGGCTTCTAACTCGAGTTTACAGTAAAGGCAGTGGCTGGACAGTGTATC	6894
Qy	6905	TACCGCTACGATGGCCTGGGGCGCGCGTGTCCAGCAAGAGCAGCCACAGCCACCCTG	6964
Db	6895	TACCGTTATGACGGCCTGGGAAGGCGTGTCTTAGCAAAACCAGTCTAGGACAGCACCTG	6954
Qy	6965	CAGTTCTTCTATGCAGACCTGACCAACCCACCAAGGTCAACCCCTGTACAACCACTCC	7024
Db	6955	CAGTTTTTTTATGCTGACTTAACTTATCCCACTAGGATTAATCATGTCTACAACCACTCG	7014
Qy	7025	AGCTCTGAGATCACCTCCCTCTACTACGACTTGCAGGACACACCTCTTTGCCATGGAGCTG	7084
Db	7015	AGTTCAGAAATTAACTCCCTGTATTATGATCTCCAAGGACATCTTTTGGCAATGGAAATC	7074
Qy	7085	AGCAGTGGTATGAGTTTATCATAGCTTGTGACAAATCGGGACCCCTCTTGTGTCTTTT	7144
Db	7075	AGCAGTGGGATGAATTTCTATATTGCATCGGATAACACAGGGACACCACCTGGCTGTGTTC	7134
Qy	7145	AGTGAACACAGTTTGTATGATCAAGCAAAATCCTGTACACAGCCCTATGGGGAGATCTACATG	7204
Db	7135	AGTAGCAATGGGCTTATGCTGAAACAGATTTCAGTACACTGCATATGGGGAAATCTATTTT	7194
Qy	7205	GATACCAACCCCAACTTTTCAGATCATATAGGCTACCATTGGTGGCCTCTATGATCCACTC	7264
Db	7195	GACTCTAATATTGACTTTCAACTGGTAATTGGATTTCATGGTGGCCTGTATGACCCACTC	7254
Qy	7265	ACCAAGCTTGTCCACATGGGCGCGGAGATTATGATGTCTGGCCGAGCGCTGGACTAGC	7324
Db	7255	ACCAATTAATCCACTTTGGAGAAAGAGATTATGACATTTTGGCAGGACGGTGGCAACA	7314
Qy	7325	CCAGACCACGAGCTGTGGAAGCACCTTAGTAGCAAGCAAGTCAATGCTTTTAACTCTAT	7384
Db	7315	CCTGACATAGAAATCTGGA--AAAGAAATTGGGAAGGACCCAGCTCCTTTTAACTGTAC	7371
Qy	7385	ATGTTCAAAAAACAACACCCCATCAGCAACTCCCAGGACATCAAGTGTCTCATGACAGAT	7444
Db	7372	ATGTTTAGGAATAACAACCCCTGCAAGCAAAATCCATGAGGTGAAAGATTACATCAAGAT	7431
Qy	7445	GTTAACAGCTGGTGTCTACCTTTTGGATTCCAGCTACACAACGCTGATCCCTGGTTATCCC	7504

Db	7432	GTTAACAGCTGGCTGGTGACATTTGGTTTCCATCTGCACAATGCTATTCTCTGGATTCCCT	7491
QY	7505	AAACCAGACATGGATGCCATGGAACCTCTCTACGAGCTCATCCACACACAGATGAAAACG	7564
Db	7492	GTTCCCAAAATTGATTAAACAGAACCTTCTTACGA-----ACTTGTGAAGAGT	7539
QY	7565	CAGGAGTGGACAAACAGCAAGTCTATCCTCGGGGTACAGTGTGAAGTACAGAAGCAGCTC	7624
Db	7540	CAGCAGTGGGATGATATACCGCCCATCTTCGGAGTCCAGCAGCAAGTGGCGCGCAGGCC	7599
QY	7625	AAGGCCTTTGTACCTTTAGAACGGTTTGACCAGCTCTATGGCTCCACAATCACAGCTGC	7684
Db	7600	AAGGCCTTTCTGTTCGTGGGGAAGATGGCGGAGGTGCAGGTGAGCGCGCCGGCCGGC	7659
QY	7685	CAGCAGGCTCCAAAGACCAAGAAGTTTGATCCAGCGGCTCAGTCTTTGGCAAGGGGGTC	7744
Db	7660	---GGCGCGCAGTCTTGGCTGTGGTTGCGCACCGTCAAGTCGCTGATCGGCAAGGGCGTC	7716
QY	7745	AAGTTTGCCTTGAAGGATGGCCGAGTGACCACAGACATCATCAGTGTGSCCAATGAGGAT	7804
Db	7717	ATGCTGGCCGTCAGCCAGGGCCGCGTGACAGACCAACGTGCTCAACATCGCCAACGAGGAC	7776
QY	7805	GGCGAAGGTTGCTGCCATCTTTGAACCATGCCCCACTACCTAGAGAACCTTGCACCTTCAAC	7864
Db	7777	TGCATCAAGGTGGCGGCCGTGCTCAACAACGCCCTTCTACCTGGAGAACCTGCACTTCAAC	7836
QY	7865	ATTGATGGGTGGATACCCATTACTTTGTGAAACCATGCCCCACTTTCAGAGGTGACCTGGCC	7924
Db	7837	ATCAGAGGCAAGGACACGCACACTACTTTCATCAAGACCACCAACGCCCGAGAGGACCTGGGC	7896
QY	7925	ATCCTGGGCCCTCAGTGGGGGCGGCGAACCCTTGAGAAATGGGGTCAACGTCACTGTGTCC	7984
Db	7897	ACGCTGCGGTTGACCAAGCGGCCGCAAGCGCTGGAGAACGGCATCAACGTGACGGTGTGCG	7956
QY	7985	CAGATCAACACAGTACTTAATGGCAGGACTAGACGCTACACAGACATCCAGCTCCAGTAC	8044
Db	7957	CAGTCCACCACGGTGGTGAAACGGCAGGACCGCCAGGTTTCGCGGACGTGGAGATGCAGTTC	8016
QY	8045	GGGCACTGTGCTTGAAACACACGCTACGGGACAACTGTGGATGAGGAGAAAGCACGGGTC	8104
Db	8017	GGCGCGCTGGCGTGCACGTGCGCTACGGCATGACCTTGGACGAGGAGAAAGCGCGCATC	8076
QY	8105	CTGGAGCTGCCCGGCAGAGAGCCGTGCGCAAGCGTGGGCCCGCGAGCAGCAGAGACTG	8164
Db	8077	CTGGAGCAGGCGCGCAGCGCGCTCGCCCGGGCCCTGGCGCGCGAGCAGCAGCGCGTG	8136
QY	8165	CGGGAAGGGAGGAAGCCCTGCGGGCCCTGGACAGAGGGGAGAAAGCAGCAGGTGCTGAGC	8224
Db	8137	CGCGACGGCAGGAGGGCGCGCCCTCTGGACGGAGGGCGAGAAAGCGGACGCTGCTGAGC	8196
QY	8225	ACAGGGCGGTGCAAGGCTACGACGGCTTTTTCGTGATCTCTGTGAGCAGTACCCAGAA	8284
Db	8197	GCCGGCAAGGTGCAGGGCTACGACGGGTACTACGTACTCTCGGTGGAGCAGTACCCCGAG	8256
QY	8285	CTGTCAGACAGCGCCAAACAACATCCACTTTCATGAGACAGAGCGAGATGGGCGGAGGTGA	8344
Db	8257	CTGGCCGACAGCGCCAAACAACATCCAGTTCTCGGCGCAGAGCGGAGATCGGCGAGGAGTAA	8316
QY	8345	C	8345
Db	8317	C	8317

RESULT 4  
US-11-096-051-7  
; Sequence 7, Application US/11096051  
; Publication No. US20050244868A1  
; GENERAL INFORMATION:  
; APPLICANT: Kekuda, Ramesh  
; APPLICANT: Maclachlan, Timothy K  
; APPLICANT: Rastelli, Luca  
; APPLICANT: Vernet, Corine



; APPLICANT: Ettenberg, Seth
; TITLE OF INVENTION: Ten-M3 Polypeptides and Polynucleotides and their Methods of Use
; FILE REFERENCE: Attorney Docket No. Cura 967
; CURRENT APPLICATION NUMBER: US/11/096,051
; CURRENT FILING DATE: 2005-03-30
; PRIOR APPLICATION NUMBER: 10/038,854
; PRIOR FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 10/455,772
; PRIOR FILING DATE: 2003-06-04
; PRIOR APPLICATION NUMBER: 60/557,978
; PRIOR FILING DATE: 2004-03-30
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: CuraseqList version 0.1
; SEQ ID NO 7
; LENGTH: 8657
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (151)..(8325)
US-11-096-051-7

Query Match 41.6%; Score 3473.8; DB 9; Length 8657;
Best Local Similarity 65.2%; Pred. No. 0;
Matches 5445; Conservative 0; Mismatches 2692; Indels 216; Gaps 14;

QY 35 ATGGACGTGAAGGAGAGGAAGCCCTTACCGCTCGCTGACCCGGCGC---CGCGACGCCGAG 91
Db ||||| ||||| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
151 ATGGATGTGAAGAAGCAGCAGGCCCTTACTGCTCCCTGACCAAGAGCAGACGAGAGAAGAA 210

QY 92 CGCCGCTACACCAGCTCGTCCGGGACAGCGAGGAGGGGCAAAG---CCCCGAGAAATCG 148
Db ||||| ||||| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
211 CGCGCTTACACAAATTCTCCGCAGACAAATGAGGAGTGCGGGTACCCACACAGAAGTCC 270

QY 149 TACAGCTCCAGCGAGACCCCTGAAGCCCTACGACCAGGA---CGCCCGCCTAGCCTATGGC 205
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
271 TACAGTTCCAGCGAGACATTGAAAGCTTTTGATCATGATTCCTCGCGGCTGCTTTACGGC 330

QY 206 AGCCCGCTCAAGGACATTGTGCGCAGGAGGCCGAGGAATTTCTCCGCACAGGTGCCAAC 265
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
331 AACAGATGAAGGATTTGGTTACAGAGAAGCAGACGAGTTCACTAGACAAGGACAGAAT 390

QY 266 TTCACCTGCGGGAGCTGGGGCTGGAAGAAGTAACGCCCCCTCACGGGACCCCTGTACCGG 325
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
391 TTTACCTTAAGGCAGTTAGGAGTTGTGAACCAAGCAACTCGAAGAGGACTGGSATTTGT 450

QY 326 ACAGACATTGGCCTGCCCCAAATGCGGCTACTCCATGSGGGCTGGCTCTGATGCGACATG 385
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
451 GCGGAAATGGGCTCCCTCAAGAGTTACTCTATCAGTGCAGGGTCAGATGCTGATACT 510

QY 386 GAGGTGACACGGTGTCTCCCTGAGCACCCCGTGGTCTGTGGGGCCCGGAGCACACGG 445
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
511 GAAATGAAGCAGTGATGTCCCAGAGCATGCCATGAGACTTTGGGGCAGGGGGTCAA 570

QY 446 TCAGGGCGCAGCTCCTGCCTGTCCAGCCGGGCCAATTCCAATCTCACACTCACCCGACACC 505
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
571 TCAGCCGCAGCTCCTGCCTGTCAAGTCCGTTCCAACTCAGCCCTCACCCCTGACAGATACG 630

QY 506 GAGCATGAAAACACTGAGACTGATCATCCGGCGGCTGCAGAACCAACGCGGGCTCCCGG 565
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
631 GAGCAGAAAACAAGTCCGACAGTGAGAAATGAGCAACTGCAAGCAATCAAGGCCAGTCT 690

QY 566 AGCCCGCGCCGCGCTCTGCGACGCCACACCCCAACCAACGACCAACGCGGCTCCATT 625
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
691 ACCGTGCAGCCCTTGCCGCTTCCCATAGCAGCACTCTGCACAGCATCATCCATCCATC 750

QY 626 AACTCCCTGAACCGGGCAACTTCACGCCGAGGAGCAACCCCAAGCCCGCCCGCCACGGAC 685
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
751 ACTTCTCTCAACAGAAACTCCCTGACCAATAGAGGAACCAAGTCCGGCCCCCGCGCT 810

QY 686 CACTCGCTCTCCGGAGAGCCCCCTGCCGGCGGCCAGGAGCCTGCCACGCCCGCCAGGAG 745
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
811 GCTTTGCCCGCCGAGCTGCAAAAC-----CACACCCGAGTCCGTCCAGCTGCAGGAC 861

QY 746 AACTGGCTGCTCAACAGCAACATCCCCCTTGAGACCAGGAACCTAGGCAAGCAGCCATTC 805
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
862 AGCTGGGTCCCTTGGCAGTAATGTACCACCTGGAAGCAGGCATTT----- 905

QY 806 CTAGGGACATTGCAGGACAACCTCATTTGAGATGGACATTTCTCGGCGCCTCCCGCCATGAT 865
Db ----- 905

QY 866 GGGGCTTACAGTGACGGGCACCTTCTCTTTCAAGCCCTGGAGGCACCTCCCCGCTCTTCTGC 925
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
906 -----CCTATTCAAACAAGAACAGGTACAAAGCCACTGTTTCAGT 945

QY 926 ACCACATCACAGGGTACCCCATGACGTCCAGCACAGTGTACTCTCTCCGCCCGCCGACCC 985
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
946 ACTGCAACCCCGAGGATACACAATGGCATCTGGCTCTGTTTATTACCACTACTCTCGCCA 1005

QY 986 CTGCCCCGAGCACCTTTCGCCCGCGCGCTTTAAACCTCAAGAAAGCCCTCCAAGTACTGT 1045
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1006 CTACCTAGAAACACCCCTATCAAGAAAGTGTCTTTAAATTCGAAGAGTCTTCAAAGTACTGT 1065

QY 1046 AACTGGAAGTGCAGCCCTGAGCGCCATCGTCATCTCAGCCACTCTGGTTCATCTCTGCTG 1105
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1066 AGCTGGAATGCATGCATGTGTCCGTAGGGTCTCGGTGCTCTCGGCAATACTCCTG 1125

QY 1106 GCATACCTTTGGCCATGCACCTGTTTGGCCCTAAACTGGCACCTTGCCACCCGATGGAGGGG 1165
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1126 TCTTATTTTATAGCAATGCATCTCTTTGGCCCTCAACTGGCAGCTACAGCAGACTGAAAT 1185

QY 1166 CAGATGTATGAGATCACGGAGGACACAGCCAGCAGTTGGCCCTGTGCCAACCCGACGTCTCC 1225
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1186 GACACATTTGAGA-----ATGGAAGAGTGAATCTGTATACCATGCCAACAAACACTGTG 1239

QY 1226 CTATACCCCTCAGGGGGCACTGGCTTAGAGACCCCTGACAGGAAGCAAGCAACCA 1285
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1240 TCATTACCTTCTGGAGACA----- 1258

QY 1286 GAAGGAAAGCCCAGTAGTTTCTTTCCAGAGGACAGTTCATAGATTTCTGGAGAAATTGAT 1345
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1259 -ATGGAATAATTAGGTGGATTTACGCAAGAAAAATAACCAATAGATTCGGAGAACTTGAT 1317

QY 1346 GTGGGAAGCGGAGCCTCCAGAAAGATTCCTCTGGCAATTTCTGGAGATCTCAAGTGTTC 1405
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1318 ATTGGCCGAAGAGCAATTCAAGAGATTCCTCCGGGATCTTCTGGAGATCACAGCTCTTC 1377

QY 1406 ATAGACCATCTGTGCATCTGAAATCAATGTGTCTCTGGGAAGGAGCCTGTGTTGGC 1465
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1378 ATTGATCAGCCACAGTTTCTTAAATTCATATCTCTCTCAGAAAGGATGCATTTGATTGGA 1437

QY 1466 ATTTATGCGAGAAAAGGCCCTCCCTCTTCACATA-----CACAGTTTGACTTT 1513
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1438 GTATATGCGCGGAAGAAGTTACCGCTTCCCATACTCAGTCTCTCCCCCAGTATGACTTC 1497

QY 1514 GTGAGCTGCTGGATGGCAGGAGGCTCCTAACCCAGGAGCGCGGAGCCTAGAGGGGACC 1573
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1498 GTGGAGCTCCTGGATGGCAGCAGGCTGATTGCCAGAGAGCAGCGGAGCCTGCTTGAGACG 1557

QY 1574 CCGGCCAGTCTCGGGGAACGTGTGCCCCCTCCAGCCATGAGACAGGCTTCATCCAGTAT 1633
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1558 GAGAGAGCCGGCGGCAGGCAGATCCGTACGCCCTTCATGAGCCCGGCTTTATCCAGTAC 1617

QY 1634 TTGGATTCAGGAATCTGGCACTTGGCTTTTTCATCAATGACGGAAGGAGTCAAGAGTGGTT 1693
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1618 TTGGATTCGGAATCTGGCATCTGGCTTTTATAATATGAGGAAAAAATGCAGAGCAGGTG 1677

QY 1694 TCCTTTCTCACCACTGCCATTCAGTTCGGTGGATTAACCTGCCCGCAGCAACTGCTATGGCAAT 1753
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1678 TCTTTTAATACCATTTGTTATAGAGTCTGTGGTGAATGTCCCCGAAATTGCCATGGAAT 1737

QY 1754 GGTGACTGCATCTCTGGGACCTGCCACTGCTTCTCTGGGTTTCTGGGCCCGACTGTGGC 1813
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1738 GGAGAAATGCGTTTCTGGAACCTGCCATTTGTTTCCAGGATTTCTGGGTCCGATTGTCA 1797

QY	1814	AGAGCCTCCTGCCCGTGCTCTGTAGCGGAAATGGCCAAATACATGAAAGGCAGATGCTTG	1877
DB	1798	AGAGCCGCCTGTCCAGTGTATGTAGTGGCAACGGGCAGTACTCCAAGGCGCTGCCTG	1857
QY	1874	TGCCACAGTGGCTGGAAAGCGCTGAGTGCAGTGTGCCCCACCACCAACCAAGTGTATCGATGTG	1933
DB	1858	TGTTTCAGCGGCTGGAAGGGCACCGAGTGTGATGTGCCGACTACCCAGTGTATTGACCCA	1917
QY	1934	GCCTGCAGCAACCATGGCACCTGCATCACGGGCACCTGCATCTGC AACCCCTGGCTACAAG	1993
DB	1918	CAGTGTGGGGTCTGGGATTTGTATCATGGGCTCTGTGCTTGCAGCTCAGGATACAAA	1977
QY	1994	GGCGAGAGCTGTGAGGAAGTGGACTGCATGGACGCCACACATGTTTCAGGCCGGGTGTCTGC	2053
DB	1978	GGAGAAAGTTGTGAAGAAAGCTGACTGTATAGACCCCTGGGTGTTCTAATCATGTGTGTGT	2037
QY	2054	GTGAGAGGCGAATGCCATTGCTTTGTGGGATGGGAGGCACCAACTCGCAGACCCCCCAGG	2113
DB	2038	ATCCACGGGGAATGTCACTGCAGTCCAGGATGGGAGGTAGCAATTGTGAAATACTGAAG	2097
QY	2114	GCCACATGCTTAGACCAGTGTTCAGGCCACCGGAACCTTCCTCCCGGACACCCGGCTTTGC	2173
DB	2098	ACCATGTGTCCAGACCAAGTGTCCGGCCACCGGAACGTATCTTCAAGAAAAGTGGCTCCTGC	2157
QY	2174	AGCTGTGACCCAAAGCTGGACTGGACACGACTGTTCTATCGAGATCTGTGCTGCCGACTGT	2233
DB	2158	ACGTGTGACCCCTAACTGGACTGGCCACGACTGCTCAAAACGAAATATGTTCTGTGGACTGT	2217
QY	2234	GGTGGCCATGGCGTGTCCGTAGGGGGCACCTGCCGCTGCGAGGATGGCTGGATGGGGCA	2293
DB	2218	GGCTCACACGGCGTTGCATGGGGGGGACGTGTCTGTGAAGAGGCTGGACGGGCCCA	2277
QY	2294	GCCTGCGACCAAGCGGCGCTGCCACCCGCGTGTGCCGAGCATGGGACCTGCCGCGACGGC	2353
DB	2278	GCCTGTAATCAGAGAGCCTGCCACCCCGCTGTGCCGAGCACGGGACCTGCAAGGATGGC	2337
QY	2354	AAGTGCAGTGCAGCCTGGCTGGAATGGCGAACACTGCACCATCGCTCACTATCTGGAT	2413
DB	2338	AAGTGTGAATGCAGCCAGGGCTGGAATGGAGAGCACTGCACATATCGCTCACTATTTGGAT	2397
QY	2414	AGGGTAGT-----TAAAGAGGGTTGCCCTGGGTTGTGCAATGGCAAC	2455
DB	2398	AAGATAGTTAAAGACAAGATAGGATATAAAGAGGGTTGTCTGCTGTGCAACAGCAAT	2457
QY	2456	GGCAGATGTACCTTAGACCTGAATGGTTGGCACTGCGTCTGCCAGCTGGGCTGGAGAGGA	2515
DB	2458	GGAAGATGTACCTGGACCACAAATGGCGGACATTGTGTGTGCCAGCCTGGATGGAGAGGA	2517
QY	2516	GCTGGCTGTGACACTTCCATGGAGACTGCCCTGCGGTGACAGCAAGACAATGATGGAGAT	2575
DB	2518	GCAGGCTGTGACGTAGCCATGGAGACTCTTTGCAAGATAGCAAGGACAATGAAGGGGAT	2577
QY	2576	GGCCTGGTGGACTGCATGGACCCCTGACTGCTGCCCTCAGGCCCTGTGCCATATCAACCCG	2635
DB	2578	GGACTCATTTGACTGCATGGATCCCGATTGCTGCTTACAGAGTTCTCTGCCAGAAATCAGCCC	2637
QY	2636	CTGTGCCCTTGGCTCCCTTAACCTCTGGACATCATCCAGGAGACACAGGTCCCTGTGTCA	2695
DB	2638	TATTGTCGGGACTGCCGGATCCTCAGGACATCATTAGCCAAAGCCTTCAATCGCCTTCT	2697
QY	2696	CAGCAGAACCTACACTCCTTCTATGACCGCATCAAGTTCCTCGTGGCAGGACAGCACG	2755
DB	2698	CAGCAAGCTGCCAAATCCTTTATGATCGAATCAGTTCTCTATAGGATCTGATAGCACC	2757
QY	2756	CACATAATCCCGGGGAGAACCCCTTTGATGGAGGGCATGCTTGTGTTATTCGTGSCCAA	2815
DB	2758	CATGTTATACCTGGAGAAAGTCTTTCAATAAGAGCCTTGCACTCTGTATCAGAGGCCAA	2817
QY	2816	GTGATGACATCAGATGGAAACCCCTCGTTGGTGTGAACATCAGTTTTTGTCAATAACCT	2875
DB	2818	GTACTGACTGCTGATGGAACTCCACTTATTGGAGTAAATGTCTCGTTTTTTCATTACCCA	2877
QY	2876	CTCTTTGGATATACAATCAGCAGGCAAGATGGCAGCTTTTGACTTGGTGACAAATGGCGGC	2935

Db	2878	GAATATGGATATACTATTACCCGCGGACGGAAATGTTTGACTTGGTGGCAAAATGGTGGG	2937
Qy	2936	ATCTCCATCATCTCGCGTTTCGAGCGGGCACCTTTTCATCACACAGGAGCACACCCCTGTGG	2995
Db	2938	GCCTCTCTAACTTTTGGTATTTGAACGATCCCCATTCCTCACTCAGTATCATACTGTGTGG	2997
Qy	2996	CTGCCATGGGATCGCTTCTTTGTTCATGGAAACCATCATCATGAGACATGAGGAGAAATGAG	3055
Db	2998	ATTCCATGGAATGTCTTTTATGTGATGGATACCCTAGTCCATGGAGAAAGAGAAATGAC	3057
Qy	3056	ATTCCAGCTGTGACCTGAGCAATTTTGCCCGCCCCCAACCCAGTCTGTCTCTCATCCCCCA	3115
Db	3058	ATTCCAGCTGTGATCTGTAGTGGATTTCGTGAGGCCAAATCCCATCATTTGTGTCTATCACCT	3117
Qy	3116	CTGAGCTCTTCGCCAGCTCCTGTGCAGAGAAAGGCCCCCATTTGTGCCGAAATTCAGGCT	3175
Db	3118	TTATCCACCTTTTTCAGATCTTCTCTGAAGACAGTCCCCTCATTTCCGAAACACAGGTA	3177
Qy	3176	TTGCAGGAGGAAATCTCTATCTCTGGCTCAAGATGAGGCTGAGCTACTCTGAGCAGCCGG	3235
Db	3178	CTCCAGGAGGAAACTACAAATCCAGGAACAGATTTGAAACTCTCCTACTTGAGTCCAGA	3237
Qy	3236	ACCCCTGGCTACAAATCTGTCTGAGGATCAGCCTCACCCACCCGACCATCCCTTCAAC	3295
Db	3238	GCTGCAGGTATAAGTCAGTTCTCAAGATCACCATGACCCAGTCTATTATTCCATTTAAT	3297
Qy	3296	CTCATGAAGGTGCACCTCATGGTAGCGGTGGAGGGCGCCCTCTTTCAGGAAGTGGTTGCT	3355
Db	3298	TTAATGAAGGTTCACTCTTATGGTAGCTGTAGTAGGAAGACTCTTCCAAAAGTGGTTTCT	3357
Qy	3356	GCAGCCCAGACCTGTCTATTATTTCATTTGGGACAAGACAGACGCTCTACAACCAAGAAG	3415
Db	3358	GCCTCACCAAACTTGGCCTATACCTTTCATATGGGATAAAAAAGATGCATATAATCAGAAA	3417
Qy	3416	GTGTTTGGGCTTTTCAGAAAGCCTTTGTTCGTGGGTATGAATATGAATCCTTGCCAGAT	3475
Db	3418	GTCTATGCTCTATCTGAAGCTGTTGTGTGAGTTGGATATGAGTATGAGTCGTGTTGGAC	3477
Qy	3476	CTAATCCTGTGGGAAAAAAGAACACAGTCGTGCAGGGCTATGAAATTCACGGCTCCAAG	3535
Db	3478	CTGACTCTGTGGGAAAAGAGGACTGCCATCTGCAGGGCTATGAATTTGGATGCGTCCAAC	3537
Qy	3536	CTTGGAGGATGGAGCCTAGACAAACATCATGCCCTCAACATTCAAAGTGGTATCCTGCAC	3595
Db	3538	ATGGTGGCTGGACATTAGATAAAACATCACGTCTGGATGTACAGAACGGTATACTGTAC	3597
Qy	3596	AAAGGGAATGGGAGAACCCAGTTTGTGTCTCAGCAGCCCTCCTGTCTATTTGGGAGCATCATG	3655
Db	3598	AAGGGAACGGGAAAAACCAGTTCACTCCAGCAGCCCTCCAGTCGTGAGTAGCATCATG	3657
Qy	3656	GGCAATGGGCGCGGAGAAGCATCTCCTGCCCCCAGCTGCAACGGCCTTGTGACGGCAAC	3715
Db	3658	GGCAATGGGCGAAGGCGCAGCATTTCTGCCCCAGTTGCAATGGTCAAGCTGATGGTAAC	3717
Qy	3716	AAGCTCTGGCCCCCAGTGGCCCTCACCTGTGGCTCTGACGGGAGCCTCTATGTGGGTGAT	3775
Db	3718	AAGTTACTGGCCCCCAGTGGCGCTAGCTTGTGGGATCGATGGCAGTCTGTACGTAGGCGAT	3777
Qy	3776	TTCAACTACATTAGAAGGATCTTCCCCTCTGGAAATGTCAACCAATCCTAGAGCTGAGG	3835
Db	3778	TTCAACTACGTGCGGCGGATATTCCCCTTCTGGAAATGTAAACAGTGTCTTAGAACTAAGA	3837
Qy	3836	AATAAAGATTTTCAGACATAGTCACAGTCCAGCACACAAAATACTACCTGGCCACAGACCCC	3895
Db	3838	AATAAAGATTTTAGACATAGCAGCAACCCAGCTCATAGATACTACCTTGCAACCGGATCCA	3897
Qy	3896	ATGAGTGGGCGCGTCTTCCTTTCTTGACGCAACAGCCGGCGGTCTTTAAAATCAAGTCC	3955
Db	3898	GTCACGGGAGATCTGTACGTTTCTTGACACAAACACCCGCAGAAATTTATCGCCCCAAAGTCA	3957
Qy	3956	ACTGTGGTGGTGAAGGACCTTGTCAAGAACTCTGAGGTGGTTGCGGGGACAGGTGACCAG	4015



Db 3958 CTTACGGGGCAAAAGACTTGACTAAAAATGCAGAAGTCGTGCGAGGGACAGGGAGCAA 4017

Qy 4016 TGCCTCCCTTTTGATGACACTCGCTGCGGGATGGTGGGAAGGCCACAGAAGCCACACTC 4075

Db 4018 TGCCTCCGTTTGACGAGCGGAGATGTGGGGATGGAGGAAGGCCGTGGAAGCCACACTC 4077

Qy 4076 ACCAATCCAGGGGTATTACAGTGGACAAAGTTTGGGCTGATCTACTTCGTGGATGGCACC 4135

Db 4078 ATGAGTCCCAAGGAATGGCAGTTGATAAGAAATGGATTAACTACTTTGTTGATGGAACC 4137

Qy 4136 ATGATCAGACGCATCGATCAGAAATGGGATCATCTCCACCCTGCTCGGCTCTAATGATCTC 4195

Db 4138 ATGATTAGGAAAGTTGACCAAAATGGAATCATATCAACTCTTCTGGGCTCTAACGATTTG 4197

Qy 4196 ACATCAGCCCGGCACTCAGCTGTGATTCTGTCTATGGATATTTCCAGGTAAGACTGGAG 4255

Db 4198 ACTTCAGCCAGACCTTTAACTTGTGACACAGCATGCACATCAGCAGGTACGTCGTGGAA 4257

Qy 4256 TGGCCACAGACTTAGCCATCAACCCAAATGGACAACTCACTTTATGTCTCTCGACAAACAT 4315

Db 4258 TGGCCCACTGACCTAGCCATTAAACCCCTATGGATAAATCCATTATGTCTCGGATAATAAT 4317

Qy 4316 GTGGTCTGCAAAATCTCTGAAAACCCACAGGTGCGCATTTGTCGCGGGAGGCCCATGCAC 4375

Db 4318 GTAGTTTTACAGATCACTGAAAATCGTCAAAGTTCGCATTGCTGTGGACGGCCCATGCAC 4377

Qy 4376 TGCCAGGTCCCTGGCATTGACCACCTTCTCTGCTAAGCAAAGGTGSCCATCCACGCAACCTTG 4435

Db 4378 TGTCAAGTTCCTGGAGTGG--AATATCCTGTGGGGAAGCACGCGGTGCAGACAACTG 4434

Qy 4436 GAGTCAGCCACCGCTTTGGCTGTTTTCAACAAATGGGTCCTGTATATTTGCTGAGACTGAT 4495

Db 4435 GAATCAGCCCACTGCCATTGCTGTCTCTACAGTGGGTCCTGTACATTACTGAAACTGAT 4494

Qy 4496 GAGAAAAAGATCAACCGCATCAGGCAGGTCAACCACCTAGTGGAGAGATCTCACTCGTTGCT 4555

Db 4495 GAGAAGAAAATTAAACCGGATAAGGCAGGTCAACAAGATGGAGAAATCTCCTTAGTGCC 4554

Qy 4556 GGGGCCCCCAGTGGCTGTGACTGTAAAAATGATGCCAACTGTGATTTGTTTTCTGGAGAC 4615

Db 4555 GGAATACCTTCAGAGTGTGACTGCAAAAATGATGCCAACTGTGACTGTTACCAGAGTGA 4614

Qy 4616 GATGGTTATGCCAAGGATGCAAAGTTAAATACCCCATCTTCCTTGGCTGTGTGCTGAT 4675

Db 4615 GATGGCTACGCCAAGGATGCCAACTCAGTGCCTCCATCCTCCTGGCTGCTTCTCCAGAT 4674

Qy 4676 GGGGAGCTCTACGTGGCCGACCTTGGGAACATCCGAAATCGGTTATCCGGAAGAACAAAG 4735

Db 4675 GGTACTGTATATTGCAGATCTAGGGAATATCCGGATCCGGCTGTGTCAAAAGAAATAAG 4734

Qy 4736 CTTTCTCTCAACACCCAGAACATGTATGAGCTGTCTTCAACCAATTTGACCAGGAGCTCTAT 4795

Db 4735 CTTTACTTAACTCTATGAACCTTCTATGAAGTTGCGTTCCTCAACTGATCAAGAACTCTAC 4794

Qy 4796 CTGTTTGATACACCGGCAAGCACTGTACACCCCAAAGCCTGCCCCACAGGAGACTACCTG 4855

Db 4795 ATCTTTGACATCAATGGTACTCACCATAATACTGTAAGTTTAGTCACTGGTGATTACCTT 4854

Qy 4856 TACAACCTTCACTACACTGGGACGGCGACATCACACTCATCACAGACAAACAAATGGCAAC 4915

Db 4855 TACAATTTTAGCTACAGCAATGACAAATGATATTACTGTCTGTGACAGACAGCAATGGCAAC 4914

Qy 4916 ATGTTAAATGTCCGCCGAGACTCTACTGGGATGCCCTCTGGCTGGTGGTCCAGATGGC 4975

Db 4915 ACCCTTAGAATTAGACGGGACCCAAATCGCATGCCAGTTCGAGTGGTGTCTCTCTGATAAC 4974

Qy 4976 CAGGTGTACTGGGTGACCAATGGGCA CCAACAGTGCACTCAAGAGTGTGACCACACAAGGA 5035

Db 4975 CAACTGATATGGTTGACAAATAGGAACAAATGGATGTTTGAAGGCATGACTGCTCAAGGA 5034

Qy 5036 CACGAGTTGGCCATGATGACATACCATGGCAATTCGGCCCTTCTGGCAACCAAAAGCAAT 5095

Db 5035 CTGGAATTAGTTTTGTTTACTTACCATGGCAATAGTGGCCCTTTTAGCCACTAAAAAGTGAT 5094

Qy 5096 GAAAAACGGATGGACAAACATTTTATGAGTACGACAGCTTTGGCCGCTTGACAAATGTGACC 5155

Db 5095 GAAACTGGATGGACAAACGTTTTTTGACTATGACAGTGAAGGTCGTCTGACAAATGTTACG 5154

Qy 5156 TTCCCTACTGSCCAGGTGAGCAGTTTCCGAAAGTGATACAGACAGTTTCAGTGCATGTCCAG 5215

Db 5155 TTTCCAACCTGGAGTGGTCACAAACCTGCATGGGACATGGACAAGGCTATACAGTGGAC 5214

Qy 5216 GTAGAGACCTCCAGC--AAGGATGATGTCAACATAACCAACCAACCTGTCTGCCTCAGGC 5272

Db 5215 ATTGAGTCATCTAGCCGAGAAAGATGTICAGCATCACTTCAAATCTGTCTCTCGATCGAT 5274

Qy 5273 GCCTTCTACACTGCTGCAAGACCAAGTCCGGAACAGCTACTACATCGGGGCCGATGGC 5332

Db 5275 TCTTTCTACACCATGGTTCAAGATCAGTTAAGAAAACAGCTACCAGATTGGTTATGACGGC 5334

Qy 5333 TCCTTGGGCTGCTGTGGCCAAACGGCATGGAGGTGGCGTGCAGACTGAGCCCCACATTG 5392

Db 5335 TCCCTCAGAAATTATCTAGCCAGTGGCCTGGACTCACACTACCAAAACAGAGCCGACGTT 5394

Qy 5393 CTGGCTGGCACCGTCAACCCACCGTGGCAAGAGGAATGTACCGTGCCTCCATCGACAAC 5452

Db 5395 CTGGCTGGCACCGCTAATCCGACGGTTGCCAAAAGAAAACATGACTTTGCCTGGCGAGAAC 5454

Qy 5453 GGCCTCAACCTGGTGGAGTGGCGCCAGCGCAAGAGCAGGCTCGSGGCCAGGTCACCTGTC 5512

Db 5455 GGTCAAAACCTGGTGAATGGAGATTCCGAAAAGAGCAAGCCCAAGGAAAAGTCAATGTC 5514

Qy 5513 TTTGGCGCGGCTGCGGCTGCACAAACCGAAATCTCCTATCTCTGGACTTTGATCGCGTA 5572

Db 5515 TTTGGCGCGAAGCTCAGGGTTAATGCGAGAAAACCTCCTTTTCAGTTGACTTTGATCGAACA 5574

Qy 5573 ACACGCCACAGAGAAGATCTATGATGACCACCGCAAGTTTCAACCTTCGGATTCTGTACGAC 5632

Db 5575 ACAAAGACAGAAAAGATCTATGACGACCACCGTAAATTTTCTACTGAGGATCGCCTACGAC 5634

Qy 5633 CAGGCGGGCGGCCAGCCTCTGTGTACCCAGCAGCAGGCTGAATGGTGTCAACGTGACA 5692

Db 5635 ACGTCTGGGCACCCGACTCTCTGGGTGCCAAGCAGCAAGCTGATGGCCGTCAATGTCAAC 5694

Qy 5693 TACTCCCTGGGGGTTACATTGTGGCATCCAGAGGGGTCATGTCTGAAAGAAATGGAA 5752

Db 5695 TATTCATCCACAGGTCAAATTTGCCAGCATCCAGCGAGGCCACTAGCGAGAAAAGTAGAT 5754

Qy 5753 TACGACCAAGCGGCGCGCATCATCCAGGATCTTCGTGATGGGAAGACATGGAGCTAC 5812

Db 5755 TATGACGGACAGGGGAGGATCGTGTCTCGGCTCTTTGTGATGGTAAACATGGAGTTAC 5814

Qy 5813 ACATACTTAGAGAAATCCATGGTGTCTACTACTACAGCCAGAGGCAGTATATCTTTGAG 5872

Db 5815 ACATAATTAGAAAAGTCCATGGTCTTCTGCTTCATAGCCAGCGCAGTACATCTTCGAA 5874

Qy 5873 TTCGACAAAGAAATGACCGCCTCTCTTCTGTGACGATGCCCAACGTGGCGCGGACACACTA 5932

Db 5875 TACGATATGTGGACCGCCTGTGCCATCACCATGCCAGTGTGGCTCGCCACACCATG 5934

Qy 5933 GAGACCATCCGCTCAGTGGGCTACTACAGAAAACATCTATCAGCCCCCTGAGGGCAATGCC 5992

Db 5935 CAGACCATCCGATCCATTTGGTACTACTCCGCAACATATACAACCCCCCGGAAAGCAACGCC 5994

Qy 5993 TCAGTCATACAGGACTTTCAGGATGGGCAACCTCTTTCACACCTTCTACCTGGGCACCT 6052

Db 5995 TCCATCATCAGGACTACACAGGAGGAAGGGCTGCTTCTACAAACAGCTTCTTGGGTACA 6054

Qy 6053 GGCGCAGGGTGATATACAGTATGGCAAACTGTCAAAGCTGGCAGAGACGCTCTATGAC 6112

Db 6055 AGTCGAGGGTCTTATTCAAATACAGAAGGCAGACTAGGCTCTCAGAAAATTTTATATGAT 6114

Qy 6113 ACCACCAAGGTCAGTTTTCACCTATGACGAGACGGCAGGCGATGCTGAAGACCATCAACCTA 6172

Db 6115 AGCACAAGAGTCAGTTTTTACCTATGATGAAACAGCAGGAGTCTCTAAGACAGTAAACCTC 6174





Db	8317	GGCAGGAGGTAAC	8329	
RESULT 5				
US-11-096-051-3				
; Sequence 3, Application US/11096051				
; Publication No. US20050244868A1				
; GENERAL INFORMATION:				
; APPLICANT: Kekuda, Ramesh				
; APPLICANT: MacLachlan, Timothy K				
; APPLICANT: Rastelli, Luca				
; APPLICANT: Vernet, Corine				
; APPLICANT: Ettenberg, Seth				
; TITLE OF INVENTION: Ten-M3 Polypeptides and Polynucleotides and their Methods of Use				
; FILE REFERENCE: Attorney Docket No. Cura 967				
; CURRENT APPLICATION NUMBER: US/11/096,051				
; CURRENT FILING DATE: 2005-03-30				
; PRIOR APPLICATION NUMBER: 10/038,854				
; PRIOR FILING DATE: 2001-12-31				
; PRIOR APPLICATION NUMBER: 10/455,772				
; PRIOR FILING DATE: 2003-06-04				
; PRIOR APPLICATION NUMBER: 60/557,978				
; PRIOR FILING DATE: 2004-03-30				
; NUMBER OF SEQ ID NOS: 38				
; SOFTWARE: CuraSeqList version 0.1				
; SEQ ID NO 3				
; LENGTH: 7786				
; TYPE: DNA				
; ORGANISM: Homo sapiens				
; FEATURE:				
; NAME/KEY: CDS				
; LOCATION: (476)..(7603)				
US-11-096-051-3				
Query Match 40.7%; Score 3396.4; DB 9; Length 7786;				
Best Local Similarity 68.1%; Pred. No. 0;				
Matches 4809; Conservative 0; Mismatches 2231; Indels 24; Gaps 5;				
QY	1287	AAGGAAAGCCAGTAGTTTCTTTCCAGAGGACAGTTTCCATAGATTCTGGAGAAATTGATG	1346	
Db	567	ATGGAATAATTAGGTGGATTACGCAAGAAAAATAACACCATAGATTCCGGAGAACTTGATA	626	
QY	1347	TGGGAAGCGGAGCCTCCAGAGAATTCTCTGGCACTTTCTGGAGATCTCAAGTGTTC	1406	
Db	627	TTGGCCGAAGAGCAATTCAAGAGATTCTCCCGGATCTTCTGGAGATCACAGCTCTTCA	686	
QY	1407	TAGACCATCCTGTGCATCTGAAATTCAATGTGTCTCTGGAAAGGCAGCCCTGGTTGGCA	1466	
Db	687	TTGATCAGCCACAGTTTCTTAAATTCAATACTCTCTTCAGAAGGATGCATTGATTGGAG	746	
QY	1467	TTTATGCGAGAAAGGCTCCCTCTCTTACATACACAGTTTGACTTTGTGGAGCTGCTGG	1526	
Db	747	TATATGCGGAAAGGCTTACCGCTTCCCATACTCAGTATGACTTCTGTGGAGCTCCTGG	806	
QY	1527	ATGGCAGAGGCTCCTAACCCAGGAGGCGGAGCCCTAGAGGGGACCCCGCCAGTCTC	1586	
Db	807	ATGGCAGAGGCTGATTGCCAGAGAGCAGCGGAGCCCTGCTTGAGACGGAGAGCCGGGC	866	
QY	1587	GGGGAAGTGTGCCCCCTCCAGCCATGAGACAGGTTTCATCCAGTATTTGGATTGAGAA	1646	
Db	867	GGCAGCGAGATCCGTACGCTTCATGAGCGCGGCTTATCCAGTACTTGGATTCTGGAA	926	
QY	1647	TCGGCACTTGGCTTTTACAAATGACGGAAAGGAGTCAGAAAGTGGTTTCTCTCACCA	1706	
Db	927	CTGGCATCTGGCTTTTATAATGATGGGAAAAATGCAGAGCAGGTGTCITTAAATACCA	986	
QY	1707	CTGCCATTGAGTCGGTGGATAACTGCCCCAGCACTGCTATGGCAATGGTGACTGCATCT	1766	
Db	987	TTGTTATAGAGTCTGTGGTGGAAATGTCCCCGAAATTGCCATGGAAATGGAGAATGCGTT	1046	
QY	1767	CTGGACCTGCCACTGCTTCCTGGTTTCTGGSCCCGACTGTGGCAGAGCCTCCTGCC	1826	
Db	1047	CTGGAACCTTGCCATTGTTTCCAGGATTCTCGGTCCGGATTGTTTCAAGAGCCGCTGTC	1106	

QY	1827	CCGTGCTCTGTAGCGGAAATGGCCAATACATGAAAGGCAGATGCTTGTGCCACAGTGGCT	1886	
Db	1107	CAGTGTATTGTAGTGGCAACGGGCAGTACTCCAAGGGCCGCTGCCTGTGTTCAGCGGCT	1166	
QY	1887	GGAAAGGCGCTGAGTGGCATGTGCCCAACCAACCAAGTGTATCGATGTGGCTGCAGCAACC	1946	
Db	1167	GGAAAGGCACCCAGTGTGTATGCCGACTACCCAGTGTATTGACCCACAGTGTGGGGTC	1226	
QY	1947	ATGGCACCTGCATCAGGGGCACCTGCATCTGCAACCTGGCTACAAGGGGAGAGCTGTG	2006	
Db	1227	GTGGGATTTGTATCATGGGCTCTTGTGCTTGCAACTCAGGATACAAAGGAGAAAGTTGTG	1286	
QY	2007	AGGAAGTGGACTGCATGGACCCACACATGTTCAGGCCGGGGTGTCTGCTGAGAGGCGAAT	2066	
Db	1287	AAGAAGCTGACTGTATAGACCCCTGGGTGTTCTAATCATGGTGTGTATCCACGGGAAT	1346	
QY	2067	GCCATTGCTTTGTGGGATGGGAGGCACCAACTCGAGACCCCCAGGSCACATGCTTAG	2126	
Db	1347	GTCACTGCAGTCCAGGATGGGAGGTAGCAATTGTGAAATACTGAAGACCATGTGTCCAG	1406	
QY	2127	ACCAGTGTTCAGSCCAGAACCTTCTCTCCGGACACCCGGGCTTTGCAGCTGTGACCCAA	2186	
Db	1407	ACCAGTGTCCGGCCACGGAACGTATCTTCAAGAAAGTGGTCTCTGCACGCTGTGACCTA	1466	
QY	2187	GCTGGACTGGACACGACTGTTTCTATCGAGATCTGTGCTGCCGACTGTGGTGGCCATGGCG	2246	
Db	1467	ACTGGACTGCCCCAGACTGCTCAACGAAATATGTTCTGTGGACTGTGGCTCACACGGCG	1526	
QY	2247	TGTGCGTAGGGGACCTGCCGCTGCCAGGATGGCTGGATGGGGCAGCCTGCGACCAGC	2306	
Db	1527	TTTGCAATGGGGGACGTGTCGCTGTGAAGAAAGCTGGACGGGCCAGCCTGTAATCAGA	1586	
QY	2307	GGGCTGCCACCCCGCTGTGCCGAGCATGGACCTGCCGCGACGGCAAGTGCAGTGCA	2366	
Db	1587	GAGCCTGCCACCCCGCTGTGCCGAGCAGCGGACCTGCAAGGATGGCAAGTGTGAATGCA	1646	
QY	2367	GCCCTGGCTGGAATGGCAACACTGCACCATCGCTCACTATCTGGATAGGGTAGTTAAAG	2426	
Db	1647	GCCAGGCTGGAATGGAGAGCACTGCACATATCGCTCACTATCGCTCACTATTGGATAAGATAGTTAAAG	1706	
QY	2427	AGGTTGCCCTGGTTGTCAATGGCAACGGCAGATGTACCTTAGACCTGAATGTTGGC	2486	
Db	1707	AGGTTGCTCTGGTCTGTGCAACAGCAATGGAAGATGTACCCCTGGACCAAAATGGCTGGC	1766	
QY	2487	ACTGCTCTGCCAGCTGGCTGGAGAGGAGCTGGCTGTGACACTTCCATGGAGACTGCCT	2546	
Db	1767	ATTGTGTGTCAGCCTGGATGGAGAGGAGCAGGCTGTGACGTAGCCATGGAGACTCTTT	1826	
QY	2547	GCGGTGACAGCAAAGACAAATGATGGAGATGGCCCTGGTGGACTGCATGGACCTGACTGCT	2606	
Db	1827	GCACAGATAGCAAGGACAAATGAAGGAGATGGACTCATTTGACTGCATGGACCCCGATTGCT	1886	
QY	2607	GCCTCCAGCCCTGTGCCATATCAACCCGCTGTGCCCTTGGCTCCCCTAACCTCTTGGACA	2666	
Db	1887	GCCTACAGAGTTCTTGCCAGAATCAGCCCTATTGTGCGGACTGCCGACCTCAGGACA	1946	
QY	2667	TCATCCAGGAGACACAGTTCCTGTGTACAGCAGAACTACACTCCTTCTATGACCGCA	2726	
Db	1947	TCATTAGCCAAAGCCTTCAATCGCCTTCTCAGCAAGCTGCCAAATCCTTTTATGATCGAA	2006	
QY	2727	TCAAGTTCCTCGTGGGAGGAGCAGCACATATAATCCCGGGGAGAACCCCTTTTGATG	2786	
Db	2007	TCAGTTTCTTATAGGATCTGATAGCACCCCATGTATACCTGGAGAAAGTCCCTTTCAATA	2066	
QY	2787	GAGGSCATGCTTGTGTTATTCTGTGGCCAAAGTATGATCATCAGATGGAACCCCTCGTTG	2846	
Db	2067	AGAGCCTTGCACTGTGCATCAGAGGCCAAGTACTGACTGCTGATGGAACCTCCACTTATG	2126	
QY	2847	GTGTGAACATCAGTTTTCGTAATAACCCCTCTCTTTGGATATACAATCAGCAGGCAAGATG	2906	
Db	2127	GAGTAAATGTCTCGTTTTTCCATTACCCAGAAATATGGATATACTATTACCCGCCAGGACG	2186	







Db 4344 ATAGTGGCCTTTTAGCCACATAAAAGTGATGAAACTGGATGGACAAACGTTTTTTTGACTATG 4403

Qy 5127 ACAGCTTTGGCGCCTGACAAATGTGACCTTCCCTACTGGCCAGGTGAGCAGTTTCCGAA 5186

Db 4404 ACAGTGAAGTGGTCTGACAAATGTACGTTTCCAACCTGGAGTGGTCACAAACCTGCAATG 4463

Qy 5187 GTGATACAGACAGTTTCAGTGCAATGTCAGGTAGAGACCTCCAGC--AAGGATGATGTCA 5243

Db 4464 GGGACATGGAACAAGCTATCACAGTGGACATTGAGTCATCTAGCCGAGAAGAATGTCA 4523

Qy 5244 CCATAACCAACCAACCTGTCTGCCTCAGGCGCCTTCTACACACTGTCTGCAAGACCAAGTCC 5303

Db 4524 GCATCACITTCAAATCTGTCTCGATCGATTCTTTCTACACCAATGGTTCGAATCAGTTAA 4583

Qy 5304 GGAACAGCTACTACATCGGGGCCGATGGCTCCTTGGCGCTGCTGCTGGCCAAACGGCATGG 5363

Db 4584 GAAACAGCTAACAGATTGGTTATGACGGCTCCCTCAGAAATTACTACGCCAGTGGCCTGG 4643

Qy 5364 AGGTGGCGCTGCAGACTGAGCCCCACTTGTCTGGCTGGCACCCTGACCGTCAACCCCACCGTGGCA 5423

Db 4644 ACTCACACTACCAAAACAGAGCCGACGTTCTGGCTGGCACCCGCTAATCCGACGGTTGCCA 4703

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Db 4704 AAAGAAACATGACTTTGCCTGSCGGAACGGTCAAAACTTGTGTGAATGGAGATTCGGAA 4763

Qy 5484 AAGAGCAGCTCGGGGCCAGGTCACTGTCTTTTGGCGCCGCTGCGGTGCACAACCGAA 5543

Db 4764 AAGAGCAAGCCCAAGGAAAGTCAATGTCTTTGGCCGCAAGCTCAGGGTTAATGGCAGAA 4823

Qy 5544 ATCTCCTATCTCTGGACTTTTGATCGCGTAAACCGCACAGAGAAGATCTATGATGACCACC 5603

Db 4824 ACCTCCTTTCAGTTGACTTTTGATCGAAACAACAAAGACAGAAAAGATCTATGACGACCACC 4883

Qy 5604 GCAAGTTACCCCTTCGGATTCTGTACGACCAAGCGGGGGCGCCAGCCTCTGGTACCCCA 5663

Db 4884 GTAAATTTCTACTGAGGATCGCCCTACGACACGCTCTGGGCACCCGACTCTCTGGCTGCCAA 4943

Qy 5664 GCAGAGGCTGAATGGTGTCAACGTGACATACTCCCCTGGGGGTTACATTGCTGGCATCC 5723

Db 4944 GCAGCAAGCTGATGGCCGTCAATGTCACTTATTCACAGAGTCAAAATGGCCAGCATCC 5003

Qy 5724 AGAGGGGCATCATGTCTGAAAGAATGGAATACGACCAGGGGGCGCCGCGCATCACATCCAGGA 5783

Db 5004 AGCGAGGCCACCACTAGCGAGAAAGTAGATTATGACGGACAGGGGAGGATCGTGTCTCGGG 5063

Qy 5784 TCTTCGCTGATGGGAAGACATGAGCTACACATACTTAGAGAAAGTCCATGGTGTCTGTAC 5843

Db 5064 TCTTTGCTGATGGTAAACATGAGTTACACATATTTAGAAAAGTCCATGGTTCTTCTGC 5123

Qy 5844 TACACAGCCAGAGGCAGTATATCTTTGAGTTCGACAAGAAATGACCGCCTCTCTTCTGTGA 5903

Db 5124 TTCATAGCCAGGGCAGTACATCTTCGAATACGATATGTGGGACCGCCTGTCTGCCATCA 5183

Qy 5904 CGATGCCCAACGTGGCGGGCAGACACTAGAGACCATCCGCTCAGTGGGCTACTACAGAA 5963

Db 5184 CCATGCCAGTGTGGCTCGCCACACCATGCAGACCATCCGATCCATTTGGCTACTACCGCA 5243

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Qy 6144 CGGAGGCATGCTGAAGACCACTCAACCTACAGAAATGAGGGCTTCACCTGCACCATCCGCT 6203

Db 5424 CAGCAGGAGTCTTAAAGACACAGTAAACCTCCAGAGTGGTTTTATTGTGCACCAATTAGAT 5483

Qy 6204 ACCGTGAGATTGGGCCCTGATTGACCGGACAGATCTTCCGCTTCACTGAGGAAGGCATGG 6263

Db 5484 ACAGGCAAAATTGGTCCCCTGATTGACAGGCAGATTTTCCGCTTTAGTGAAGATGGGATGG 5543

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Qy 6384 CAGAGCAGTTTGGGAAGTTTGGTGTCAITTTACTATGACATTAACCAGATCATCACACAG 6443

Db 5664 TTGAGCAGTTTGGAAAAGTTTGGAGTTATATATATATGATATTAACCAGATCATTTCTACAG 5723

Qy 6444 CTGTCAATGACCAACCAAGCATTTTGTGATGTCATATGGCAGGATGAAGGAAGTGCAGTATG 6503

Db 5724 CTGTAATGACCTATAGCAAGCATTTTGTATGCTCATGGCCGTATCAAGGAGATTCATATG 5783

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Db 5784 AGATATTCAAGTCCGCTCATGTACTGGATTACAAATTCAGTATGATAACATGGGTCCGGTAA 5843

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Db 5904 ATGTTGATGGACAGCTCCAAACAGTTTACCTCAATGAAAAGATAATGTGGCGGTACAAC 5963

Qy 6684 ACGACCTCAATGGGAACCTGCACCTTACTGAGCCCTGGGAACAGTGCACGGCTCACACCAC 6743

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Qy 6864 TCATCAAGGCCTACAA CCGGCTGGCAGTGGAGTGT CAGGTACCGTACGATGGCCTGG 6923

Db 6144 TAACTCGGTTTACAGTAAAGGCAGTGGTGGA CAGTGATCTACCGTTATGACGGCCTGG 6203

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Qy 7044 TCTACTACGACTTGCAAGGACACCTCTTTGCCATGGAGCTGAGCAGTGGTGTGATGATTTT 7103

Db 6324 TGTATTATGATCTCCAAGGACATCTTTTGGCCATGGAAATCAGCAGTGGGATGAATTCT 6383

Qy 7104 ACATAGCTTGTGA CAAACATCGGGA CCCCCTCTTGCTGTCTTTAGTGGAA CAGGTTTGATGA 7163

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Db 6504 AACTGGTAAATGGATTTTCATGGTGGCCTGTATGACCCACTCACCAAAATTAATCCACTTTC 6563





Db 2961 GTCAAATTGCCAGCATCCAGCGAGGCCACCACCTAGCGAGAAAGTAGATTATGACGGACAGG 2902

Qy 5766 GCCGCATCACATCCAGGATCTTTCGCTGATGGGAAGACATGGAGCTACACATACTTAGAGA 5825

Db 2901 GGAGGATCGTGTCTCGSGTCTTTGCTGATGGTAAACAATGGAGTTACACATATTTAGAAA 2842

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Db 2841 AGTCCATGGTTCCTCTGCTTCATAGCCAGCGCAGTACATCTTCGAATACGATATGTGG 2782

Qy 5886 ACCGCCTCTCTTCTGTGACGATGCCCAACGTGGCGCGGACACACTPAGAGACCATCCGCT 5945

Db 2781 ACCGCCTGTCTGCCATCACCATGCCCATGCCAGTGTGGCTCGCCACACCATGCCATCCGAT 2722

Qy 5946 CAGTGGGCTACTACAGAAAACATCTATCAGCCCCCTGAGGGCAATGCTCAGTCATACAGG 6005

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Qy 6006 ACTTCACTGAGGATGGGCACCTCCTTCACACCTTCTACCTGGGCACTGGCCGAGGGTGA 6065

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Qy 6366 ATGATGTGTCAAGCAAGACAGAGCAGTTTGGGAAGTTTGGTGTCTATTTACTATGACATTA 6425

Db 2301 ATGACATTTCTGGCAAAAGTTGAGCAGTTTGGAAGTTTGGAGTTATATATTTATGATATTA 2242

Qy 6426 ACCAGATCATCACACAGCTGTGATCAACGAGACCCCACTGAGTGAAGCATTTTGATGATATGSCAGGA 6485

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Qy 6606 GCTACTCTCTATGAGTATGATGCTGACGGCCAGCTGCAGACAGTCTCCATCAATGACAAAGC 6665

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Qy 6726 GTGCACGGCTCACACCCTACGGTATGACATCCGGACCGCATCACTCGGCTGGGTGACG 6785

Db 1941 GTGCGGTCTGACACCCCTTCGCTATGACCTCGAGACAGAACTCACTCGACTGGGTGATG 1882

Qy 6786 TGCAATACAAGATGGATGAGGATGGCTTCCCTGAGGACGGGGCGGTGATATCTTTGAGT 6845

Db 1881 TTCAATATCGGTTGGATGAAGATGGTTTCCTACGTCAAAGGGGCAACGGGAATCTTTGAAT 1822

Qy 6846 ACAACTCAGCTGSCCTGTCTCATCAAGGCCTACAACCGGCTGGCAGCTGGAGTGTCAAGT 6905

Db 1821 ATAGCTCCAAGGGCTTCTAACTCGAGTTTACAGTAAGGCAGTGGCTGGACAGTGATCT 1762

Qy 6906 ACCGCTACGATGGCCTGGGGCGCGCTGTCCAGCAAGAGCAGCCACAGCCACCACCTGC 6965

Db 1761 ACCGTTATGACGGCCTGGGAAGCGGTGTTTCTAGCAAAACCAGTCTAGGACAGCACCTGC 1702

Qy 6966 AGTTCTTCTATGACAGCCTGACCAACCCCAACCAAGGTCACCCACCTGTACAACCACTCCA 7025

Db 1701 AGTTTTTTTATGCTGACTTAACTTATCCCCACTAGGATTACTCATGTCTACAACCATTCGA 1642

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Db 1581 GCAGTGGGATGAATTTCTATATTGTCATCGGATAACACAGGGACACCCACTGGCTGTGTTCA 1522

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Db 1284 TGTTTAGGAATAAACAAACCCCTGCAAGCAAAAATCCATGACGTGAAGAGATTACATCACAGATG 1225

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Db 1224 TTAACAGCTGGCTGGTGACATTTGGTTTCCATCTGCACAAATGCTATTCCTGGATTCCCTG 1165

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Qy 7566 AGGAGTGGGACAAACAGCAAGTCTATCCTCGGGGTACAGTGTGAAGTACAGAAGCAGCTCA 7625

Db 1116 AGCAGTGGGATGATATACCGCCCATCTTCGGAGTCCAGCAGCAAGTGGCGCGGAGGCCA 1057

Qy 7626 AGGCCTTTGTACCTTAGAACCGTTTGACCAGCTCTATGGCTCCACAATCACCAAGCTGCC 7685

Db 1056 AGGCCTTCCTGTCTGGTGGGAAGATGGCCGAGGTGCAAGTCAAGTCGCTGATCGGAAGGCCGC- 998

Qy 7686 AGCAGGCTCCAAAGACCAAGAAAGTTTGTCATCCAGCGCTCAGTCTTTTGGCAAGGGGTCA 7745

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Db 939 TGCTGGCCGTGAGCCAGGGCCGCTGCAGACCAACGTGCTCAACATCGCCCAACGAGGACT 880

Qy 7806 GGCAAGGGTTGTGCCCATTCTTGAACCATATGCCACTACCTAGAGAACTTGCACCTTCAACA 7865

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Db 1349 ATTGTGTGTGCCAGCCTGGATGGAGGAGCAGGCTGTGACGTAGCCATGGAGACTCTTT 1408

Qy 2547 GCGGTGACAGCAAAAGACAATGATGGAGATGGCCTGGTGGACTGCATGGACCCCTGACTGCT 2606

Db 1409 GCACAGATAGTAAGGACAAATGAAGGAGATGGACTCATTTGACTGCATGGATCCCGATTGCT 1468

Qy 2607 GCCTCCAGCCCTGTGCCATATCAACCCGCTGTGCCCTTGGCTCCCCCTAAACCCCTCTGGACA 2666

Db 1469 GCCTACAGAGTTCCTGCCAGAAATCAGCCCTATTGTGCGGGAAGTCCCGATCCTCAGGACA 1528

Qy 2667 TCATCCAGGAGACACAGGTCCTGTGTACAGCAGAAACCTACACTCCTTCTATGACCGCA 2726

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Db 1589 TCAGTTTTCCTTATAGGATCTGATAGCACCCCATGTTATACCTGGAGAAAGTCCTTTCAATA 1648

Qy 2787 GAGGGCATGCTTGTGTTATTTCGTGGCCAAAGTATGACATCAGATGGAACCCCTCGTTG 2846

Db 1649 AGAGCCTTGCACTGTCTATCAGAGGCCAAAGTACTGACTGTGATGGAACCTCCACTATTG 1708

Qy 2847 GTGTGAACATCAGTTTTTGTCAATAACCCCTCTCTTTGGATATACAATCAGCAGGCAAGATG 2906

Db 1709 GAGTAAATGTCTCGTTTTTCCATTACCCAGAAATATGGATATACTATTACCCGCCAGGACG 1768

Qy 2907 GCAGCTTTGACTTGGTGACAAATGGCGGCATCTCCATCACTCTCGGTTTCGAGCGGGCAC 2966

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Qy 2967 CTTTCATCACACAGGAGCACACCTGTGGCTGCCATGGATCGCTTCTTTGTCAATGGAAA 3026

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Qy 3027 CCATCATCATGAGACATGAGGAGAAATGAGATTCCCAGCTGTGACCTGAGCAATTTTGCCC 3086

Db 1889 CCCTAGTCATGAAGAAAGAGAGAAATGACATTCCCAGCTGTGATCTGAGTGGATTCTGTA 1948

Qy 3087 GCCCAACCCAGTCGTCTCTCCATCCCCACTGACGTCTCTCGCCAGCTCCTGTGCAGAGA 3146

Db 1949 GGCCAAATCCCATCATTTGTGTATCACCCTTTATCCACCTTTTTCAGATCTTCTCTGAAG 2008

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Db 2009 ACAGTCCCATCATTTCCCGAAACACAGGTACTCCACGAGGAAACTACAATTCAGGAACAG 2068

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Db 2069 ATTTGAAACTCTCCTACTTTGAGTTCAGAGCTGCAGGGTATAAGTCAGTTCTCAAGATCA 2128

Qy 3267 GCCTCACCCACCCGACCATCCCTTCAACCTCATGAAGGTGCACCTCATGTGAGCGGTGG 3326

Db 2129 CCATGACCCAGTCTATTATTCCATTTAAATTTAATGAAGGTTTCATCTTATGGTAGCTGTAG 2188

Qy 3327 AGGCGCGCCTCTTCAGGAAGTGGTTGCTGCAGCCCAGACCTGTCTCTATTATTCAATTT 3386

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Db 2309 TTGGATATGAGTATGAGTCGTGTTTGGACCTGACTCTGTGGGAAAAGAGGACTGCCATTTC 2368

Qy 3507 TGCAGGGCTATGAAATTGACGCGTCCAAGCTTGGAGGATGGAGCCTAGACAAACATCATG 3566

Db 2369 TGCAGGGCTATGAATTGGATGGTCCCAACATGGGTGGCTGGACATTAGATAAACATCAAG 2428

Qy 3567 CCCTCAACATTCAAAGTGGTATCCTGCAACAAAGGGAATGGGAGAACCAAGTTTGTGTCTC 3626

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Qy 3627 AGCAGCCTCCTGTCAATTTGGGAGCATCATGGGCAA 3660

Db 2489 AGCAGCCTCCAGTCGTGAGTAGCCTCGAGGGTAA 2522

RESULT 8

US-11-096-051-5

; Sequence 5, Application US/11096051

; Publication No. US20050244868A1

; GENERAL INFORMATION:

; APPLICANT: Kekuda, Ramesh

; APPLICANT: MacLachlan, Timothy K

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; TITLE OF INVENTION: Ten-M3 Polypeptides and Polynucleotides and their Methods of Use

; FILE REFERENCE: Attorney Docket No. Cura 967

; CURRENT APPLICATION NUMBER: US/11/096,051

; CURRENT FILING DATE: 2005-03-30

; PRIOR APPLICATION NUMBER: 10/038,854

; PRIOR FILING DATE: 2001-12-31

; PRIOR APPLICATION NUMBER: 10/455,772

; PRIOR FILING DATE: 2003-06-04

; PRIOR APPLICATION NUMBER: 60/557,978

; PRIOR FILING DATE: 2004-03-30

; NUMBER OF SEQ ID NOS: 38

; SOFTWARE: CuraSeqList version 0.1

; SEQ ID NO 5

; LENGTH: 2482

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (11)..(2473)

US-11-096-051-5

Query Match 13.8%; Score 1151.2; DB 9; Length 2482;

Best Local Similarity 67.8%; Pred. No. 1.2e-277;

Matches 1609; Conservative 0; Mismatches 763; Indels 0; Gaps 0;

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Db 111 ATGGAATAATTAGGTGGATTACGCAAGAAAAATAACCCATAGATTCCGGAGAACTTGATA 170

Qy 1347 TGGGAAGGCGAGCCTCCCAGAAGATTCTCTCGGACATTTCTGGAGATCTCAAGTGTTC 1406

Db 171 TTGGCCGAAGAGCAATTCAAGAGATTCTCTCCGGGATCTTCTCGAGATCACAGCTCTTCA 230

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Qy 1467 TTTATGGCAGAAAAGGCCTCCCTCTTTCACATACACAGTTTGTGAGCTGCTGG 1526

Db 291 TATATGGCCGAAAGGCTTACCGCCTTCCCATACTCAGTATGACTTCGTGGAGCTCCTGG 350

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Db 351 ATGGCAGCAGGCTGATTGCCAGAGAGCAGCGGAGCCTGCTTGAGACGGAGAGAGCCGGGC 410

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Db 411 GGCAGCGGAGATCCGTGAGCCTTCATGAGCCCGGCTTTATCCAGTACTTTGGATTCTGGAA 470

Qy 1647 TCTGGCACTTGGCTTTTACAAATGACGGAAAGGAGTTCAGAAAGTGGTTTCTTTCTCACCA 1706

Db 471 TCTGGCATCTGGCTTTTATAATGATGGGAAAAATGCAGAGCAGGTGTCTTTTAATACCA 530

Qy 1707 CTGCCAATTGAGTCGGTGGATAACTGCCCCAGCAACTGCTATGGCAATGGTGACTGCATCT 1766

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QY	1767	CTGGGACCTGCCACTGCTTCCTTGGGTTTCCTGGGCCCCGACTGTGGCAGAGSCTCCTGCC	1826
Db	591	CTGGAACCTTGCCATTGTTTCCAGGATTTCTGGTCCGGATTGTTCAAGAGCGCCTGTC	650
QY	1827	CCGTGCTCTGTAGCGGAAATGGCCAAATACATGAAAAGGCAGATGCTTGTGCCACAGTGGCT	1886
Db	651	CAGTGTATGTAGTGGCAACGGGCAGTACTCCAAGGGCCGCTGCCTGTGTTTTCAGCGGCT	710
QY	1887	GGAAAGGCGTGAAGTGCATGTGCCCCAACCAACAGTGTATCGATGTGGCTGCAGCAACC	1946
Db	711	GGAGGGCACCGAGTGTGATGTGCCGACTACCCAGTGTATTGACCCACAGTGTGGGGGTC	770
QY	1947	ATGGCACCTGCATCACGGGCACCTGTCATCTGCAACCCCTGGCTACAAGGGCGAGAGCTGTG	2006
Db	771	GTGGGATTTGTATCATGGGCTCTTGTGCTTGCAACTCAGGATACAAAAGGAGAAAGTTGTG	830
QY	2007	AGGAAGTGGACTGCATGGACCCCAACATGTTTCAGSCCGGGGTGTCTGCGTGAGAGCGGAAT	2066
Db	831	AAGAAAGCTGACTGTATAGACCCCTGGGTGTTCTTAATCATGGTGTGTATCCACGGGAAT	890
QY	2067	GCCATTGCTTTGTGGGATGGGGAGGCCAACACTGCCGAGACCCCCAGGGCCACATGCTTAG	2126
Db	891	GTCACTGCAGTCCAGGATGGGGAGGTAGCAATTGTGAAATACTGAAGACCATGTGTCCAG	950
QY	2127	ACCAGTGTTTACGGCACGGAACTTCCTCCCGGACACCGGGCTTTGACGTGTGACCCAA	2186
Db	951	ACCAGTGCTCCGGCCACGGAACGTATCTTCAAGAAAGTGGCTCCTGCACGTGTGACCCCTA	1010
QY	2187	GCTGGAAGTGGACGACTGTTCTATCGAGATCTGTGCTGCCGACTGTGTTGGCCATGGCG	2246
Db	1011	ACTGGACTGGCCCCAGACTGCTCAAACGAAATATGTTCTGTGGACTGTGGCTCACACGGCG	1070
QY	2247	TGTGCGTAGGGGGACCTGCCGCTGCGAGGATGGCTGGATGGGGGACGCTTGCACCCAGC	2306
Db	1071	TTTGCATGGGGGGACGTGTGCTGTGAAGAGGTGGACGGGCCACGCTGTAATCAGA	1130
QY	2307	GGGCTGCCACCCGGCTGTGCCGAGCATGGGACTGCTGCCGACGGCAAGTGCAGTGCA	2366
Db	1131	GAGCCTGCCACCCCGCTGTGCCGAGCACGGGACCTGCAAGGATGGCAAGTGTGAATGCA	1190
QY	2367	GCCCTGGCTGGAATGSGAAACACTGCACCACCTCGCTCACTATCTGGATAGGGTAGTTAAAG	2426
Db	1191	GCCAGGGCTGGAATGGAGAGCACTGCACATACTCGCTCACTATTTGGATAAGATAGTTAAAG	1250
QY	2427	AGGGTTGCCCTGGTTGTGCAATGGCAAACGGCAGATGTACCTTAGACCTGAATGGTTGGC	2486
Db	1251	AGGGTTGTCTGGTCTGTGCAAACAGCAAATGGAAGATGTACCTTGACCAAATGGCTGGC	1310
QY	2487	ACTGCGTCTGCCAGCTGGGCTGGAGAGGAGCTGGCTGTGACACTTCCATGGAGACTGCCT	2546
Db	1311	ATTGTGTGTGCCAGCCTGGATGGAGAGGAGCAGGCTGTGACGTAGCCATGGAGACTCTTT	1370
QY	2547	GCGGTGACAGCAAAGACAATGATGGAGATGGCCCTGGTGGACTGCATGGACCCCTGACTGCT	2606
Db	1371	GCACAGATAGTAAGGACAATGAAGGAGATGGACTCATGACTGCATGGATCCCGATTGCT	1430
QY	2607	GCCTCCAGCCCTGTGCCATATCAACCCGCTGTGCCCTTGGCTCCCTTAACCTCTGAGACA	2666
Db	1431	GCCTACAGAGTTCCTGCCAGAAATCAGCCCTATTGTCCGGGACTGCCGGATCCTCAGGACA	1490
QY	2667	TCATCCAGGAGACACAGGTCCCTGTGTACAGCAGAACTACACTCCTTCTATGACCGCA	2726
Db	1491	TCATTAGCCAAAGCCTTCAATCGCCTTCTCAGCAAGCTGCAAAATCCTTTTATGATCGAA	1550
QY	2727	TCAAGTTCCCTCGTGGSCAGGGACAGCACGACATATCCCGGGGAGAACCCCTTTTGATG	2786
Db	1551	TCAGTTTCTTATAGGATCTGATAGCACCCCATGTTTATACCTGGAGAAAGTCTCTTCAATA	1610
QY	2787	GAGGGCATGCTTGTGTTATTCTGTGGCCAAAGTATGATGACATCAGATGGAACCCCTTGTG	2846
Db	1611	AGAGCCTTGCACTCTGTCATCAGAGGCCAAGTACTGACTGCTGATGGAACTCCACITATTG	1670
QY	2847	GTGTGAACATCAGTTTGTGTAATAAACCCCTCTCTCTTTGGATATACAATCAGCAGGCAAGATG	2906

Db	1671	GAGTAAATGCTCGTTTTTCCATTACCCAGAAATATGGATATACATAATACCGCCAGGACG	1730
Qy	2907	GCAGCTTTGACTTGGTGACAAATGGCGSCATCTCCATCATCTCTCGGTTTCGAGCGGCAC	2966
Db	1731	GAATGTTGACTTGGTGGCAAAATGGTGGGCGCTCTCTAACTTTGGTATTGAACGATCCC	1790
Qy	2967	CTTTTCATCACACAGGAGCACACCCCTGTGGCTGCCATGGGATCGCTTCCTTGTCTATGGAAA	3026
Db	1791	CATTCTCACTCAGTATCATACTGTGTGGATTCCATGGAAATGTCTTTTATGTGATGGATA	1850
Qy	3027	CCATCATCATGAGACATGAGGAGAAATGAGATTCCCAGCTGTGACCTGAGCAATTTTCCCC	3086
Db	1851	CCCTAGTCATGAAGAAAGAGAAATGACATTTCCAGCTGTGATCTGAGTGGATTCTGTGA	1910
Qy	3087	GCCCCAACCCAGTCGTCTCTCCATCCCACACTGACGTCTCTTCGCCAGCTCCTGTGCGAGAGA	3146
Db	1911	GGCCAAATCCCATCATGTGTATCATCACCTTTATCCACCTTTTTCAGATCTTCTCCTGAAG	1970
Qy	3147	AAGGCCCAATGTGCCGGAATTCAGGCTTTGAGGAGGAAATCTCTATCTCTGGCTGCA	3206
Db	1971	ACAGTCCCATCATTTCCGAAACACAGGTACTCCACGAGGAAACTACAATTCAGGAACAG	2030
Qy	3207	AGATGAGGCTGAGCTACCTGAGCAGCCGSCCCCTGGCTACAAATCTGTCTCTGAGGATCA	3266
Db	2031	ATTTGAAACTCTCCTACTTGAGTTCAGAGCTGCAGGTATAAGTCAGTTCATCTCAAGATCA	2090
Qy	3267	GCCTCACCCACCCGACCATCCCCCTTCAACCTCATGAAGTGCACCTCATGCTAGCGGTGG	3326
Db	2091	CCATGACCCAGTCTATTATTCATTTAATTAATGAAGTTTCATCTTTATGGTAGCTGTAG	2150
Qy	3327	AGGGCCGCTCTTTCAGGAAGTGGTTCGTGTCAGCCCCAGACCTGTCTCTATTATTTTCATTT	3386
Db	2151	TAGGAAGACTCTTCCAAAAGTGGTTTCTCGCTCACCAAACCTTGGCCTATACCTTTCATAT	2210
Qy	3387	GGGACAAAGACAGACGTCTACAAACAGAAAGTGTTTGGGCTTTTCAGAAAGCCTTTGTTTCCG	3446
Db	2211	GGGATAAAACAGATGCATATAAATCAGAAAGTCTATGGTCTATCTGAAGCTGTTGTGTGAG	2270
Qy	3447	TGGGTTATGAATATGAATCTGCCCCAGATCTAATCTGTGGGAAAAAAGAACACAGTGC	3506
Db	2271	TTGGATATGAGTATGAGTCGTGTTTGGACCTGACTCTGTGGGAAAAAGGAGCTGCCATTC	2330
Qy	3507	TGCAGGGCTATGAAATTGACGCGTCCAAAGCTTGGAGGATGGAGCCTAGACAAACATCATG	3566
Db	2331	TGCAGGGCTATGAATTGGATGCGTCCAAACATGGGTGGCTGGACATTAGATATAAACATCAG	2390
Qy	3567	CCCTCAACATTCAAAGTGGTATCCTGCACAAAGGGAATGGGGAGAACCGATTGTGTCTC	3626
Db	2391	TGCTGGATGTACAGAACGGTATACTGTACAAGGGAAACGGGGAAAAACGAGTTCACTCTCC	2450
Qy	3627	AGCAGCCTCCTGTCAATTGGGAGCATCATGGGC	3658
Db	2451	AGCAGCCTCCAGTCGTGAGTAGCCTCGAGGC	2482

## RESULT 9

US-11-096-051-13  
; Sequence 13, Application US/11096051  
; Publication No. US20050244868A1  
; GENERAL INFORMATION:  
; APPLICANT: Kekuda, Ramesh  
; APPLICANT: MacLachlan, Timothy K  
; APPLICANT: Rastelli, Luca  
; APPLICANT: Vernet, Corine  
; APPLICANT: Ettenberg, Seth  
; TITLE OF INVENTION: Ten-M3 Polypept  
; FILE REFERENCE: Attorney Docket No.  
; CURRENT APPLICATION NUMBER: US/11/0  
; CURRENT FILING DATE: 2005-03-30  
; PRIOR APPLICATION NUMBER: 10/038,85  
; PRIOR FILING DATE: 2001-12-31  
; PRIOR APPLICATION NUMBER: 10/455,77



; PRIOR FILING DATE: 2003-06-04									
; PRIOR APPLICATION NUMBER: 60/557,978									
; PRIOR FILING DATE: 2004-03-30									
; NUMBER OF SEQ ID NOS: 38									
; SOFTWARE: CuraSeqList version 0.1									
; SEQ ID NO 13									
; LENGTH: 1833									
; TYPE: DNA									
; ORGANISM: Homo sapiens									
; FEATURE:									
; NAME/KEY: CDS									
; LOCATION: (7)..(1827)									
US-11-096-051-13									
Query Match 10.1%; Score 842.2; DB 9; Length 1833;									
Best Local Similarity 66.7%; Pred. No. 1.7e-200;									
Matches 1229; Conservative 0; Mismatches 593; Indels 21; Gaps 1;									
QY	2469	TAGACCTGAATGGTTGGCACTGCGTCTGCGCAGCTGGGCTGGAGAGGAGCTGGCTGTGACA	2528						
Db	5	TTGACCAAAATGGCGACATTGTGTGTGCCAGCCTGGATGGAGAGGAGCAGGCTGTGACG	64						
QY	2529	CTTCCATGGAGACTGCTGCGGTGACAGCAAAAGACAATGATGAGAGATGGCCTGGTGGACT	2588						
Db	65	TAGCCATGGAGACTCTTTGCACAGATAGCAAGGACAATGAAGGAGATGGACTCAATTGACT	124						
QY	2589	GCATGGACCCCTGACTGCTGCCCTCCAGCCCCCTGTGCCATATCAACCCGCTGTGCCCTTGGCT	2648						
Db	125	GCATGGATCCCGATTGCTGCCCTACAGAGTTCTTGCCAGAGATCAGCCCTATTGTGCGGGAC	184						
QY	2649	CCCCTAACCCCTCTGGACATCATCCAGGAGACACAGGTCCTGTGTCAACAGCAGAACTTAC	2708						
Db	185	TGCCGGATCCTCAGGACATCATTAGCCAAAGCCTTCAATCGCCTTCTCAGCAAGCTGCCA	244						
QY	2709	ACTCCTTCTATGACCGCATCAAGTTCTCTGTTGGCAGGACAGCACGCACATAATCCCCG	2768						
Db	245	AATCCCTTTATGATCGAATCGATTTCCTTATAGGATCTGATAGCACCCCATGTTATACCTG	304						
QY	2769	GGGAGAACCCCTTTGATGGAGGCAATGCTTGTGTTATTCTGGCCAAAGTGATGACATCAG	2828						
Db	305	GAGAAAGTCCTTTCAATAAGAGCCTTGTCATCTGTATCAGAGGCCAAAGTACTGACTGCTG	364						
QY	2829	ATGGAACCCCTCGTTGGTGTGAACATCAGTTTGTGTCATAAACCCCTCTCTTTGGATATA	2888						
Db	365	ATGGAACTCCACTTATTGGAGTAAATGTCTCGTTTTTCCATTACCCAGAATATGGATATA	424						
QY	2889	CAATCAGCAGGCAAGATGGCAGCTTTGACTTGGTGACAAATGGCGGCATCTCCATCATCC	2948						
Db	425	CTATTACC CGCCAGGACGGAATGTTGACTTGGTGGCAAAATGGTGGGCCCTCTCTAACTT	484						
QY	2949	TGCGGTTGAGCGGGCACCTTTTCATCACACAGGAGCACACCCTGTGGCTGCCATGGGATC	3008						
Db	485	TGGTATTGAACGATCCCCCATTCCTCACTCAGTATCATACTGTGTGGATTCCATGGAAATG	544						
QY	3009	GCTTCTTTGTCATGGAAACCATCATCATGAGACATGAGGAGAAATGAGATTCACAGCTGTG	3068						
Db	545	TCITTTTATGTGATGGATAACCTAGTCATGAAGAAAGAGAAATGACATTCCCAGCTGTG	604						
QY	3069	ACCTGAGCAATTTTGGCCGCCCCCAACCCAGTCGTCTCTCCATCCCCACTGACGTCCTTCG	3128						
Db	605	ATCTGAGTGGATTCTGTAGGCCAAATCCCATCAATTGTGTCAATCACCTTTATCCACCTTTT	664						
QY	3129	CCAGCTCCTGTGCAGAGAAAGGCCCCCATTTGTCCGGAAATTCAGGCTTTGCAGGAGGAAA	3188						
Db	665	TCAGATCTTCTCCTGAAGACAGTCCCATCATTTCCCGAAACACAGGTACTCCACGAGGAAA	724						
QY	3189	TCTCTATCTCTGGCTGCAAGATGAGGCTGAGCTACCTGAGCAGCCGGACCCCTGGCTACA	3248						
Db	725	CTACAATTCAGGAACAGATTTGAAACTCTCCTACTTGAGTCCAGAGCTGCGGGTATA	784						
QY	3249	AATCTGTCTGAGGATCAGCCTCACCCACCCGACCATCCCTTCAACCTCATGAAGGTGC	3308						
Db	785	AGTCAGTTCTCAAGATCACCATGACCCAGTCATTATTCATTATTCATTAAATGAAGGTTTC	844						

RESULT 10

US-11-096-051-11

; Sequence 11, Application US/11096051

QY	3309	ACCTCATGGTAGCGGTGGAGGGCCGCTCTTCAGGAAGTGGTTCGCTGCAGCCCCAGACC	3368
Db	845	ATCTTATGGTAGCTGTAGTAGGAAGACTCTTCCAAAAGTGGTTTCCTGCCTCACCAAACT	904
QY	3369	TGTCCCTATTATTTCATTTGGACAAGACAGACGCTCTACAACCAGAAAGGTGTGTGGCCTTT	3428
Db	905	TGGCCTATACITTTTCATATGGGATAAAACACAGATGCATATAATCAGAAAAGTCTATGGTCTAT	964
QY	3429	CAGAAAGCCTTTTGTTCCTGGGTTATGAATATGAATCCTGCCCAGATCTAAATCCTGTGGG	3488
Db	965	CTGAAGCTGTTGTGTAGTTGGATATGAGTATGAGTCGTGTTGGACCTGACTCTGTGGG	1024
QY	3489	AAAAAAGAACACAGTCTGCAGGGCTATGAAATTTGACGCTCCAAAGCTTGGAGGATGGA	3548
Db	1025	AAAAGAGGACTGCCATTTCTGCAGGGCTATGAATTTGGATGCGTCCAAACATGGGTGGCTGGA	1084
QY	3549	GCCTAGACAAACATCATGCCCTCAACATTTCAAAAGTGGTATCCTGCACAAAGGGAATGGGG	3608
Db	1085	CATTAGATAAACATCACGTGCTGGATGTACAGAAACGGTATACTGTACAAGGGAACGGGG	1144
QY	3609	AGAACCCAGTTTGTGTCTCAGCAGCCTCCTGTCTATTTGGGAGCATCATGGGCAATGGCGCC	3668
Db	1145	AAAACCAGTTCATCTCCAGCAGCCTCCAGTCTGAGTAGCATCATGGGCAATGGGCGAA	1204
QY	3669	GGAGAAAGCATCTCCTGCCCCAGCTGCAACGGCCCTTGTGACGGCAACAAGCTCCTGGCCC	3728
Db	1205	GGCGCAGCATTTCTGCCCCAGTTGCAATGGTCAAGCTGATGGTAACAAGTTACTGGCCC	1264
QY	3729	CAGTGGCCCTCACCTGTGGCTCTGACGGGAGCCCTCTATGTGGGTGATTTCAACTACATTA	3788
Db	1265	CAGTGGCGCTAGCTTGTGGGATCGATGGCAGTCTGTACGTAGGCGATTTCAACTATGTGC	1324
QY	3789	GAAGGATCTTCCCCTCTGGAAATGTCAACCAACATCCTAGAGCTGAGGAATAAGATTTCA	3848
Db	1325	GGCGGATATTCCCTTCTGGAAATGTAAACAAAGTGTCTTAGAACTAAGCAGCAA-----	1376
QY	3849	GACATAGTCACAGTCCAGCACACAAATACTACTCCTGGCCAAGAGCCCATGAGTGGGGCCG	3908
Db	1377	-----CCCAGCTCATAGATACTACTCTTGCAACGGATCCAGTACGGGAGATC	1423
QY	3909	TCTTCCCTTCTGACAGCAACAGCCGGCGGTCTTTAAAAATCAAGTCCACTGTGGTGTGA	3968
Db	1424	TGTACGTTTCTGACACAAACACCCCGCAGAAATTTATCGCCCAAAGTCACTTACGGGGCAA	1483
QY	3969	AGGACCTTGTCAAGAACTCTGAGGTGGTTGGGGGACAGGTGACCAAGTGCCTCCCTTTG	4028
Db	1484	AAGACTTGACTAAAAATGCAGAAAGTCGTGCGAGGGACAGGGGAGCAATGCCTTCCGTTTG	1543
QY	4029	ATGACACTCGCTCGGGGATGGTGGGAAGGCCACAGAAAGCCACACTCAACATCCCAGGG	4088
Db	1544	ACGAGGCGAGATGTGGGATGGAGGAAGGCCGTGGAAGCCACACTCATGAGTCCCAAAG	1603
QY	4089	GTATTACAGTGGACAAGTTTGGGCTGATCTACTTCGTGGATGGCACCATTGATCAGACGCA	4148
Db	1604	GAATGGCAGTTGATAAGAAATGGATTAATCTACTTTTGTGATGGAAACCATGATTAGGAAAG	1663
QY	4149	TCGATCAGAAATGGGATCATCTCCACCCTGCTCGGCTCTAATGATCTCACATCAGCCCGGC	4208
Db	1664	TTGACCAAAATGGAATCATATCAACTCTTCTGGGTTCTAACGATTTGACTTCAGCCAGAC	1723
QY	4209	CACCTAGCTGTGATTCTGTCTATGGATATTTCCAGGTAAAGACTGGAGTGGCCCCACAGACT	4268
Db	1724	CTTTAACTTGTGACACCAGCATGCACATCAGCCAGGTACGTCTGGAATGGCCCACTGACC	1783
QY	4269	TAGCCATCAACCCCAATGGACAACCTCACTTTTATGTCTCGACAA	4311
Db	1784	TAGCCATTAACCCCTATGGATAAATCCATTTATGTCTCGGATAA	1826



Db 343 GGGTGTCTTAATCATGTTGTGTGTATCCACGGGGAATGTCACTGCAGTCCAGGATGGGGA 402

QY 2090 GGCACCAACTGCGAGACCCCGAGGGCCACATGCTTAGACCAGTGTTCAGGGCCACGGAACC 2149

Db 403 GGTAGCAATTGTGAATACTACTGAAGACCATGTGTCCAGACCATGTCTCGGCCACGGAACG 462

QY 2150 TTCTCCCGGACACCGGGCTTTGACAGCTGTGACCCAAAGCTGGACTGGACACGACTGTTCT 2209

Db 463 TATCTTCAAGAAAGTGGCTCCTGCACGTGTGACCCCTAACTGGACTGGCCACAGACTGCTCA 522

QY 2210 ATCGAGATCTGTGCTGCCGACTGTGGTGGCCATGGCGTGTGCGTAGGGGGCACCTGCCGC 2269

Db 523 AACGAAATATGTTCTGTGGACTGTGGCTCACACGGCGTTTGCATGGGGGGGACGTGTGCG 582

QY 2270 TCGGAGGATGGCTGGATGGGGGACGCTTGGACCCAGCGGGCCTGCCACCCGCGTGTGCC 2329

Db 583 TGTGAAGAAGCTGGACGGGCCAGCCTGTGAATCAGAGAGCCTGCCACCCCGCTGTGCC 642

QY 2330 GAGCATGGGACCTGCCGCGACGGCAAGTGGGAGTGCAGCCCTGGCTGGAATGGCGAACAC 2389

Db 643 GAGCACGGGACCTGCAAGGATGGCAAGTGAATGCAGCCAGGCTGGAATGGAGAGCAC 702

QY 2390 TGCACCATCGCTCACTATCTGGATAGGTAAGTAAAGAGGGTTGCCCTGGTTGTGCAAT 2449

Db 703 TGCACATATC-----GAGGGTTGCTCCTGGTCTGTGCAAC 735

QY 2450 GGCAACGGCAGATGTACCTTAGACCTGAATGGTTGGCACTGGCTGTGCCAGCTGGGCTGG 2509

Db 736 AGCAATGGAAGATGTACCCCTGGACCAAAATGGCTGGCATTTGTGTGCCAGCCTGGATGG 795

QY 2510 AGAGGAGCTGGCTGTGAC 2527

Db 796 AGAGGAGCAGGCTGTGAC 813

RESULT 12

US-11-096-051-15

; Sequence 15, Application US/11096051

; Publication No. US20050244868A1

; GENERAL INFORMATION:

; APPLICANT: Kekuda, Ramesh

; APPLICANT: MacLachlan, Timothy K

; APPLICANT: Rastelli, Luca

; APPLICANT: Vernet, Corine

; APPLICANT: Ettenberg, Seth

; TITLE OF INVENTION: Ten-M3 Polypeptides and Polynucleotides and their Methods of Use

; FILE REFERENCE: Attorney Docket No. Cura 967

; CURRENT APPLICATION NUMBER: US/11/096,051

; CURRENT FILING DATE: 2005-03-30

; PRIOR APPLICATION NUMBER: 10/038,854

; PRIOR FILING DATE: 2001-12-31

; PRIOR APPLICATION NUMBER: 10/455,772

; PRIOR FILING DATE: 2003-06-04

; PRIOR APPLICATION NUMBER: 60/557,978

; PRIOR FILING DATE: 2004-03-30

; NUMBER OF SEQ ID NOS: 38

; SOFTWARE: CuraSeqList version 0.1

; SEQ ID NO 15

; LENGTH: 768

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (65)..(706)

US-11-096-051-15

Query Match 2.0%; Score 168.2; DB 9; Length 768;

Best Local Similarity 63.1%; Pred. No. 2.5e-32;

Matches 311; Conservative 0; Mismatches 173; Indels 9; Gaps 3;

QY 35 ATGGACGTGAAGGAGAGGAGGAGCTTACCGCTCGCTGACCCGGCGC---CGCGACGCCGAG 91

Db 65 ATGGATGTGAAGAACCGCAGGCTTACTGCTCCCTGACCAAGACGACGAGAGAAGAA 124

QY 92 CGCCGCTACACAGCTCGTCCGCGGACAGCGAGAGGGCAAAG---CCCCGAGAAATCG 148

Db 125 CGGCGCTACACAAATTCTCCGCAGACAATGAGGAGTGCCGGGTACCCACACAGAAGTCC 184

QY 149 TACAGCTCCAGCGAGACCCCTGAAGGCCTACGACCAGGA---CGCCCCCCTAGCCTATGGC 205

Db 185 TACAGTTCACGCGAGACATTTGAAAGCTTTTGATCATGATTTCTCTCGCGGCTGCTTTACGGC 244

QY 206 AGCCGCGTCAAGGACATTTGTCCGCGCAGGAGGCGGAGGAATTCTGCCGACAGGTGCCAAC 265

Db 245 AACAGAGTGAAGGATTTGGTTTACAGAGAAGCAGACGAGTTCACTAGACAAGGACAGAAT 304

QY 266 TTCACCCCTGCGGAGCTGGGGCTGGAAGAAAGTAAACGCCCTCTCACGGGACCCCTGTACCGG 325

Db 305 TTTACCCCTAAGGCAGTTAGGAGTTTGTGAACCCAGCAACTCGAAGAGGACTGGCATTTTGT 364

QY 326 ACAGACATTTGGCTGCCCCCAATCGGGCTACTCCATGGGGCTGGCTCTGATGCCGACATG 385

Db 365 GCGAAATGGGGCTCCCTCACAGAGGTTACTCTATCAGTGCAGGTCAGATGCTGATACT 424

QY 386 GAGGCTGACACGGTGTCTCCCTGAGCAACCCCGTGCCTGTGTGGGCGGAGCACACGG 445

Db 425 GAAATGAAGCAGTGTATGCCAGAGCATGCCATGAGACTTTGGGGCAGGGGGTCAAA 484

QY 446 TCAGGGCGCAGCTCCTGCTGTCCAGCCGGGCCAAATTCCAATCTCACACTCACCGACACC 505

Db 485 TCAGGCCGCGAGCTCCTGCCTGTCAAGTCGGTCCAACTCAGCCCTCACCCCTGACAGATACG 544

QY 506 GAGCATGAAAAACA 518

Db 545 GAGCACGAAAAACA 557

RESULT 13

US-10-750-185-39327/c

; Sequence 39327, Application US/10750185

; Publication No. US20050260603A1

; GENERAL INFORMATION:

; APPLICANT: MMI GENOMICS, INC.

; APPLICANT: Denise, Sue K.

; APPLICANT: KERR, Richard

; APPLICANT: ROSENFELD, David

; APPLICANT: HOLM, Tom

; APPLICANT: BATES, Stephen

; APPLICANT: FANTIN, Dennis

; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS

; FILE REFERENCE: MM1100-2

; CURRENT APPLICATION NUMBER: US/10/750,185

; CURRENT FILING DATE: 2003-12-31

; PRIOR APPLICATION NUMBER: US 60/437,482

; PRIOR FILING DATE: 2002-12-31

; NUMBER OF SEQ ID NOS: 64922

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 39327

; LENGTH: 2064

; TYPE: DNA

; ORGANISM: Bovine 19866880711171

US-10-750-185-39327

Query Match 1.7%; Score 144; DB 6; Length 2064;

Best Local Similarity 67.1%; Pred. No. 4.4e-26;

Matches 204; Conservative 0; Mismatches 100; Indels 0; Gaps 0;

QY 3139 TGCAGAGAAAGGCCCCCATTTGTGCCGAAATTCAGGCTTTGCAGGAGGAAATCTCTATCTC 3198

Db 1322 TGCACGTGTTCCACCTGTGTCTCTCTCTCCAGGTTCTTCATGAAGAAATTGAGCTCCC 1263

QY 3199 TGGCTGCAAGATGAGGCTGAGTACCTGAGCAGCCGACCCCTGGCTACAAATCTGTCTC 3258

Db 1262 TGGTTCCACCGTGAAGCTTCGCTACCTGAGCTCCAGGACCCGAGGCTACAAGTCACTGCT 1203

QY 3259 GAGGATCAGCCTCACCCACCCGACCATTCCCTTCAACCTCATGAAGGTGCACCTCATGGT 3318



Db 1202 GAAGATCACCATGACCCCAATCCACAGTGCCCCCTGAACCTCATCAAGGTTTCATCTCATGGT 1143  
QY 3319 AGCGGTGGAGGGCCGCTCTTTCAGGAAGTGGTTTCGCTGCAGCCCCCAGACCTGTCTCTATTA 3378  
Db 1142 TGCTGTAGAGGGGCACCTCTTCCAGAAAGTCATTCCAGGCCTCTCCTAACCTGGCCTACAC 1083  
QY 3379 TTTCATTTGGGACAAGACAGACGCTCTACAACCAGAAAGTGTTTGGGCTTTTCAGAAAGCCTT 3438  
Db 1082 CTTTCATCTGGGACAAGACAGATGCCTACGGCCAAAGGGTCTATGGACTCTCTGATGCTGT 1023  
QY 3439 TGTT 3442  
Db 1022 TGGT 1019

RESULT 14  
US-10-750-185-39351  
; Sequence 39351, Application US/10750185  
; Publication No. US20050260603A1  
; GENERAL INFORMATION:  
; APPLICANT: MMI GENOMICS, INC.  
; APPLICANT: DENISE, Sue K.  
; APPLICANT: KERR, Richard  
; APPLICANT: ROSENFELD, David  
; APPLICANT: HOLM, Tom  
; APPLICANT: BATES, Stephen  
; APPLICANT: FANTIN, Dennis  
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS  
; FILE REFERENCE: MM1100-2  
; CURRENT APPLICATION NUMBER: US/10/750,185  
; CURRENT FILING DATE: 2003-12-31  
; PRIOR APPLICATION NUMBER: US 60/437,482  
; PRIOR FILING DATE: 2002-12-31  
; NUMBER OF SEQ ID NOS: 64922  
; SOFTWARE: PatentIN version 3.1  
; SEQ ID NO 39351  
; LENGTH: 972  
; TYPE: DNA  
; ORGANISM: Bovine 19866881410938  
US-10-750-185-39351

Query Match 1.2%; Score 101.6; DB 6; Length 972;  
Best Local Similarity 76.2%; Pred. No. 1.2e-15;  
Matches 125; Conservative 0; Mismatches 39; Indels 0; Gaps 0;  
QY 4088 GGTATTACAGTGGACAAGTTTGGGCTGATCTACTTCGTGGATGGCACCATGATCAGACGC 4147  
Db 272 GGTATTGCAGTTGACAAGAAATGGGCTCATGTACTTTGTCGACGCCACCATGATCCGCAAG 331  
QY 4148 ATCGATCAGAATGGGATCATCTCCACCCTGCTCGGCTCTAATGATCTCATACAGCCCGG 4207  
Db 332 GTCGACCAGAATGGAATCATCTCCACCTTGCTGGGCTCCAACGACCTCACCGCTGTCCGG 391  
QY 4208 CCACTCAGCTGTGATTCTGTCTATGGATATTTCCCAGGTAAGACT 4251  
Db 392 CCCCTGAGCTGTGACTCCAGCATGGATGTGGCCCCAGGTGGGATT 435

RESULT 15  
US-10-750-185-28736/c  
; Sequence 28736, Application US/10750185  
; Publication No. US20050260603A1  
; GENERAL INFORMATION:  
; APPLICANT: MMI GENOMICS, INC.  
; APPLICANT: DENISE, Sue K.  
; APPLICANT: KERR, Richard  
; APPLICANT: ROSENFELD, David  
; APPLICANT: HOLM, Tom  
; APPLICANT: BATES, Stephen  
; APPLICANT: FANTIN, Dennis  
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS  
; FILE REFERENCE: MM1100-2

; CURRENT APPLICATION NUMBER: US/10/750,185  
; CURRENT FILING DATE: 2003-12-31  
; PRIOR APPLICATION NUMBER: US 60/437,482  
; PRIOR FILING DATE: 2002-12-31  
; NUMBER OF SEQ ID NOS: 64922  
; SOFTWARE: PatentIN version 3.1  
; SEQ ID NO 28736  
; LENGTH: 1835  
; TYPE: DNA  
; ORGANISM: Bovine 19866880998125  
US-10-750-185-28736  
Query Match 1.1%; Score 92.6; DB 6; Length 1835;  
Best Local Similarity 62.1%; Pred. No. 2.9e-13;  
Matches 146; Conservative 0; Mismatches 89; Indels 0; Gaps 0;  
QY 1816 AGCCTCCTGCCCCGTCTCTGTAGCGGAAATGGCCCAATACATGAAAAGSCAGATGCTTGTG 1875  
Db 273 AGATTCTGTCCTGTCTGTGTGGTGGGAATGGAGAATATGAAAAAGGACACTGTGTCTG 214  
QY 1876 CCACAGTGGCTGGAAGGGCGCTGAGTGCATGTCGCCACCAACCAAGTGTATCGATGTGGC 1935  
Db 213 CCGAAATGGCTGGAAGGGGCCAGAGTCCGATGTTCCAGAAGCAATGCATTGATCCAAC 154  
QY 1936 CTGCAGCAACCATGGCACCTGTCATCACGGGCACCTGTCATCTGCAACCCCTGGCTACAAGG 1995  
Db 153 GTGCTTTGGCCACGCGCACCTGTCATCATGCGAGTTCGATCTGTGTGCCAGGATACAAAG 94  
QY 1996 CGAGAGCTGTGAGGAAGTGGACTGCATGCGATGGACCCCAACATGTTTCAGGCCGGGTGTC 2050  
Db 93 AGAAATATGCGAGGAAGGTGAGAGCCCTGTGTTAATATATATTGCTTCAGGCTTTTC 39

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Job time : 641 secs

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OM nucleic - nucleic search, using sw model

Run on: December 9, 2005, 19:44:14 ; Search time 5839 Seconds  
(without alignments)  
11831.201 Million cell updates/sec

Title: US-10-029-020-13  
Perfect score: 8354  
Sequence: 1 gtttgtgatgtggaggac.....ccggaggtgacagagggac 8354

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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10: /cgn2\_6/ptodata/1/pubpna/US11\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES				
Result No.	Score	Query Match	Length DB ID	Description
1	8354	100.0	8354	7 US-10-383-201-43 Sequence 43, Appl
2	8354	100.0	8354	7 US-10-029-020-13 Sequence 13, Appl
3	8225	98.5	8645	7 US-10-467-535-22 Sequence 22, Appl
4	7991.2	95.7	8355	7 US-10-383-201-55 Sequence 55, Appl
5	7779.2	93.1	8438	7 US-10-042-865-1 Sequence 1, Appli
6	3680.8	44.1	8624	8 US-10-723-860-3169 Sequence 3169, Ap
7	3680.8	44.1	8624	9 US-10-756-149-2959 Sequence 2959, Ap
8	3621.6	43.4	8774	8 US-10-723-860-7176 Sequence 7176, Ap
9	3502.2	41.9	8645	7 US-10-038-854-37 Sequence 37, Appl
10	3473.8	41.6	8675	7 US-10-038-854-35 Sequence 35, Appl
11	3422	41.0	8473	7 US-10-038-854-39 Sequence 39, Appl
12	3398.8	40.7	8487	7 US-10-038-854-41 Sequence 41, Appl
13	3397.8	40.7	8689	3 US-09-808-602-78 Sequence 78, Appl
14	3397.8	40.7	8689	3 US-09-800-198-66 Sequence 66, Appl
15	3385	40.5	9826	3 US-09-808-602-7 Sequence 7, Appli
16	3385	40.5	9826	3 US-09-800-198-7 Sequence 7, Appli
17	3384.8	40.5	8797	3 US-09-808-602-74 Sequence 74, Appl
18	3384.8	40.5	8797	3 US-09-808-602-77 Sequence 77, Appl
19	3384.8	40.5	8797	3 US-09-800-198-62 Sequence 62, Appl
20	3384.8	40.5	8797	3 US-09-800-198-65 Sequence 65, Appl
21	3384.8	40.5	8797	9 US-10-631-467-1171 Sequence 1171, Ap
22	3351.4	40.1	9729	3 US-09-808-602-12 Sequence 12, Appl
23	3351.4	40.1	9729	3 US-09-800-198-12 Sequence 12, Appl



Db 1 |||||GTGTGGATGTGGAGGAGCGCGGCGGAGGCCATGGACGTGAAGGAGAGAACCTTA 60

QY 61 CCGCTCGTGAACCCGCGCGCCGAGCGCGAGCGCGCTACACAGACTCGTCCGCGGACAG 120

Db 61 CCGCTCGTGAACCCGCGCGCCGAGCGCGAGCGCGCTACACAGACTCGTCCGCGGACAG 120

QY 121 CGAGGAGGCAAGCCCCCGCAGAAATCGTACAGCTCCAGCGAGACCCCTGAAGGCCCTACGA 180

Db 121 CGAGGAGGCAAGCCCCCGCAGAAATCGTACAGCTCCAGCGAGACCCCTGAAGGCCCTACGA 180

QY 181 CCAGGACGCCGCCCTAGCCCTATGGCAGCCGCGTCAAGGACATTTGTCCGCGAGGAGGCCGA 240

Db 181 CCAGGACGCCGCCCTAGCCCTATGGCAGCCGCGTCAAGGACATTTGTCCGCGAGGAGGCCGA 240

QY 241 GGAATTCTGCGGCACAGGTGCCAACTTCAACCTGCGGGAGCTGGGGCTGGAAGAGTAAC 300

Db 241 GGAATTCTGCGGCACAGGTGCCAACTTCAACCTGCGGGAGCTGGGGCTGGAAGAGTAAC 300

QY 301 GCCCCCTACGGGACCCCTGTACCGGACAGACATTGGCCCTGCCCAATGCGGCTACTCCAT 360

Db 301 GCCCCCTACGGGACCCCTGTACCGGACAGACATTGGCCCTGCCCAATGCGGCTACTCCAT 360

QY 361 GGGGGCTGGTCTGATGCCGACATGGAGGCTGACACGGTGTCTCCCTGAGCACCCCGT 420

Db 361 GGGGGCTGGTCTGATGCCGACATGGAGGCTGACACGGTGTCTCCCTGAGCACCCCGT 420

QY 421 GCGTCTGSGGGCCGGAGCACACGGTCAAGGGCGCAGCTCCTGCTGTCCAGCCGGGCCAA 480

Db 421 GCGTCTGSGGGCCGGAGCACACGGTCAAGGGCGCAGCTCCTGCTGTCCAGCCGGGCCAA 480

QY 481 TTCCAATCTCACACTCACCGACACCGAGCATGAAAACACTGAGACTGATCATCCGSGCGG 540

Db 481 TTCCAATCTCACACTCACCGACACCGAGCATGAAAACACTGAGACTGATCATCCGSGCGG 540

QY 541 CCTGCAGAACCA CGCGCGGCTCCGGACGCCCGCGCGCTCTCGCA CGCCCCACACCCC 600

Db 541 CCTGCAGAACCA CGCGCGGCTCCGGACGCCCGCGCGCTCTCGCA CGCCCCACACCCC 600

QY 601 CAACCAAGCACCGCGGCTCCATTAACTCCCTGAACCGGGGCAACTTCA CGCCGAGGAG 660

Db 601 CAACCAAGCACCGCGGCTCCATTAACTCCCTGAACCGGGGCAACTTCA CGCCGAGGAG 660

QY 661 CAACCCAGCCCGGCCCCCAGGACCACTCGCTCTCCGAGAGCCCCCTGCGCGGCGCGC 720

Db 661 CAACCCAGCCCGGCCCCCAGGACCACTCGCTCTCCGAGAGCCCCCTGCGCGGCGCGC 720

QY 721 CCAGGAGCTGCCACGCCCGGAGAACTGGCTGCTCAACAGCAACATCCCCCTGGAGAC 780

Db 721 CCAGGAGCTGCCACGCCCGGAGAACTGGCTGCTCAACAGCAACATCCCCCTGGAGAC 780

QY 781 CAGGAACCTAGGCAAGCAGCCATTCTAGGGACATTGCAAGGACAACTCA TTGAGATGGA 840

Db 781 CAGGAACCTAGGCAAGCAGCCATTCTAGGGACATTGCAAGGACAACTCA TTGAGATGGA 840

QY 841 CATTCTCGGCGCTCCCGCCATGATGGGCTTACAGTGACGGGCACCTTCTCTTCAAGCC 900

Db 841 CATTCTCGGCGCTCCCGCCATGATGGGCTTACAGTGACGGGCACCTTCTCTTCAAGCC 900

QY 901 TGGAGGCACCTCCCGGCTCTTCTGCACCACTACACAGGGTACCCACTGACGTCCAGCAC 960

Db 901 TGGAGGCACCTCCCGGCTCTTCTGCACCACTACACAGGGTACCCACTGACGTCCAGCAC 960

QY 961 AGTGACTCTCTCCGCCCCGACCCCTGCCCGCAGCACTTCCGCCCCGGGCTTTAA 1020

Db 961 AGTGACTCTCTCTCCGCCCCGACCCCTGCCCGCAGCACTTCCGCCCCGGGCTTTAA 1020

QY 1021 CCTCAAGAACCCCTCCAAGTACTGTAAGTGAAGTGGCAGCCCTGAGCGCCATCGTCAAT 1080

Db 1021 CCTCAAGAACCCCTCCAAGTACTGTAAGTGAAGTGGCAGCCCTGAGCGCCATCGTCAAT 1080

QY 1081 CTCAAGCCACTCTGGTCAATCCTGTGGCATACTTTGTGSCCATGCACCTGTTTGGCCTAAA 1140

Db 1081 CTCAGCCACTCTGTGTCATCCTGTCTGGCATACTTTGTGGCCATGCACCTGTTTGGCCTAAA 1140

QY 1141 CTGGCACCTGCAGCCGATGGAGGGGCAGATGTATGAGATCACGGAGGACACAGCCAGCAG 1200

Db 1141 CTGGCACCTGCAGCCGATGGAGGGGCAGATGTATGAGATCACGGAGGACACAGCCAGCAG 1200

QY 1201 TTGGCCTGTGCCAACCGACGTCTCCCTATACCCCTCAGGGGGCACTGGCTTAGAGACCCC 1260

Db 1201 TTGGCCTGTGCCAACCGACGTCTCCCTATACCCCTCAGGGGGCACTGGCTTAGAGACCCC 1260

QY 1261 TGACAGGAAAGGCAAGGAACCA CAGAAGGAAGCCCTAGTAGTTCTTTCCAGAGGACAG 1320

Db 1261 TGACAGGAAAGGCAAGGAACCA CAGAAGGAAGCCCTAGTAGTTCTTTCCAGAGGACAG 1320

QY 1321 TTTCATAGATTCTGGAGAAATTGATGTGGGAAGCGCCTCCAGAAAGATTCCTCTGG 1380

Db 1321 TTTCATAGATTCTGGAGAAATTGATGTGGGAAGCGAGCCTCCAGAAAGATTCCTCTGG 1380

QY 1381 CACTTTCTGGAGATCTCAAGTGTTCATAGACCATCTCTGTCATCTGAAATTCATGTGTC 1440

Db 1381 CACTTTCTGGAGATCTCAAGTGTTCATAGACCATCTCTGTCATCTGAAATTCATGTGTC 1440

QY 1441 TCTGGAAAGGCAGCCCTGTTGGCATTTATGGCAGAAAGCCCTCCCTCTCACATAC 1500

Db 1441 TCTGGAAAGGCAGCCCTGTTGGCATTTATGGCAGAAAGCCCTCCCTCTCACATAC 1500

QY 1501 ACAGTTTGACTTTGTGGAGCTGCTGGATGGCAGGAGGCTCTTAACCCAGGAGCGCGGAG 1560

Db 1501 ACAGTTTGACTTTGTGGAGCTGCTGGATGGCAGGAGGCTCTTAACCCAGGAGCGCGGAG 1560

QY 1561 CCTAGAGGGGACCCCGCCAGTCTCGGGGAACCTGTGCCCCCTCCAGCCATGAGACAGG 1620

Db 1561 CCTAGAGGGGACCCCGCCAGTCTCGGGGAACCTGTGCCCCCTCCAGCCATGAGACAGG 1620

QY 1621 CTTCAATCCAGTATTTGGATTTCAGGAATCTGGCACTTGCGCTTTTACAAATGACGGAAGGA 1680

Db 1621 CTTCAATCCAGTATTTGGATTTCAGGAATCTGGCACTTGCGCTTTTACAAATGACGGAAGGA 1680

QY 1681 GTCAGAAAGTGTTTCTTCTCACCACTGCATTCGATCGGTGGATAACTGCCCCAGCAA 1740

Db 1681 GTCAGAAAGTGTTTCTTCTCACCACTGCATTCGATCGGTGGATAACTGCCCCAGCAA 1740

QY 1741 CTGCTATGGCAATGGTGACTGCATCTCTGGGACCTGCCACTGCTTCTCTGGTTCCTGGG 1800

Db 1741 CTGCTATGGCAATGGTGACTGCATCTCTGGGACCTGCCACTGCTTCTCTGGTTCCTGGG 1800

QY 1801 CCCCCACTGTGGCAGAGCCCTCCTGCCCCGTGCTCTGTAGCGGAAATGGCCAATACATGAA 1860

Db 1801 CCCCCACTGTGGCAGAGCCCTCCTGCCCCGTGCTCTGTAGCGGAAATGGCCAATACATGAA 1860

QY 1861 AGGCAGATGCTTGTGCCACAGTGGCTGGAAAGGCGCTGAGTGGATGTGCCCAACCA 1920

Db 1861 AGGCAGATGCTTGTGCCACAGTGGCTGGAAAGGCGCTGAGTGGATGTGCCCAACCA 1920

QY 1921 GTGTATCGATGTGGCCTGCAGCAACCA TGGCACTGTCATCACGGGCACTGTCATCTGCAA 1980

Db 1921 GTGTATCGATGTGGCCTGCAGCAACCA TGGCACTGTCATCACGGGCACTGTCATCTGCAA 1980

QY 1981 CCCTGGCTACAAGGGCGAGAGCTGTAGGAAGTGGACTGTCATGGACCCCACTGTTTCAAG 2040

Db 1981 CCCTGGCTACAAGGGCGAGAGCTGTAGGAAGTGGACTGTCATGGACCCCACTGTTTCAAG 2040

QY 2041 CCGGGTGTCTGCGTGAGAGGCGAATGCCATTGCTTTGGGATGGGAGGCCAACACTG 2100

Db 2041 CCGGGTGTCTGCGTGAGAGGCGAATGCCATTGCTTTGGGATGGGAGGCCAACACTG 2100

QY 2101 CGAGACCCCGAGGGCCACATGCTTAGACCAGTGTTCAGGCCACGGAACCTTCTCCCGGA 2160

Db 2101 CGAGACCCCGAGGGCCACATGCTTAGACCAGTGTTCAGGCCACGGAACCTTCTCCCGGA 2160

QY 2161 CACCGGGCTTTCAGCTGTGACCCCAAGCTGGA CTGGACACGACTGTTCTATCGAGATCTG 2220

Db 2161 CACCGGGCTTTCAGCTGTGACCCCAAGCTGGA CTGGACACGACTGTTCTATCGAGATCTG 2220

QY	2221	TGCTGCCGACTGTGGCCATGGCGTGTGCGTAGGGGGCACCTGCCGCTGCGAGGATGG	2280
Db	2221		
QY	2281	CTGGATGGGGGACGCTGCGACCGAGCGGGCTGCCACCGCGCTGTGCCGAGCATGGGAC	2340
Db	2281		
QY	2341	CTGCCGACGGCAAGTGCAGACCGGGCTGCCCTGGCTGGAATGGCGAACACTGCACCATCGC	2400
Db	2341		
QY	2401	TCACATCTGGATAGGGTAGTTAAAGAGGGTTGCCCTGGGTTGTGCAATGGCAACGGCAG	2460
Db	2401		
QY	2461	ATGTACCTTAGACCTGAATGGTTGGCACTGCGTCTGCCAGCTGGGCTGGAGAGGACTGG	2520
Db	2461		
QY	2521	CTGTGACACTTCCATGGAGACTGCCCTGGGTGACAGCAAAAGACAATGATGGAGATGGCCT	2580
Db	2521		
QY	2581	GGTGGACTGCATGGACCTGACTGTGCCCTCCAGCCCCCTGTGCCATATCAACCCGCTGTG	2640
Db	2581		
QY	2641	CCTTGGCTCCCCCTAACCCTCTGGACATCATCCAGGAGACACAGGTCCTGTGTACAGCA	2700
Db	2641		
QY	2701	GAACCTACACTCCTTCTATGACCGCATCAAGTTCCTCGTGGCAGGACAGCACGCACAT	2760
Db	2701		
QY	2761	AATCCCCGGGAGAACCCCTTTGATGGAGGGCATGCTTGTGTTATTCGTGGCCAAAGTGAT	2820
Db	2761		
QY	2821	GACATCAGATGGAAACCCCTCTGGTGTGAGCAATCAGTTTTGTCAATAACCCCTCTCTT	2880
Db	2821		
QY	2881	TGGATATACAATCAGCAGGCAAGATGGCAGCTTTTGACTTGGTGACAAATGGCGGCATCTC	2940
Db	2881		
QY	2941	CATCATCCTGCGGTTGAGCGGGCACCTTTTCATCACAGGAGCACACCCCTGTGGCTGCC	3000
Db	2941		
QY	3001	ATGGGATCGCTTCTTTGTATGGAAACCATCATATGAGACATGAGGAGAAATGAGATTCC	3060
Db	3001		
QY	3061	CAGCTGTGACCTGAGCAATTTTGCCCGCCCCAACCCAGTCTCTCCATCCCCACTGAC	3120
Db	3061		
QY	3121	GTCCCTCGCCAGCTCCTGTGCAGAGAAAGGCCCCCATTTGTCCGGAAATTCAGGCTTTGCA	3180
Db	3121		
QY	3181	GGAGGAAATCTCTATCTCTGGCTGCAAGATGAGGCTGAGCTACCTGAGCAGCGGACCCC	3240
Db	3181		
QY	3241	TGGCTACAAATCTGTCTGAGGATCAGCCTCACCCACCGACCATCCCCCTTCAACCTCAT	3300
Db	3241		

QY	3301	GAAGTGCACCTCATGGTAGCGGTGAGGGCCGCCCTCTTTCAGGAAGTGGTTCGCTGCAGC	3360
Db	3301		
QY	3361	CCCAGACCTGTCTATTATTTCATTGGGACAAGACAGACGCTGTACAAACCAGAAAGGTGTT	3420
Db	3361		
QY	3421	TGGGCTTTCAGAAAGCCTTTGTTTCOGTGGGTTATGAATATGAATCTGCTGCCAGATCTAAT	3480
Db	3421		
QY	3481	CCTGTGGAAAAAAGAACACAGTCTGCAGGGCTATGAAATTTGACGCTTCAAAGCTTGG	3540
Db	3481		
QY	3541	AGGATGGAGCCTAGACAAACATCATGCCCTCAACATTTCAAAAGTGGTATCCTGCACAAAGG	3600
Db	3541		
QY	3601	GAATGGGAGAACCAAGTTTGTGTCTCAGCAGCCTCCTGTCAATTTGGAGCATCATGGGCAA	3660
Db	3601		
QY	3661	TGGCGCGGAGAAAGCATCTCCTGCCAGCTGCAACGGCCTTGTGACGGCAACAAGCT	3720
Db	3661		
QY	3721	CCTGGCCCCAGTGGCCCTCACCTGTGCTCTGACGGAGCCTCTATFTGGGTGATTTCAA	3780
Db	3721		
QY	3781	CTACATTAGAAAGGATCTTCCCCTCTGGAAATGTCACCAACATCCTAGAGCTGAGGAATAA	3840
Db	3781		
QY	3841	AGATTTCAGACATAGTCACAGTCCAGCACACAAATACTACCTGGGCCACAGACCCCATGAG	3900
Db	3841		
QY	3901	TGGGGCCGCTTCTTCTGTACAGCAACAGCCGGCGGTCTTTTAAATCAAGTCCACTGT	3960
Db	3901		
QY	3961	GGTGTGAAGACCTTGTCAAGAACTCTGAGGTGGTTGCGGGACAGGTGACCACTGCCT	4020
Db	3961		
QY	4021	CCCCCTTTGATGACACTCGCTGCGGGGATGGTGGGAAGGCCACAGAGCCACACTCACCAA	4080
Db	4021		
QY	4081	TCCCAGGGGTATTACAGTGGACAAGTTTGGGCTGATCTACTTCGTGGATGGCACCATGAT	4140
Db	4081		
QY	4141	CAGACGCATCGATCAGAAATGGGATCATCTCCACCCCTGCTCGGCTCTAATGATCTCACATC	4200
Db	4141		
QY	4201	AGCCCGGCCACTCAGCTGTGATTCTGTCAATGGATATTTCCCAGGTAAGACTGGAGTGGCC	4260
Db	4201		
QY	4261	CACAGACTTAGCCATCAACCCCAATGGACAACTCACTTTATGTCTCGACAACAATGTGGT	4320
Db	4261		
QY	4321	CCTGCAAAATCTCTGAAAAACCAACAGGTGGCATTTGTCCCGGGAGGCCCATGCACTGCCA	4380
Db	4321		
QY	4381	GGTCCCCTGGCATTTGACCACTTCTCTGTCTAAGCAAGGTGGCCATCCACGGCAACCCCTGGAGTC	4440



Db	4381	GGTCCCTGGCATTGACCACCTTCCTGCTAAGCAAGGTGGCCATCCACGCAACCCCTGGAGTC	4440
QY	4441	AGCCACCGCTTTGGCTGTTTCACACAATGGGGTCCTGTATATATGCTGAGACTGATGAGAA	4500
Db	4441	AGCCACCGCTTTGGCTGTTTCACACAATGGGGTCCTGTATATATGCTGAGACTGATGAGAA	4500
QY	4501	AAAGATCAACCGCATCAGGCAGGTACCACTAGTGGAGAGATCTCACTCGTTGCTGGGGC	4560
Db	4501	AAAGATCAACCGCATCAGGCAGGTACCACTAGTGGAGAGATCTCACTCGTTGCTGGGGC	4560
QY	4561	CCCCAGTGGTGTGACTGTAAAAATGATGCCAACTGTGATGTTTTCTTGAGACGATGG	4620
Db	4561	CCCCAGTGGTGTGACTGTAAAAATGATGCCAACTGTGATGTTTTCTTGAGACGATGG	4620
QY	4621	TTATGCCAAGGATGCAAAAGTTAAATACCCCATCTTCCTTGGCTGTGTGCTGATGGGA	4680
Db	4621	TTATGCCAAGGATGCAAAAGTTAAATACCCCATCTTCCTTGGCTGTGTGCTGATGGGA	4680
QY	4681	GCTCTACGTGGCCGACCTTGGGAACATCCGAATTCGGTTTATCCGGAAGAACAAAGCCTTT	4740
Db	4681	GCTCTACGTGGCCGACCTTGGGAACATCCGAATTCGGTTTATCCGGAAGAACAAAGCCTTT	4740
QY	4741	CCTCAACACCCAGAACATGTATGAGCTGTCTTCAACCAATTGACCAGGAGCTCTATCTGTT	4800
Db	4741	CCTCAACACCCAGAACATGTATGAGCTGTCTTCAACCAATTGACCAGGAGCTCTATCTGTT	4800
QY	4801	TGATACACCCGGCAAGCACCTGTACACCCAAAGCCTGCCACAGGAGACTACCTGTACAA	4860
Db	4801	TGATACACCCGGCAAGCACCTGTACACCCAAAGCCTGCCACAGGAGACTACCTGTACAA	4860
QY	4861	CTTACCTPACACTGGGGACGGCAGCATCACACTCATCACAGACAAACAATGGCAACATGGT	4920
Db	4861	CTTACCTPACACTGGGGACGGCAGCATCACACTCATCACAGACAAACAATGGCAACATGGT	4920
QY	4921	AAATGTCGCGCAGACTCTACTGGGATGCCCTCTGGCTGGTGGTCCCAGATGGCCAGGT	4980
Db	4921	AAATGTCGCGCAGACTCTACTGGGATGCCCTCTGGCTGGTGGTCCCAGATGGCCAGGT	4980
QY	4981	GTACTGGGTGACCATTGGGCACCAACAGTGCACCTCAAGAGTGTGACCAACAAGGACACGA	5040
Db	4981	GTACTGGGTGACCATTGGGCACCAACAGTGCACCTCAAGAGTGTGACCAACAAGGACACGA	5040
QY	5041	GTTGGCCATGATGACATACCATGGCAATTCCGGCCCTTCGGCAACCAAAAGCAATGA AAA	5100
Db	5041	GTTGGCCATGATGACATACCATGGCAATTCCGGCCCTTCGGCAACCAAAAGCAATGA AAA	5100
QY	5101	CGGATGGACAAACATTTTATGAGTACGACAGCTTTGGCCGCTTGACAAAATGTGACCTTCCC	5160
Db	5101	CGGATGGACAAACATTTTATGAGTACGACAGCTTTGGCCGCTTGACAAAATGTGACCTTCCC	5160
QY	5161	TACTGGCCAGGTGAGCAGTTTCCGAAGTGATACAGACAGTTTCCAGGTAGATGATGATGAGT	5220
Db	5161	TACTGGCCAGGTGAGCAGTTTCCGAAGTGATACAGACAGTTTCCAGGTAGATGATGATGAGT	5220
QY	5221	GACCTCCAGCAAGGATGATGTCACCAATAACCAACCACTGTCTGCCTCAGGCGCCTTCTA	5280
Db	5221	GACCTCCAGCAAGGATGATGTCACCAATAACCAACCACTGTCTGCCTCAGGCGCCTTCTA	5280
QY	5281	CACACTGCTGCAAGACCAAGTCCGGAACAGCTACTACATCGGGGCCGATGGCTCTTGGC	5340
Db	5281	CACACTGCTGCAAGACCAAGTCCGGAACAGCTACTACATCGGGGCCGATGGCTCTTGGC	5340
QY	5341	GCTGCTGCTGGCCAAACGGCATGGAGGTGGCGCTGCAGACTGAGCCCCACTTGTGCTGGTGG	5400
Db	5341	GCTGCTGCTGGCCAAACGGCATGGAGGTGGCGCTGCAGACTGAGCCCCACTTGTGCTGGTGG	5400
QY	5401	CACCGTCAACCCCAACCGTGGCAAGAGGAATGTACGCTGCCCATCGACAAACGGCCTCAA	5460
Db	5401	CACCGTCAACCCCAACCGTGGCAAGAGGAATGTACGCTGCCCATCGACAAACGGCCTCAA	5460
QY	5461	CTGCTGGAGTGGCCAGCGCAAGAGCAGGCTCGGGCCAGGTCACTGTCTTTGGGCG	5520
Db	5461	CTGCTGGAGTGGCCAGCGCAAGAGCAGGCTCGGGCCAGGTCACTGTCTTTGGGCG	5520

Db	5461	CCTGGTGGAGTGGCGCCAGCGCAAAAGAGCAGGCTCGGGCCAGGTCACTGTCTTTGGGCG	5520
QY	5521	CCGGCTGCGGGTGCACAAACCGAAAATCTCCTATCTCTGGACTTTGATCGCGTAACACGCAC	5580
Db	5521	CCGGCTGCGGGTGCACAAACCGAAAATCTCCTATCTCTGGACTTTGATCGCGTAACACGCAC	5580
QY	5581	AGAGAAAGATCTATGATGACCACCCGCAAGTTCAACCCCTTCGGATTCTGTACGACGAGCGGG	5640
Db	5581	AGAGAAAGATCTATGATGACCACCCGCAAGTTCAACCCCTTCGGATTCTGTACGACGAGCGGG	5640
QY	5641	GCGGCCCCAGCCTCTGGTCAACCCAGCAGCAAGCTGAATGGTGTCAACGTGACATACTCCCC	5700
Db	5641	GCGGCCCCAGCCTCTGGTCAACCCAGCAGCAAGCTGAATGGTGTCAACGTGACATACTCCCC	5700
QY	5701	TGGGGTTTACATTGCTGGCATCCAGAGGGGCATCATGTCTGAAAAGATGGAATACGACCA	5760
Db	5701	TGGGGTTTACATTGCTGGCATCCAGAGGGGCATCATGTCTGAAAAGATGGAATACGACCA	5760
QY	5761	GGCGGGCCGCATCACATCCAGGATCTTCGCTGATGGGAAGACATGGAGCTACACATACTT	5820
Db	5761	GGCGGGCCGCATCACATCCAGGATCTTCGCTGATGGGAAGACATGGAGCTACACATACTT	5820
QY	5821	AGAGAAAGTCCATGGTGTCTGTACTACACAGCCAGAGGCAGTATATCTTTGAGTTCGACAA	5880
Db	5821	AGAGAAAGTCCATGGTGTCTGTACTACACAGCCAGAGGCAGTATATCTTTGAGTTCGACAA	5880
QY	5881	GAATGACCGCCTCTCTTCTGTGACGATGCCCAACGTTGGCGCGGCAGACACTAGAGACCAT	5940
Db	5881	GAATGACCGCCTCTCTTCTGTGACGATGCCCAACGTTGGCGCGGCAGACACTAGAGACCAT	5940
QY	5941	CCGCTCAGTGGGCTACTACAGAAAACATCTATCAGCCCCCTTGAGGGCAATGCCTCAGTCAT	6000
Db	5941	CCGCTCAGTGGGCTACTACAGAAAACATCTATCAGCCCCCTTGAGGGCAATGCCTCAGTCAT	6000
QY	6001	ACAGGACTTCACTGAGGATGGGCACCTCCTTCAACACTTTCACACCTTCTACCTGGGCACTGGCCG	6060
Db	6001	ACAGGACTTCACTGAGGATGGGCACCTCCTTCAACACTTCTACCTGGGCACTGGCCG	6060
QY	6061	GGTGATATACAAGTATGGCAAACTGTCAAAAGCTGGCAGAGACGCTCTATGACACCAACCA	6120
Db	6061	GGTGATATACAAGTATGGCAAACTGTCAAAAGCTGGCAGAGACGCTCTATGACACCAACCA	6120
QY	6121	GGTCAGTTTCACCTATGACGAGACGCGCAGGCATGCTGAAGACCACTCAACCTACAGAAATGA	6180
Db	6121	GGTCAGTTTCACCTATGACGAGACGCGCAGGCATGCTGAAGACCACTCAACCTACAGAAATGA	6180
QY	6181	GGGCTTCACTGCACCATCCGCTACCGTCAGATTGGGCCCCCTTGATGACCGACAGATCTT	6240
Db	6181	GGGCTTCACTGCACCATCCGCTACCGTCAGATTGGGCCCCCTTGATGACCGACAGATCTT	6240
QY	6241	CCGCTTCACTGAGGAAAGGCATGGTCAACGCCCCGTTTGGACTACAACTATGACAAACAGCTT	6300
Db	6241	CCGCTTCACTGAGGAAAGGCATGGTCAACGCCCCGTTTGGACTACAACTATGACAAACAGCTT	6300
QY	6301	CCGGTGACCAAGCATGCAGGCTGTGATCAACGAGACCCCACTGCCCATTTGATCTCTATCG	6360
Db	6301	CCGGTGACCAAGCATGCAGGCTGTGATCAACGAGACCCCACTGCCCATTTGATCTCTATCG	6360
QY	6361	CTATGATGATGTGTGAGGCAAGACAGAGCAGTTTGGGAAGTTTGGTGTCTTTTACTATGA	6420
Db	6361	CTATGATGATGTGTGAGGCAAGACAGAGCAGTTTGGGAAGTTTGGTGTCTTTTACTATGA	6420
QY	6421	CATTAAACCAGATCATCACCACAGCTGTGATGACCCACACCAAGCATTTTGTGATATGG	6480
Db	6421	CATTAAACCAGATCATCACCACAGCTGTGATGACCCACACCAAGCATTTTGTGATATGG	6480
QY	6481	CAGGATGAAGGAAGTGCAGTATGAGATCTTCCGCTCGCTCATGTGATGATGACCGCTCCA	6540
Db	6481	CAGGATGAAGGAAGTGCAGTATGAGATCTTCCGCTCGCTCATGTGATGATGACCGCTCCA	6540
QY	6541	GTATGATAACATGGGGCGAGTAGTGAAGAAAGGAGCTGAAGGTAGGACCCCTACGCCAATAC	6600
Db	6541	GTATGATAACATGGGGCGAGTAGTGAAGAAAGGAGCTGAAGGTAGGACCCCTACGCCAATAC	6600



QY 6601 CACTCGCTACTCCTATGAGTATGATGCTGACGGCCAGCTGCAGACAGTCTCCATCAATGA 6660  
Db 6601 CACTCGCTACTCCTATGAGTATGATGCTGACGGCCAGCTGCAGACAGTCTCCATCAATGA 6660  
QY 6661 CAAGCCACTCTGGCGCTACAGCTACGACTCAATGGGAACCTGCACTTACTGAGCCCTGG 6720  
Db 6661 CAAGCCACTCTGGCGCTACAGCTACGACTCAATGGGAACCTGCACTTACTGAGCCCTGG 6720  
QY 6721 GAACAGTGACGGCTCACACCCTACGGTATGACATCCGGACCGCATCACTCGGCTGG 6780  
Db 6721 GAACAGTGACGGCTCACACCCTACGGTATGACATCCGGACCGCATCACTCGGCTGG 6780  
QY 6781 TGACGTGCAATACAAGATGGATGAGATGGCTTCTGAGGACGGGGCGGTGATATCTT 6840  
Db 6781 TGACGTGCAATACAAGATGGATGAGATGGCTTCTGAGGACGGGGCGGTGATATCTT 6840  
QY 6841 TGAGTACAACTCAGCTGGCCTGCTCATCAAGGCCCTACAACCGGCTGGCAGCTGGAGTGT 6900  
Db 6841 TGAGTACAACTCAGCTGGCCTGCTCATCAAGGCCCTACAACCGGCTGGCAGCTGGAGTGT 6900  
QY 6901 CAGGTACCGCTACGATGGCCTGGGGCGGCGGTGTCCAGCAAGAGCAGCCACCA 6960  
Db 6901 CAGGTACCGCTACGATGGCCTGGGGCGGCGGTGTCCAGCAAGAGCAGCCACCA 6960  
QY 6961 CCTGCAGTCTTCTATGCAGACCTGACCAAGCCCAACCAAGGTCAACCCACCTGTACAACCA 7020  
Db 6961 CCTGCAGTCTTCTATGCAGACCTGACCAAGCCCAACCAAGGTCAACCCACCTGTACAACCA 7020  
QY 7021 CTCCAGCTCTGAGATCACCTCCCTCTACTAGCACTTGAAGGACACCTTTGCCATGGA 7080  
Db 7021 CTCCAGCTCTGAGATCACCTCCCTCTACTAGCACTTGAAGGACACCTTTGCCATGGA 7080  
QY 7081 GCTGAGCAGTGGTGATGAGTTTACATAGCTTGTGACAAATCGGGACCCCTCTTGTCTGT 7140  
Db 7081 GCTGAGCAGTGGTGATGAGTTTACATAGCTTGTGACAAATCGGGACCCCTCTTGTCTGT 7140  
QY 7141 CTTTAGTGGAACAGGTTTGATGATCAAGCAAAATCCTGTACACAGCCATATGGGAGATCTA 7200  
Db 7141 CTTTAGTGGAACAGGTTTGATGATCAAGCAAAATCCTGTACACAGCCATATGGGAGATCTA 7200  
QY 7201 CATGGATACCAACCCAACTTTAGATCATATAGGCTACCATGGTGGCCTCTATGATCC 7260  
Db 7201 CATGGATACCAACCCAACTTTAGATCATATAGGCTACCATGGTGGCCTCTATGATCC 7260  
QY 7261 ACTCACCAGCTTTGTCCACATGGGCGCGGAGATTATGATGTGTGCGCGGACGCTGGAC 7320  
Db 7261 ACTCACCAGCTTTGTCCACATGGGCGCGGAGATTATGATGTGTGCGCGGACGCTGGAC 7320  
QY 7321 TAGCCCAGACCAGAGCTGTGGAAGCACCTTTAGTAGCAGCAACGTCATGCTTTTAAATCT 7380  
Db 7321 TAGCCCAGACCAGAGCTGTGGAAGCACCTTTAGTAGCAGCAACGTCATGCTTTTAAATCT 7380  
QY 7381 CTATATGTTCAAAAACAACACCCCATCAGCAACTCCCAGGACATCAAGTGCTTCATGAC 7440  
Db 7381 CTATATGTTCAAAAACAACACCCCATCAGCAACTCCCAGGACATCAAGTGCTTCATGAC 7440  
QY 7441 AGATGTTAACAGCTGGCTGCTCACCTTTGGATTCCAGCTACACAACGTTGATCCCTGGTTA 7500  
Db 7441 AGATGTTAACAGCTGGCTGCTCACCTTTGGATTCCAGCTACACAACGTTGATCCCTGGTTA 7500  
QY 7501 TCCCAAACCCAGACATGGATGCCATGGAACCCCTCCTACGAGCTCATCCACACAGATGAA 7560  
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Db 8221 GAGCACAGGGCGGTGCAAGGCTACGACGGCTTTTCTGTGATCTCTGTGAGCAGTACCC 8280  
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RESULT 2

US-10-029-020-13  
; Sequence 13, Application US/10029020  
; Publication No. US20040033971A1  
; GENERAL INFORMATION:  
; APPLICANT: Gangolli et al.  
; TITLE OF INVENTION: Polypeptides and Nucleic Acids Encoding Same  
; FILE REFERENCE: 21402-225  
; CURRENT APPLICATION NUMBER: US/10/029,020  
; CURRENT FILING DATE: 2001-12-19  
; PRIOR APPLICATION NUMBER: 60/256,704  
; PRIOR FILING DATE: 2000-12-19  
; PRIOR APPLICATION NUMBER: 60/311,590  
; PRIOR FILING DATE: 2001-08-10  
; PRIOR APPLICATION NUMBER: 60/257,314  
; PRIOR FILING DATE: 2000-12-20  
; PRIOR APPLICATION NUMBER: 60/311,613  
; PRIOR FILING DATE: 2001-08-10  
; PRIOR APPLICATION NUMBER: 60/315,617  
; PRIOR FILING DATE: 2001-08-29  
; PRIOR APPLICATION NUMBER: 60/307,506  
; PRIOR FILING DATE: 2001-07-24  
; PRIOR APPLICATION NUMBER: 60/322,358  
; PRIOR FILING DATE: 2001-09-14

like as file  
same

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; PRIOR APPLICATION NUMBER: 60/294,075
; PRIOR FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: 60/288,153
; PRIOR FILING DATE: 2001-05-02
; NUMBER OF SEQ ID NOS: 190
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 8354
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-029-020-13

Query Match      100.0%; Score 8354; DB 7; Length 8354;
Best Local Similarity 100.0%; Pred. No. 0;
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QY 61 CCGCTCGCTGACCCCGCGCGGACGCGAGCGCGCTACACAGACTCGTCCGCGGACAG 120
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QY 421 GCGTCTGTGGGCGGAGCACACGGTCAGGGCGCAGCTCTGCTGTCCAGCCGGGCCAA 480
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Db 1801 CCCCAGCTGTGGCAGAGCCTCCTGCCCCCGTGTCTGTAGCGGAAATGGCCAATACATGAA 1860
QY 1861 AGGCAGATGCTTGTGCCACAGTGGTGGAAAGGCGCTGAGTCGATGTGCCCAACCA 1920
Db 1861 AGGCAGATGCTTGTGCCACAGTGGTGGAAAGGCGCTGAGTCGATGTGCCCAACCA 1920
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QY	4261	CACAGACTTAGCCATCAACCCCAATGGACAACTCACTTTATGTCTCTCGACAACAATGTGGT	4320
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QY	4621	TTATGCCAAGGATGCAAAAGTTAAATACCCCATCTTCCCTGGCTGTGTGCTGATGGGGA	4680
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Db	4921		
QY	4981	GTACTGGGTGACCATGGGCACCAACAGTGCATCTCAAGAGTGTGACCAACAGGACACGA	5040
Db	4981		
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Db	5041		
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Db	5161		
QY	5221	GACCTCCAGCAAGGATGATGTACCCATAAACCAACCTGTCTGCCTCAGGCGCCTTCTA	5280
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Db	5401		
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QY	5821	AGAGAAAGTCCAATGGTGTCTACTACAGCCAGAGGCAGTATATCTTTGAGTTTCGACAA	5880
Db	5821		
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QY	6001	ACAGGACTTCACTGAGGATGGGCACCTCTTACACCTTCTACCTGGGCACGTGGCCGCGAG	6060
Db	6001		
QY	6061	GGTGATATACAAAGTATGGCAAACTGTCAAAGCTGGCAGAGACGCTCTATGACACCAACAA	6120
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QY 6421 CATTAACCAGATCATCACCACAGCTGTCTATGACCCACACCAGCAATTTTGATGCATATGG 6480

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QY 8341 GTGACAGAGAGGAC 8354

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RESULT 3  
US-10-467-535-22  
; Sequence 22, Application US/10467535  
; Publication No. US20040146970A1  
; GENERAL INFORMATION:  
; APPLICANT: YUE, Henry; YAO, Monique G.  
; APPLICANT: ISON, Craig H.; LU, Yan



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; APPLICANT: LU, Dyung Aina M.; RICHARDSON, Thomas W.
; APPLICANT: TRAN, Uyen K.; KHARE, Reena
; APPLICANT: CHAWLA, Narinder K.
; TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL GROWTH, DIFFERENTIATION, AND DEATH
; FILE REFERENCE: PF-0903 USN
; CURRENT APPLICATION NUMBER: US/10/467,535
; CURRENT FILING DATE: 2003-08-08
; PRIOR APPLICATION NUMBER: PCT/US02/03715
; PRIOR FILING DATE: 2002-08-02
; PRIOR APPLICATION NUMBER: US 60/268,111
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/271,175
; PRIOR FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: US 60/274,503
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: US 60/274,552
; PRIOR FILING DATE: 2001-03-09
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PERL Program
; SEQ ID NO 22
; LENGTH: 8645
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No: 7488573CB1
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 93
; OTHER INFORMATION: a, t, c, g, or other
US-10-467-535-22

Query Match 98.5%; Score 8225; DB 7; Length 8645;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 8300; Conservative 0; Mismatches 21; Indels 33; Gaps 3;

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Qy 61 CCGTCGCTGACCCGGCGCCGGACGCCCGGCTACAGCTCCAGGAGACCCCTGAAGGCCTACGA 120
Db |||||||
143 CCGCTCGCTGACCCGGCGCCGGACGCCCGGCTACAGCTCGTCCGCGGACAG 202
Qy 121 CGAGGAGGGCAAAGCCCCCGCAGAAATCGTACAGCTCCAGGAGACCCCTGAAGGCCTACGA 180
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Qy 181 CCAGGACGCCCGCCTAGCCTATGGCAGCCGCGTCAAGGACATTTGTCGCGCAGGAGCCGA 240
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Qy 361 GGGGCTGGCTCTGATGCCGACATGGAGGCTGACACGGTGTCTCCCTGAGCACCCCGT 420
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Qy 421 GCGTCTGTGGGCGCGGAGCACACGGTCAGGGCGCAGCTCGCTGTCCAGCCGGGCCAA 480
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Db |||||||
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Qy 721 CCAGGAGCCTGCCACGCCCCAGGAGAACTGGTGCTCAACAGCAACATCCCCCTGGAGAC 780
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Qy 781 CAGGAACCTAGGCAAGCAGCCATTCTCTAGGACATTCAGGACAACCTCATTTGAGATGA 840
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Qy 1381 CACTTTCTGGAGATCTCAAGTGTTCATAGACCATCTCTGTGCATCTGAAATTCAATGTGTC 1440
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Qy 1681 GTCAGAAAGTGGTTTCCTTTCTCACCACCTGCCATTGAGTCGGTGGATAACTGCCCCAGCAA 1740  
Db 1751 GTCAGAAAGTGGTTTCCTTTCTCACCACCTGCCATTGAGTCGGTGGATAACTGCCCCAGCAA 1810  
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Db 1871 CCCCAGACTGTGGCAGAGCCTCTGCCCCGTGCTCTGTAGCGGAATGGCCAAATACATGAA 1930  
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Db 1931 AGGCAGATGCTTGTGTCACAGTGGCTGGAAAGGCGCTGAGTGCATGTGCCCCACCAACCA 1990  
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Qy	3781	CTACATTAGAAGGATCTTCCCCTCTGGAAATGTCAACAACTCCTAGAGCTGAGGAATAA	3840
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Db	3903	-----AGTCACAGTCCAGCACACAAATACTACCTGGCCACAGACCCCATGAG	3949
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Db	3950	TGGGGCCGTCTTCCTTTCTGACAGCAACAGCCGGGGTCTTTAAAAATCAAGTCCACTGT	4009
Qy	3961	GGTGGTAAGGACCTTGTCAAGAACTCTGAGGTGTTGCGGGGACAGGTGACCAGTGCCT	4020
Db	4010	GGTGGTAAGGACCTTGTCAAGAACTCTGAGGTGTTGCGGGGACAGGTGACCAGTGCCT	4069
Qy	4021	CCCCTTTGATGACACTCGCTCGGGGGATGGTGGGAAGGCCACAGAAGCCACACTCACAA	4080
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Qy	4081	TCCCAGGGGTATTACAGTGGACAAGTTTGGGCTGATCTACTTCGTGGATGGCACCATGAT	4140
Db	4130	TCCCAGGGGCATTACAGTGGACAAGTTTGGGCTGATCTACTTCGTGGATGGCACCATGAT	4189
Qy	4141	CAGACGCATCGATCAGAA TGGGATCATCTCCACCCTGTCTCGGCTCTAAATGATCTCACATC	4200
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Qy	4201	AGCCCCGCCACTCAGCTGTGATTTCTGTCAATGATATTTCCAGSTAAAGACTGGAGTGGCC	4260
Db	4250	AGCCCCGCCACTCAGCTGTGATTTCTGTCAATGATATTTCCAGSTTACCTGGAGTGGCC	4309
Qy	4261	CACAGACTTAGCCATCAACCCCAATGGACAACTCACTTTATGTCTCGACAACAATGTGGT	4320
Db	4310	CACAGACTTAGCCATCAACCCCAATGGACAACTCACTTTATGTCTCGACAACAATGTGGT	4369
Qy	4321	CCTGCAAAATCTTGAAAACCCACCAGGTGCGCATTTGTCGCGGGAGGCCCATGCAC TGCCA	4380
Db	4370	CCTGCAAAATCTTGAAAACCCACCAGGTGCGCATTTGTCGCGGGAGGCCCATGCAC TGCCA	4429
Qy	4381	GGTCCCTGGCATTTGACCACTTCCCTGTAAAGCAAGGTGGCCATCCACGCAACCCCTGGAGTC	4440
Db	4430	GGTCCCTGGCATTTGACCACTTCCCTGTAAAGCAAGGTGGCCATCCACGCAACCCCTGGAGTC	4489
Qy	4441	AGCCACCGCTTTGGCTGTTTCAACAATGGGGTCTGTATATTTGCTGAGACTGATGAGAA	4500
Db	4490	AGCCACCGCTTTGGCTGTTTCAACAATGGGGTCTGTATATTTGCTGAGACTGATGAGAA	4549
Qy	4501	AAAGATCAACCGCATCAGGCAGGTCAACCACTAGTGGAGAGATCTCACTCGTTGCTGGGGC	4560
Db	4550	AAAGATCAACCGCATCAGGCAGGTCAACCACTAGTGGAGAGATCTCACTCGTTGCTGGGGC	4609
Qy	4561	CCCCAGTGGCTGTGACTGTAAAAATGATGCCAACTGTGATTTTCTGGAGACGATGG	4620
Db	4610	CCCCAGTGGCTGTGACTGTAAAAATGATGCCAACTGTGATTTTCTGGAGACGATGG	4669
Qy	4621	TTATGCCAAGGATGCAAAGTTAAATACCCCATCTTCCCTGGCTGTGTGTGCTGATGGGA	4680
Db	4670	TTATGCCAAGGATGCAAAGTTAAATACCCCATCTTCCCTGGCTGTGTGTGTTGATGGGA	4729
Qy	4681	GCTCTACGTGGCCGACCTTGGGAACATCCGAATTCGGTTTATCCGGAAGAACAAAGCCTTT	4740
Db	4730	GCTCTACGTGGCCGACCTTGGGAACATCCGAATTCGGTTTATCCGGAAGAACAAAGCCTTT	4789
Qy	4741	CCTCAACACCCAGAACATGTATGAGCTGTCTTCAACCAATTGACCAGGAGCTCTATCTGTT	4800
Db	4790	CCTCAACACCCAGAACATGTATGAGCTGTCTTCAACCAATTGACCAGGAGCTCTATCTGTT	4849
Qy	4801	TGATACCA CCGGCAAGCACCTGTACCCAAAGCCTGCCACAGGAGACTACCTGTACAA	4860
Db	4850	TGATACCA CCGGCAAGCACCTGTACACCCAAAGCCTGCCACAGGAGACTACCTGTACAA	4909
Qy	4861	CTTCACTACACTGGGACGGCAGCATCACACTCATCACAGACAACAATGSCAACATGGT	4920
Db	4910	CTTCACTACACTGGGACGGCAGCATCACACTCATCACAGACAACAATGSCAACATGGT	4969
Qy	4921	AAATGTCCGCCGAGACTCTACTGGGATGCCCCCTCTGGCTGGTGGTCCCAGATGGCCAGGT	4980
Db	4970	AAATGTCCGCCGAGACTCTACTGGGATGCCCCCTCTGGCTGGTGGTCCCAGATGGCCAGGT	5029
Qy	4981	GTACTGGGTGACCAATGGGCACCAACAGTGCACTCAAGAGTGTGACCAACAAGGACACGA	5040
Db	5030	GTACTGGGTGACCAATGGGCACCAACAGTGCACTCAAGAGTGTGACCAACAAGGACACGA	5089
Qy	5041	GTTGGCCATGATGACATACCATGGCAAATTCGGGCCCTTCTGGCAACCACAAAGCAATGAAAA	5100
Db	5090	GTTGGCCATGATGACATACCATGGCAAATTCGGGCCCTTCTGGCAACCACAAAGCAATGAAAA	5149
Qy	5101	CGGATGGACAACATTTATGAGTACGACAGCTTTGGCCGCTTGACAAATGTGACCTTCCC	5160
Db	5150	CGGATGGACAACATTTATGAGTACGACAGCTTTGGCCGCTTGACAAATGTGACCTTCCC	5209
Qy	5161	TACTGGCCAGGTGAGCAGTTTCCGAAGTGATACAGACAGTTTCAGTGCATGTCTCCAGGTAGA	5220
Db	5210	TACTGGCCAGGTGAGCAGTTTCCGAAGTGATACAGACAGTTTCAGTGCATGTCTCCAGGTAGA	5269
Qy	5221	GACCTCCAGCAAGGATGATGTCACCCATTAACCAACCACTGTCTGCCCTCAGGCGCCTTCTA	5280
Db	5270	GACCTCCAGCAAGGATGATGTCACCCATTAACCAACCACTGTCTGCCCTCAGGCGCCTTCTA	5329
Qy	5281	CACACTGCTGCAAGACCAGTCCGGAAACAGCTACTACATCGGGGCCGATGGCTCCTTGCG	5340
Db	5330	CACACTGCTGCAAGACCAGTCCGGAAACAGCTACTACATCGGGGCCGATGGCTCCTTGCG	5389
Qy	5341	GCTGCTGTGGCCAA CCGCATGGAGTGGCGCTGCAGACTGAGCCCACCTTGCTGGCTGG	5400
Db	5390	GCTGCTGTGGCCAA CCGCATGGAGTGGCGCTGCAGACTGAGCCCACCTTGCTGGCTGG	5449
Qy	5401	CACCGTCAACCCACCCGTGGGCAAGAGGAATGTACGCTGCCCATCGACAAACGGCCTCAA	5460
Db	5450	CACCGTCAACCCACCCGTGGGCAAGAGGAATGTACGCTGCCCATCGACAAACGGCCTCAA	5509
Qy	5461	CCTGGTGGAGTGGCGCCAGCGCAAAGAGCAGGCTCGGGGCCAGGTCACTGTCTTTGGGCG	5520
Db	5510	CCTGGTGGAGTGGCGCCAGCGCAAAGAGCAGGCTCGGGGCCAGGTCACTGTCTTTGGGCG	5569
Qy	5521	CCGGCTCGGGTGCACAACCCGAAATCTCTATCTCTGGACTTTGATCGCGTAACACGCAC	5580
Db	5570	CCGGCTCGGGTGCACAACCCGAAATCTCTATCTCTGGACTTTGATCGCGTAACACGCAC	5629
Qy	5581	AGAGAAAGATCTATGATGACCA CCGCAAGTTCACCCCTTCGGATTCTGTACGACGAGCGGG	5640
Db	5630	AGAGAAAGATCTATGATGACCA CCGCAAGTTCACCCCTTCGGATTCTGTACGACGAGCGGG	5689
Qy	5641	GCGGCCACGCTCTGGTCA CCGAGCAGGCTGAATGGTGTCAACGTGACATACTCCCC	5700
Db	5690	GCGGCCACGCTCTGGTCA CCGAGCAGGCTGAATGGTGTCAACGTGACATACTCCCC	5749
Qy	5701	TGGGGTTACATTTGTCGTCATCCAGAGGGGCATCATGTCTGAAAGAAATGGAATACGACCA	5760
Db	5750	TGGGGTTACATTTGTCGTCATCCAGAGGGGCATCATGTCTGAAAGAAATGGAATACGACCA	5809
Qy	5761	GGCGGGCCGCATCACATCCAGGATCTTCGCTGATGGGAAGACATGGAGCTACACATACTT	5820
Db	5810	GGCGGGCCGCATCACATCCAGGATCTTCGCTGATGGGAAGACATGGAGCTACACATACTT	5869
Qy	5821	AGAGAAAGTCCATGGTGTCTGTACTACAGCCAGAGGCAGTATATCTTTGAGTTCGACAA	5880
Db	5870	AGAGAAAGTCCATGGTGTCTGTACTACAGCCAGAGGCAGTATATCTTTGAGTTCGACAA	5929
Qy	5881	GAATGACCGCCTCTCTTCTGTGACGATGCCCAACGTTGGCGCGCAGACACTAGAGACCAT	5940
Db	5930	GAATGACCGCCTCTCTTCTGTGACGATGCCCAACGTTGGCGCGCAGACACTAGAGACCAT	5989
Qy	5941	CCGCTCAGTGGGGCTACTACAGAAACATCTATCAGCCCCCTTGAGGGCAATGCCTCAGTCAT	6000



Db 5990 CCGCTCAGTGGGCTACTACAGAAA CATCTATCAGCCCCCTGAGGGCAATGCGCTCAGTCAT 6049  
QY 6001 ACAGGACTTCACTGAGGATGGGCACCTCCTTTCACACCTTCTACCTGGGCACTGGCCGCAG 6060  
Db 6050 ACAGGACTTCACTGAGGATGGGCACCTCCTTTCACACCTTCTACCTGGGCACTGGCCGCAG 6109  
QY 6061 GGTGATATACAAAGTATGGCAAACTGTCAAAGCTGGCAGAGACGCTCTATGACACCAACCAA 6120  
Db 6110 GGTGATATACAAAGTATGGCAAACTGTCAAAGCTGGCAGAGACGCTCTATGACACCAACCAA 6169  
QY 6121 GGTGAGTTTCACTATGACGAGACGGCAGGCAATGCTGAAGACCATCAACCTACAGAAATGA 6180  
Db 6170 GGTGAGTTTCACTATGACGAGACGGCAGGCAATGCTGAAGACCATCAACCTACAGAAATGA 6229  
QY 6181 GGGCTTCACTGCACCATCCGCTACCGTTCAGATTGGGCCCCCTGATTGACCGACAGATCTT 6240  
Db 6230 GGGCTTCACTGCACCATCCGCTACCGTTCAGATTGGGCCCCCTGATTGACCGACAGATCTT 6289  
QY 6241 CCGCTTCACTGAGGAAGGCATGGTCAACGCCCGCTTTTGACTACAACTATGACAAACAGCTT 6300  
Db 6290 CCGCTTCACTGAGGAAGGCATGGTCAACGCCCGCTTTTGACTACAACTATGACAAACAGCTT 6349  
QY 6301 CCGGGTGACAGCATGAGGCTGTGATCAACGAGACCCCACTGCCCAATGATCTCTATCG 6360  
Db 6350 CCGGGTGACAGCATGAGGCTGTGATCAACGAGACCCCACTGCCCAATGATCTCTATCG 6409  
QY 6361 CTATGATGATGTGTCAAGCAAGACAGAGCAGTGTGGGAAGTTTGGTGCAATTTACTATGA 6420  
Db 6410 CTATGATGATGTGTCAAGCAAGACAGAGCAGTGTGGGAAGTTTGGTGCAATTTACTATGA 6469  
QY 6421 CATTAAACAGATCATCAACACAGCTGTCTATGACCCACACCAAGCATTTTGTGATGCATATGG 6480  
Db 6470 CATTAAACAGATCATCAACACAGCTGTCTATGACCCACACCAAGCATTTTGTGATGCATATGG 6529  
QY 6481 CAGGATGAAGGAAGTGCAGTATGAGATCTTCCGCTCGCTCATGTACTGGATGACCGTCCA 6540  
Db 6530 CAGGATGAAGGAAGTGCAGTATGAGATCTTCCGCTCGCTCATGTACTGGATGACCGTCCA 6589  
QY 6541 GTATGATAACATGGGGCGAGTAGTGAAGAAGGAGCTGAAGGTAGGACCTACGCCAATAC 6600  
Db 6590 GTATGATAACATGGGGCGAGTAGTGAAGAAGGAGCTGAAGGTAGGACCTACGCCAATAC 6649  
QY 6601 CACTCGCTACTCCTATGAGTATGATGCTGACGGCCAGCTGCAGACAGTCTCCATCAATGA 6660  
Db 6650 CACTCGCTACTCCTATGAGTATGATGCTGACGGCCAGCTGCAGACAGTCTCCATCAATGA 6709  
QY 6661 CAAGCCACTCTGGCGCTACAGCTACGACCTCAATGSGAACCTGCACTTACTGAGCCCTGG 6720  
Db 6710 CAAGCCACTCTGGCGCTACAGCTACGACCTCAATGSGAACCTGCACTTACTGAGCCCTGG 6769  
QY 6721 GAAACAGTGCACGGCTCACACCACACTACGGTATGACATCCGCGACCGCATCACTCGGCTGG 6780  
Db 6770 GAAACAGTGCACGGCTCACACCACCTACGGTATGACATCCGCGACCGCATCACTCGGCTGG 6829  
QY 6781 TGACGTGCAATACAAAGATGGATGAGGATGGCTTCTGAGGCAGCGGGCGGTGATATCTT 6840  
Db 6830 TGACGTGCAATACAAAGATGGATGAGGATGGCTTCTGAGGCAGCGGGCGGTGATATCTT 6889  
QY 6841 TGAGTACAACTCAGCTGGCTGCTCATCAAGGCCTACAAACGGGCTGGCAGCTGGAGTGT 6900  
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QY 6901 CAGGTACCGCTACGATGGCCTGGGGCGGCGGTGTCCAGCAAGAGCAGCCACAGCCACCA 6960  
Db 6950 CAGGTACCGCTACGATGGCCTGGGGCGGCGGTGTCCAGCAAGAGCAGCCACAGCCACCA 7009  
QY 6961 CCTGCAGTTCTTCTATGCAGACCTGACCAACCCCAACCAAGGTCACCCCACCTGTACAACCA 7020  
Db 7010 CTTGCAGTTCTTCTATGCAGACCTGACCAACCCCAACCAAGGTCACCCCACCTGTACAACCA 7069  
QY 7021 CTCCAGCTCTGAGATCACCTCCCTCTACTACGACTTGCAGGGAACACCTCTTTGCCATGGA 7080

Db 7070 CTCCAGCTCTGAGATCACCTCCCTCTACTACGACTTGCAAGGACACCTCTTTGCCATGGA 7129  
QY 7081 GCTGAGCAGTGGTATGAGTTTTTACATAGCTTTGTGACAAACATCGGAGACCCCTCTTTGCTGT 7140  
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QY 7141 CTTTAGTGGAAACAGGTTTGTATGATCAAGCAAATCCTGTACACAGCCTATGGGGAGATCTA 7200  
Db 7190 CTTTAGTGGAAACAGGTTTGTATGATCAAGCAAATCCTGTACACAGCCTATGGGGAGATCTA 7249  
QY 7201 CATGGATACCAACCCCAACTTTTCAGATCATATAGGCTACCATGGTGGCCTCTATGATCC 7260  
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QY 7261 ACTCACCAAGCTTGTCCACATGGGCCGCGAGATTATGATGTGCTGSCCGACGCTGGAC 7320  
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QY 7321 TAGCCCCAGACCAAGCTGTGGAAAGCACTTTAGTAGCAGCAACGTCATGCTGCTTTTAATCT 7380  
Db 7370 TAGCCCCAGACCAAGCTGTGGAAAGCACTTTAGTAGCAGCAACGTCATGCTTTTAATCT 7429  
QY 7381 CTATATGTTCAAAAAACAAACCCCATCAGCAACTCCAGGACATCAAGTCTTCATGAC 7440  
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QY 7441 AGATGTTAACAGCTGGCTGCTCACCTTTGGATTCCAGCTACACAACGTCATCCCTGGTTA 7500  
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QY 7501 TCCCAAAACCAAGATGGATGCCATGGAAACCTCTACGAGCTCATCCACACACAGATGAA 7560  
Db 7550 TCCCAAAACCAAGATGGATGCCATGGAAACCTCTACGAGCTCATCCACACACAGATGAA 7609  
QY 7561 AACGCAGGATGGGACAAACAGCAAGTCTATCTCTCGGGGTACAGTGTGAAGTACAGAAGCA 7620  
Db 7610 AACGCAGGATGGGACAAACAGCAAGTCTATCTCTCGGGGTACAGTGTGAAGTACAGAAGCA 7669  
QY 7621 GCTCAAGGCCTTTGTCACTTAGAACGGTTTGACAGCTCTATGGCTCCACAATCACCAG 7680  
Db 7670 GCTCAAGGCCTTTGTCACTTAGAACGGTTTGACAGCTCTATGGCTCCACAATCACCAG 7729  
QY 7681 CTGCCAGCAGGCTCCAAAAGACCAAGAGTTTGCATCCAGCGGCTCAGTCTTTGGCAAGGG 7740  
Db 7730 CTGCCAGCAGGCTCCAAAAGACCAAGAGTTTGCATCCAGCGGCTCAGTCTTTGGCAAGGG 7789  
QY 7741 GGTCAAGTTTGCCTTGAAGGATGGCCGAGTGACCAACAGACATCATCAGTGTGSCCAATGA 7800  
Db 7790 GGTCAAGTTTGCCTTGAAGGATGGCCGAGTGACCAACAGACATCATCAGTGTGSCCAATGA 7849  
QY 7801 GGATGGCGGAAGGTTGCTGCCATCTTTGAACCATGCCCACTACCTAGAGAACCTGCACCTT 7860  
Db 7850 GGATGGCGGAAGGTTGCTGCCATCTTGAAACCATGCCCACTACCTAGAGAACCTGCACCTT 7909  
QY 7861 CACCATTTGATGGGTGGATACCCATTACTTTGTGAAACCAGGACCTTCAGAAAGGTGACCT 7920  
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QY 7921 GGCCATCCTGGGCTCAGTGGGGCGGCGAACCCTGGAGAAATGGGTCAACGTCACCTGT 7980  
Db 7970 GGCCATCCTGGGCTCAGTGGGGCGGCGAACCCTGGAGAAATGGGTCAACGTCACCTGT 8029  
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Db 8030 GTCCCAGATCAACACAGTACTTAATGGCAGGACTAGACGCTACACAGACATCCAGCTCCA 8089  
QY 8041 GTACGGGGCACTGTGCTTGAAACACACGCTACGGGACAACTTTGGATGAGGAAGGCACG 8100  
Db 8090 GTACGGGGCACTGTGCTTGAAACACACGCTACGGGACAACTTTGGATGAGGAAGGCACG 8149  
QY 8101 GGTCTTGAGCTGGCCCGGCAGAGCCGTCGCCAAAGCGTGGGCCCGGCAGCAGCAGAG 8160  
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QY      8221 GAGCACAGGGCGGTGCAAGGCTACGACGGCTTTTCGTGATCTCTGTCGAGCAGTACCC 8280
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Db      8270 GAGCACAGGGCGGTGCAAGGCTACGACGGCTTTTCGTGATCTCTGTCGAGCAGTACCC 8329
      |||
QY      8281 AGAACTGTCAGACAGCGCCAAACAACATCCACTTCATGAGACAGAGCGAGATGGGCCGGAG 8340
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Db      8330 AGAACTGTCAGACAGCGCCAAACAACATCCACTTCATGAGACAGAGCGAGATGGGCCGGAG 8389
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QY      8341 GTGACAGAGAGGAC 8354
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RESULT 4
US-10-383-201-55
; Sequence 55, Application US/10383201
; Publication No. US20040029226A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook II, John et al.
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-568A
; CURRENT APPLICATION NUMBER: US/10/383,201
; CURRENT FILING DATE: 2003-03-06
; PRIOR APPLICATION NUMBER: 10/029020
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/365,984
; PRIOR FILING DATE: 2002-03-20
; PRIOR APPLICATION NUMBER: 60/372,022
; PRIOR FILING DATE: 2002-04-12
; PRIOR APPLICATION NUMBER: 60/389,143
; PRIOR FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: 60/391,779
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: 60/410,755
; PRIOR FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: 60/412,957
; PRIOR FILING DATE: 2002-09-23
; PRIOR APPLICATION NUMBER: 10/051,874
; PRIOR FILING DATE: 2002-01-16
; PRIOR APPLICATION NUMBER: 60/366,928
; PRIOR FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: 10/055,877
; PRIOR FILING DATE: 2002-01-22
; NUMBER OF SEQ ID NOS: 155
; SOFTWARE: CuraseqList version 0.1
; SEQ ID NO 55
; LENGTH: 8355
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(8325)
US-10-383-201-55

Query Match      95.7%; Score 7991.2; DB 7; Length 8355;
Best Local Similarity 98.3%; Pred. No. 0;
Matches 8248; Conservative 0; Mismatches 18; Indels 126; Gaps 12;

QY      35 ATGGACGTGAAGGAGAGGAAGCCTTACCGCTCGCTGACCCGGCGCCGCGACGCCGAGCGC 94
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Db      1 ATGGACGTGAAGGAGAGGAAGCCTTACCGCTCGCTGACCCGGCGCCGCGACGCCGAGCGC 60
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QY      95 CGGTACACCACTCGTCCGGGACAGCGAGGAGGGCAAGCCCCCGCAGAAATCGTACAGC 154
      |||
Db      61 CGGTACACCACTCGTCCGGGACAGCGAGGAGGGCAAGCCCCCGCAGAAATCGTACAGC 120
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QY      155 TCCAGCGAGACCCCTGAAGGCCCTACGACCGCCCGCTAGCCCTATGGCAGCGCGCTC 214
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Db      121 TCCAGCGAGACCCTGAAGCCCTACGACCAGGACGCCCGCCTAGCCTATGGCAGCCGCGTC 180
QY      215 AAGGACATTGTCCCGCAGGAGGCCGAGGAATTCTGCGGCACAGGTCGCAACTTCACCCCTG 274
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Db      181 AAGGACATTGTCCCGCAGGAGGCCGAGGAATTCTGCGGCACAGGTCGCAACTTCACCCCTG 240
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QY      275 CGGGAGCTGGGGCTGGAAGAAAGTAACGCCCCCTACGGGACCCTGTACCGGACAGACATT 334
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Db      241 CGGGAGCTGGGGCTGGAAGAAAGTAACGCCCCCTCACGGGACCCTGTACCGGACAGACATT 300
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QY      335 GGCCTGCCCAATGCGGCTACTCCATGGGGGTGGCTCTGATGCCGACATGGAGGCTGAC 394
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QY      395 ACGGTGCTGTCCCTGAGCACCCCGTGCCTGTGTGGGGCCGGAGCACACGGTCAGGGCGC 454
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QY      455 AGCTCCTGCCTGTCAGCGCGGCCAATTCCAATCTCACACTCACCGACACCGAGCATGAA 514
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Db      421 AGCTCCTGCCTGTCCAGCGGGCCAATTCCAATCTCACACTCACCGACACCGAGCATGAA 480
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QY      515 AACACTGAGACTGATCATCCGGGCGGCTTCAGAAACCACGCGCGGCTCCGGACGCCGCCG 574
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Db      481 AACACTGAGACTGATCATCCGGGCGGCTTCAGAAACCACGCGCGGCTCCGGACGCCGCCG 540
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QY      575 CCGCGCTCTCGCACGCCACACCCCCAACCCCAACAGCAGCACACGCGGCTCCATTAACTCCCTG 634
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Db      541 CCGCGCTCTCGCACGCCACACCCCCAACCCCAACAGCAGCACACGCGGCTCCATTAACTCCCTG 600
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QY      635 AACCAGGGCAACTTCACGCGGAGGAGCAACCCAGCCCCAGCCCCCAGCCCACTCGCTC 694
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Db      601 AACCAGGGCAACTTCACGCGGAGGAGCAACCCAGCCCCAGCCCCCAGCCCACTCGCTC 660
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QY      695 TCCGAGAGCCCTGCGGCGGCCAGGAGCCTGCCACGCCCAGGAGAACTGGCTG 754
      |||
Db      661 TCCGAGAGCCCTGCGGCGGCCAGGAGCCTGCCACGCCCAGGAGAACTGGCTG 720
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QY      755 CTCAACAGCAACATCCCCCTGGAGACCAGGAACCTTAGGCAAGCAGCAGCATTCTTAGGGACA 814
      |||
Db      721 CTCAACAGCAACATCCCCCTGGAGACCAGGAACCTTAGGCAAGCAGCAGCATTCTTAGGGACA 780
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QY      815 TTGCAGGACAACTCATTGAGATGGACATTCTCGGCGCCTCCCGCCATGATGGGCTTAC 874
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QY      875 AGTGACGGGCACTTCCTCTTCAAGCCTGGAGGCACCTCCCGGCTTCTTGCACCACATCA 934
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Db      841 AGTGACGGGCACTTCCTCTTCAAGCCTGGAGGCACCTCCCGGCTTCTTGCACCACATCA 900
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QY      935 CCAGGGTACCCACTGACGTCCAGCACAGTGTACTCTCTCCGCCCCGACCCCTGCCCGCG 994
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Db      901 CCAGGGTACCCACTGACGTCCAGCACAGTGTACTCTCTCCGCCCCGACCCCTGCCCGCG 960
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QY      995 AGCACCTTCGCGCGCGGCTTTAACTCAAGAGCCCTCCAACTGTAAGTGGGAG 1054
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QY      1055 TCGCAGCCCTGAGCGCCATCGTCATCTCAGCCACTCTGTCTATCTCTGGCATACTTT 1114
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Db      1021 TCGCAGCCCTGAGCGCCATCGTCATCTCAGCCACTCTGTCTATCTCTGGCATACTTT 1080
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QY      1115 GTGGCCATGCACCTGTTTGGCCTAACTGGCACCTGCAGCCGATGGAGGGCAGATGTAT 1174
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Db      1081 GTGGCCATGCACCTGTTTGGCCTAACTGGCACCTGCAGCCGATGGAGGGCAGATGTAT 1140
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QY      1175 GAGATCAGGAGGACACAGCCAGCAGTGGCCTGTGCCAACCCGACGCTCTCCCTATACCCC 1234
      |||
Db      1141 GAGATCAGGAGGACACAGCCAGCAGTGGCCTGTGCCAACCCGACGCTCTCCCTATACCCC 1200
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QY      1235 TCAGGGGCACTGGCTTAGAGACCCCTGACAGGAAAGGCAAGCAACAGAAAGGAAAG 1294
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Db      1201 TCAGGGGCACTGGCTTAGAGACCCCTGACAGGAAAGGCAAGCAACAGAAAGGAAAG 1260
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QY	1295	CCCAGTAGTTTCTTTCCAGAGGACAGTTTTCATAGATTCTGGAGAAATTGATGTGGGAAGG	1354
Db	1261	CCCAGTAGTTTCTTTCCAGAGGCCAGTTTTCATAGATTCTGGAGAAATTGATGTGGGAAGG	1320
QY	1355	CGAGCCTCCAGAAAGATTCTCTCTGGCACCTTCTTGAGATCTCAAGTGTTTCATAGACCAT	1414
Db	1321	CGAGCTTCCAGAAAGATTCTCTCTGGCACCTTCTTGAGATCTCAAGTGTTTCATAGACCAT	1380
QY	1415	CCTGTGCATCTGAAATTCAAATGTGTCTCTGGGAAGGCAGCCCTGGTTGGCATTTATGGC	1474
Db	1381	CCTGTGCATCTGAAATTCAAATGTGTCTCTGGGAAGGCAGCCCTGGTTGGCATTTATGGC	1440
QY	1475	AGAAAAGGCCTCCCTCTTCACATACACAGTTTGACTTTGTGGAGCTGTGGATGGCAGG	1534
Db	1441	AGAAAAGGCCTCCCTCTTCACATACACAGTTTGACTTTGTGGAGCTGTGGATGGCAGG	1500
QY	1535	AGGCTCCTAACCCAGGAGCGCGGAGCCTAGAGGGGACCCCGCCAGTCTCGGGGAAC	1594
Db	1501	AGGCTCCTAACCCAGGAGCGCGGAGCCTAGAGGGGACCCCGCCAGTCTCGGGGAAC	1560
QY	1595	GTGCCCCCTCCAGCCATGAGACAGGCTTCATCCAGTATTGGATTTCAGGAATCTGGCAC	1654
Db	1561	GTGCCCCCTCCAGCCATGAGACAGGCTTCATCCAGTATTGGATTTCAGGAATCTGGCAC	1620
QY	1655	TTGGCTTTTACAAATGACGGAAGGAGTCAAGTGGTTTCTTTCTCACCACTGCCATT	1714
Db	1621	TTGGCTTTTACAAATGACGGAAGGAGTCAAGTGGTTTCTTTCTCTCCCC-----A	1674
QY	1715	GAGTCGGTGGATAACTGCCCCAGCAACTGCTATGSCAATGGTGACTGCATCTCTGGGACC	1774
Db	1675	GAGTCGGTGGATAACTGCCCCAGCAACTGCTATGSCAATGGTGACTGCATCTCTGGGACC	1734
QY	1775	TGCCACTGCTTCCTGGGTTTCTTGGGCCCCGACTGTGGCAGAGCCTCCTGCCCGTGCTC	1834
Db	1735	TGCCACTGCTTCCTGGGTTTCTTGGGCCCCGACTGTGGCAGAGCCTCCTGCCCGTGCTC	1794
QY	1835	TGTAGCGGAAATGGCCAAATACATGAAAGGCAGATGCTTGTGCCACAGTGGCTGGAAAGGC	1894
Db	1795	TGTAGCGGAAATGGCCAAATACATGAAAGGCAGATGCTTGTGCCACAGTGGCTGGAAAGGC	1854
QY	1895	GCTGAGTGCAGTGTGCCACCAACCAGTGATCGATGTGGCCTGCAGCAACCATGGCAC	1954
Db	1855	GCTGAGTGCAGTGTGCCACCAACCAGTGATCGATGTGGCCTGCAGCAACCATGGCAC	1914
QY	1955	TGCATCAGGGGCACCTGCATCTGCAACCTGGCTACAAGGGCGAGAGCTGTGAGGAAGTG	2014
Db	1915	TGCATCAGGGGCACCTGCATCTGCAACCTGGCTACAAGGGCGAGAGCTGTGAGGAA---	1971
QY	2015	GACTGCATGGACCCACATGTTCAGGCCGGGTGTCTGCGTGAGAGGCGAATGSCATTGC	2074
Db	1972	GACTGCATGGACCCACATGTTCAGGCCGGGTGTCTGCGTGAGAGGCGAATGSCACTGC	2031
QY	2075	TTTGTGGGATGGGAGGACCAACTGCGAGACCCCGAGGCCACATGCTTAGACCAGTGT	2134
Db	2032	TCTGTGGGATGGGAGGACCAACTGCGAGACCCCGAGGCCACATGCTTAGACCAGTGT	2091
QY	2135	TCAGGCCACGGAACTTCTCCCGGACACCGGGCTTTGCAGCTGTGACCCCAAGCTGGACT	2194
Db	2092	TCAGGCCACGGAACTTCTCCCGGACACCGGGCTTTGCAGCTGTGACCCCAAGCTGGACT	2151
QY	2195	GGACACGACTGTTCTATCGAGATGTGTGCTGCCGACTGTGGTGGCCATGGCGTGTGCGTA	2254
Db	2152	GGACACGACTGTTCTATCGAGATGTGTGCTGCCGACTGTGGTGGCCATGGCGTGTGCGTA	2211
QY	2255	GGGGGCACCTGCGGATGGCTGGATGGGGGCGAGCCTGCGACCAGCGGSCCTGC	2314
Db	2212	GGGGGCACCTGCGGATGGCTGGATGGGGGCGAGCCTGCGACCAGCGGSCCTGC	2271
QY	2315	CACCCGCGCTGTGCCGAGCATGGGACCTGCCCGGACGGCAAGTGCAGTGCAGCCCTGGC	2374
Db	2272	CACCCGCGCTGTGCCGAGCATGGGACCTGCCCGGACGGCAAGTGCAGTGCAGCCCTGGC	2331

QY	2375	TGGAATGGCGAACACTGCACCATC-----GCTCACTATCTGGATAGGGTAGTTAA----	2424
Db	2332	TGGAATGGCGAACACTGCACCATCTCCCTAGCTCACTATCTGGATAGGGTAGTTAACTT	2391
QY	2425	--AGAGGGTTGCCCTGGGTTGTGCAATGGCAACGGCAGATGTACCTTAGACCTGAATGGT	2482
Db	2392	TCAGAGGGTTGCCCTGGGTTGTGCAATGGCAACGGCAGATGTACCTTAGACCTGAATGGT	2451
QY	2483	TGGCACTGCGTCTGCCAGCTGGGCTGGAGAGGAGCTGGCTGTGACACTTCCATGGAGACT	2542
Db	2452	TGGCACTGCGTCTGCCAGCTGGGCTGGAGAGGAGCTGGCTGTGACACTTCCATGGAGACT	2511
QY	2543	GCCTGCGGTGACAGCAAAAGACAATGATGGAGATGGCCTGGTGGACTGACATGGACCCCTGAC	2602
Db	2512	GCCTGCGGTGACAGCAAAAGACAATGATGGAGATGGCCTGGTGGACTGACATGGACCCCTGAC	2571
QY	2603	TGCTGCCCTCCAGCCCCCTGTGCCATATCAACCCGCTGTGCCCTTGGCTCCCTAAACCCCTCTG	2662
Db	2572	TGCTGCCCTCCAGCCCCCTGTGCCATATCAACCCGCTGTGCCCTTGGCTCCCTAAACCCCTCTG	2631
QY	2663	GACATCATCCAGGAGACACAGGTCCTGTGTCAACAGCAGAACCTACACTCCTTCTATGAC	2722
Db	2632	GACATCATCCAGGAGACACAGGTCCTGTGTCAACAGCAGAACCTACACTCCTTCTATGAC	2691
QY	2723	CGCATCAAGTTCTCTGTGGGAGGACAGCACGACACATAATCCCCGGGAGAACCCCTTTT	2782
Db	2692	CGCATCAAGTTCTCTGTGGGAGGACAGCACGACACATAATCCCCGGGAGAACCCCTTTT	2751
QY	2783	GATGGAGGGCATGCTTGTGTTATTCTGTCGCCAAAGTGATGACATCAGATGGAACCCCCCTG	2842
Db	2752	GATGGAGGGCATGCTTGTGTTATTCTGTCGCCAAAGTGATGACATCAGATGGAACCCCCCTG	2811
QY	2843	GTTGGTGTGAACATCAGTTTTTGTCAATAACCCCTCTCTTTGGATATACAAATCAGCAGGCAA	2902
Db	2812	GTTGGTGTGAACATCAGTTTTTGTCAATAACCCCTCTCTTTGGATATACAAATCAGCAGGCAA	2871
QY	2903	GATGGCAGCTTTGAATTGGTGACAAATGGCGGCATCTCCATCATCCTGCGGTTTCGAGCGG	2962
Db	2872	GATGGCAGCTTTGAATTGGTGACAAATGGCGGCATCTCCATCATCCTGCGGTTTCGAGCGG	2931
QY	2963	GCACCTTTCATCACACAGGAGCACACCTCTGTGGCTGCCATGGGATCGCTTCTTTGTTCATG	3022
Db	2932	GCACCTTTCATCACACAGGAGCACACCTCTGTGGCTGCCATGGGATCGCTTCTTTGTTCATG	2991
QY	3023	GAAACCATCATCATGAGACATGAGGAGAAATGAGATTCCCAGCTGTGACCTGAGCAATTTT	3082
Db	2992	GAAACCATCATCATGAGACATGAGGAGAAATGAGATTCCCAGCTGTGACCTGAGCAATTTT	3051
QY	3083	GCCCGCCCCAACCCAGTCGTCTCTCCATCCCCACTGACGTCCTTCGCCAGCTCCTGTGCA	3142
Db	3052	GCCCGCCCCAACCCAGTCGTCTCTCCATCCCCACTGACGTCCTTCGCCAGCTCCTGTGCA	3111
QY	3143	GAGAAAGGCCCCCATTTGTGCCGGAATTACGGTTTGCAGGAGGAAATCTCTATCTCTGGC	3202
Db	3112	GAGAAAGGCCCCCATTTGTGCCGGAATTACAGGCTTTGCAGGAGGAAATCTCTATCTCTGGC	3171
QY	3203	TGCAAGATGAGGCTGAGCTACCTGAGCAGCCGGACCCCTGGCTACAAATCTGTCCTGAGG	3262
Db	3172	TGCAAGATGAGGCTGAGCTACCTGAGCAGCCGGACCCCTGGCTACAAATCTGTCCTGAGG	3231
QY	3263	ATCAGCCTCACCCACCCGACCATCCCTTCAACCTCATGAAGGTGCACCTCATGGTAGCG	3322
Db	3232	ATCAGCCTCACCCACCCGACCATCCCTTCAACCTCATGAAGGTGCACCTCATGGTAGCG	3291
QY	3323	GTGAGGGCGCGCCTCTTCAGGAAGTGGTTGCTGCGAGCCCCAGACCTGTCTTATTTTC	3382
Db	3292	GTGAGGGCGCGCCTCTTCAGGAAGTGGTTGCTGCGAGCCCCAGACCTGTCTTATTTTC	3351
QY	3383	ATTTGGGACAAAGACAGACGTCTACAACCCAGAGGTGTTTGGGCTTTCAGAAACCTTTGTT	3442
Db	3352	ATTTGGGACAAAGACAGACGTCTACAACCCAGAGGTGTTTGGGCTTTCAGAAACCTTTGTT	3411
QY	3443	TCCGTGGGTTATGAATATGAATCCTGCCACAGATCTAAATCCTGTGGGAAAAAAGAACACA	3502



Db 3412 TCCGTGGGTTATGAATATGAATCCTGCCCAGATCTAATCCTGTGGGAAAAAGAACAA 3471  
QY 3503 GTGCTGCAGGGCTATGAATTTGACCGTCCAAGCTTGGAGGATGGAGCTAGACAAACAT 3562  
Db 3472 GTGCTGCAGGGCTATGAATTTGATGCGTCCAAAGCTTGGAGGATGGAGCTAGACAAACAT 3531  
QY 3563 CATGCCCTCAACATTCAAAGTGGT--ATCCTGCACAAAGGGAAATGGGAGAACCCAGTTT 3619  
Db 3532 CATGCCCTCAACATTCAAAGTGGTGGCATCCTGCACAAAGGGAAATGGGAGAACCCAGTTT 3591  
QY 3620 GTGTCTCAGCAGCCTCCTGTCAATTGGGAGCATATGGGCAATGGGCGCGGAGAGCATC 3679  
Db 3592 GTGTCTCAGCAGCCTCCTGTCAATTGGGAGCATATGGGCAATGGGCGCGGAGAGCATC 3651  
QY 3680 TCCTGCCCCAGCTGCAACGGCCTTGTGTACGGCAACAAGCTCCTGSCCCCAGTGGCCCTC 3739  
Db 3652 TCCTGCCCCAGCTGCAACGGCCTTGTGTACGGCAACAAGCTCCTGSCCCCAGTGGCCCTC 3711  
QY 3740 ACCTGTGGCTCTGACGGGAGCCTCTATGTGGTGATTTCAACTACATTAGAAGGATCTTC 3799  
Db 3712 ACCTGTGGCTCTGACGGGAGCCTCTATGTGGTGATTTCAACTACATTAGAAGGATCTTC 3771  
QY 3800 CCTCTGGAAATGTACCAACATCCTAGAGCTGAGG-----ATAAAGATTTTCAGACAT 3853  
Db 3772 CCTCTGGAAATGTACCAACATCCTAGAGCTGAGGTCAGAAATAAAGATTTTCAGACAT 3831  
QY 3854 AGTCACAGTCCAGCACACAAATACTACCTGGCCACAGACCCCAATGAAGTGGGCCGTCTTC 3913  
Db 3832 AGTCACAGTCCAGCACACAAATACTACCTGGCCACAGACCCCAATGAAGTGGGCCGTCTTC 3891  
QY 3914 CTTTCTGACAGCAACAGCCGGCGGTCTTTTAAATCAAGTCCACTGTGGTGAAGGAC 3973  
Db 3892 CTTTCTGACAGCAACAGCCGGCGGTCTTTTAAATCAAGTCCACTGTGGTGAAGGAC 3951  
QY 3974 CTTGTCAAGAACTCTGAGGTGGTTGCGGGACAGGTGACCAAGTCCCTCCCCTTTGATGAC 4033  
Db 3952 CTTGTCAAGAACTCTGAGGTGGTTGCGGGACAGGTGACCAAGTCCCTCCCCTTTGATGAC 4011  
QY 4034 ACTCGCTCGGGGATGGTGGGAAGGCCACAGAAGCCACACTCACCAATCCCAGGGGT--- 4090  
Db 4012 ACTCGCTCGGGGATGGTGGGAAGGCCACAGAAGCCACACTCACCAATCCCAGGGGTCCC 4071  
QY 4091 -----ATTACAGTGGACAAAGTTTGGGCTGATCTACTTCGTGGATGGCACCATTGATCAGA 4144  
Db 4072 CCAGGCATTACAGTGGACAAAGTTTGGGCTGATCTACTTCGTGGATGGCACCATTGATCAGA 4131  
QY 4145 CGCATCGATCAGAAATGGGATCATCTCCACCCTGCTCGGCTCTAATGATCTCATACTAGCC 4204  
Db 4132 CGCATCGATCAGAAATGGGATCATCTCCACCCTGCTCGGCTCTAATGATCTCATACTAGCC 4191  
QY 4205 CGGCCACTCAGCTGTGATTCTGTATGGATATTTCCCAGGTAAGA-----CTGGAG 4255  
Db 4192 CGGCCACTCAGCTGTGATTCTGTATGGATATTTCCCAGGTAAGACAGGTTTCACCTGGAG 4251  
QY 4256 TGGCCACAGACTTAGCCATCAACCAATGGACAACTCACTTTATGTCTCGACAAACAAT 4315  
Db 4252 TGGCCACAGACTTAGCCATCAACCAATGGACAACTCACTTTATGTCTCGACAAACAAT 4311  
QY 4316 GTGGTCTGCAAAATCTCTGAAAACCAACAGGTGCGCATTTGCGCGGAGGCCCATGAC 4375  
Db 4312 GTGGTCTGCAAAATCTCTGAAAACCAACAGGTGCGCATTTGCGCGGAGGCCCATGAC 4371  
QY 4376 TGCCAGGTCCCTGGCATTGACCACTTCCGTCTAAGCAAGGTGGCCATCCACGCAACCCCTG 4435  
Db 4372 TGCCAGGTCCCTGGCATTGACCACTTCCGTCTAAGCAAGGTGGCCATCCACGCAACCCCTG 4431  
QY 4436 GAGTCAGCCACCGCTTTGGCTGTTTACACAAATGGGGTCTGTATTTGCTGAGACTGAT 4495  
Db 4432 GAGTCAGCCACCGCTTTGGCTGTTTACACAAATGGGGTCTGTATTTGCTGAGACTGAT 4491  
QY 4496 GAGAAAAAGATCAACCGCATCAGGCAGGTCAACCACTAGTGGAGAGATCTCACTCGTTGCT 4555

Db 4492 GAGAAAAAGATCAACCCGATCAGGCAGGTCACCACATAGTGGAGAGATCTCACTCGTTGCT 4551  
QY 4556 GGGGCCCCCAGTGGCTGTGACTGTAAAAATGATGCCAACTGTGATTTGTTCTGGAGAC 4615  
Db 4552 GGGGCCCCCAGTGGCTGTGACTGTAAAAATGATGCCAACTGTGATTTGTTCTGGAGAC 4611  
QY 4616 GATGGTTATGCCAAGGATGCAAAAGTTAAATACCCCATCTTCCTTGGCTGTGTGCTGAT 4675  
Db 4612 GATGGTTATGCCAAGGATGCAAAAGTTAAATACCCCATCTTCCTTGGCTGTGTGCTGAT 4671  
QY 4676 GGGGAGCTCTACGTGGCCGACCTTGGGAACATCCGAATTCGGTTTATCCGGAAGAACAA 4735  
Db 4672 GGGGAGCTCTACGTGGCCGACCTTGGGAACATCCGAATTCGGTTTATCCGGAAGAACAA 4731  
QY 4736 CCTTTCTCAACACCCAGAACATGTATGAGCTGTCTTCACCAATTGACAGGAGCTCTAT 4795  
Db 4732 CCTTTCTCAACACCCAGAACATGTATGAGCTGTCTTCACCAATTGACAGGAGCTCTAT 4791  
QY 4796 CTGTTTGATACCCCGCAAGCACCTGTACACCCCAAGCCTGCCACAGGAGACTACCTG 4855  
Db 4792 CTGTTTGATACCCCGCAAGCACCTGTACACCCCAAGCCTGCCACAGGAGACTACCTG 4851  
QY 4856 TACAACTTCACCTACACTGGGACGGCGACATCACACTCATCACAGACAAACAATGGCAAC 4915  
Db 4852 TACAACTTCACCTACACTGGGACGGCGACATCACACTCATCACAGACAAACAATGGCAAC 4911  
QY 4916 ATGGTAAATGTCCGCCGAGACTCTACTGGGATGCCCCCTCTGGCTGGTGGTCCCAGATGGC 4975  
Db 4912 ATGGTAAATGTCCGCCGAGACTCTACTGGGATGCCCCCTCTGGCTGGTGGTCCCAGATGGC 4971  
QY 4976 CAGGTGTACTGGGTGACCATGGGCACCAACAGTGCACTCAAGAGTGTGACCAACAAGGA 5035  
Db 4972 CAGGTGTACTGGGTGACCATGGGCACCAACAGTGCACTCAAGAGTGTGACCAACAAGGA 5031  
QY 5036 CACGAGTTGGCCATGATGACATACCATGGCAATTCGGCCTTCTGGCAACCAAAAGCAAT 5095  
Db 5032 CACGAGTTGGCCATGATGACATACCATGGCAATTCGGCCTTCTGGCAACCAAAAGCAAT 5091  
QY 5096 GAAAACGGATGGACAAACATTTTATGAGTACGACAGCTTTGGCCGCTGACAAATGTGACC 5155  
Db 5092 GAAAACGGATGGACAAACATTTTATGAGTACGACAGCTTTGGCCGCTGACAAATGTGACC 5151  
QY 5156 TTCCCTACTGGCCAGGTGAGCAGTTTCCGAAAGTGATACAGACAGTTTCAGTGCATGTCCAG 5215  
Db 5152 TTCCCTACTGGCCAGGTGAGCAGTTTCCGAAAGTGATACAGACAGTTTCAGTGCATGTCCAG 5211  
QY 5216 GTAGAGACCTCCAGCAAGGATGATGTACACCATAACCAACCACTGTCTGCCTCAGGCGCC 5275  
Db 5212 GTAGAGACCTCCAGCAAGGATGATGTACACCATAACCAACCACTGTCTGCCTCAGGCGCC 5271  
QY 5276 TTCTACACACTGCTGCAAGACCAAGTCCGGAACAGCTACTACATCGGGGCCGATGGCTCC 5335  
Db 5272 TTCTAC-----GACCAAGTCCGGAACAGCTACTACATCGGGGCCGATGGCTCC 5319  
QY 5336 TTGGCGCTGCTGTGGCCAAACGGCATGGAGGTGGCGTGCAGACTGAGCCCCCACTTGTCTG 5395  
Db 5320 TTGGCGCTGCTGTGGCCAAACGGCATGGAGGTGGCGTGCAGACTGAGCCCCCACTTGTCTG 5379  
QY 5396 GCTGGCACCGTCAACCCCAACCGTGGGCAAGAGGAATGTACAGTGCCTGCCATCGACAAACGGC 5455  
Db 5380 GCTGGCACCGTCAACCCCAACCGTGGGCAAGAGGAATGTACAGTGCCTGCCATCGACAAACGGC 5439  
QY 5456 CTCAACCTGGTGGAGTGGCGCCAGCGCAAGAGCAGGCTCGGGGCCAGGTCACTGTCTTT 5515  
Db 5440 CTCAACCTGGTGGAGTGGCGCCAGCGCAAGAGCAGGCTCGGGGCCAGGTCACTGTCTTT 5499  
QY 5516 GGGCGCCGCTGCGGGTG-----CACAAACCGAAATCTCCTATCTCTGGACTTTGAT 5566  
Db 5500 GGGCGCCGCTGCGGGTGCTCCAGGTTCAAAACCGAAATCTCCTATCTCTGGACTTTGAT 5559  
QY 5567 CGCGTAACACGCACAGAGAAGATCTATGATGACCACCGCAAGTTACCCCTTCGGATTCTG 5626  
Db 5560 CGCGTAACACGCACAGAGAAGATCTATGATGACCACCGCAAGTTACCCCTTCGGATTCTG 5619









Db 661 |||||CTCTCCGGAGAGCCCCCTGCGGCGGCGCCAGAGACCTGCCACGCCCCAGGAGAACTGG 720

QY 752 CTGCTCAACAGCAACATCCCCCTGGAGACCAAGGAACCTAGGCAAGCAGCCATTCTTAGGG 811

Db 721 CTGCTCAACAGCAACATCCCCCTGGAGACCAAGAACTAGGCAAGCAGCCATTCTTAGGG 780

QY 812 ACATTGCAGGACAACTCATTTGAGATGGACATTTCTGGCGCCTCCCCGCCATGATGGGGCT 871

Db 781 ACATTGCAGGACAACTCATTTGAGATGGACATTTCTGGCGCCTCCCCGCCATGATGGGGCT 840

QY 872 TACAGTGACGGGCACTTCCTCTTCAAGCCTGGAGGACCTCCCCGCTCTTTCTGACCCACA 931

Db 841 TACAGTGACGGGCACTTCCTCTTCAAGCCTGGAGGACCTCCCCGCTCTTTCTGACCCACA 900

QY 932 TCACCAGGGTACCCACTGACGTCCAGCACAGTGTACTCTCTCCGCCCGACCCCTGCC 991

Db 901 TCACCAGGGTACCCACTGACGTCCAGCACAGTGTACTCTCTCCGCCCGACCCCTGCC 960

QY 992 CGCAGCACCTTCGCCCGCGCGCCCTTTAACTCAAGAACCCCTCCAAGTACTGTAACCTGG 1051

Db 961 CGCAGCACCTTCGCCCTGCGCGCGCCCTTTAACTCAAGAACCCCTCCAAGTACTGTAACCTGG 1020

QY 1052 AAGTGCAGCCCTGAGCGCATCGTCATCTCAGCCACTCTGGTCATCTCTGCGCATAC 1111

Db 1021 AAGTGCAGCCCTGAGCGCATCGTCATCTCAGCCACTCTGGTCATCTCTGCGCATAC 1080

QY 1112 TTTGTGGCCATGCACCTGTTGGCCCTAACTGGCACCTGCAGCCCGATGGAGGCGAGATG 1171

Db 1081 TTTGTGGCCATGCACCTGTTGGCCCTAACTGGCACCTGCAGCCCGATGGAGGCGAGATG 1140

QY 1172 -----TATGAGATCACGAGGACACAGCCAGCAGTTGGCCTGTGCCAACCGACGTCTC 1224

Db 1141 ACGGATTTATGAGATCACGAGGACACAGCCAGCAGTTGGCCTGTGCCAACCGACGTCTC 1200

QY 1225 CCTATACCCCTCAGGGGGCACTGGCTTAGAGACCCCTGACAGGAAAGGCAAGGAACCCAC 1284

Db 1201 CCTATACCCCTCAGGGGGCACTGGCTTAGAGACCCCTGACAGGAAAGGCAAGGAACCCAC 1260

QY 1285 AGAAGGAAAGCCAGTAGTTCTTTCCAGAGGACAGTTTCATAGATTTCTGGAGAAATTGA 1344

Db 1261 AGAAGGAAAGCCAGTAGTTCTTTCCAGAGGCCAGTTTCATAGATTTCTGGAGAAATTGA 1320

QY 1345 TGTGGGAAAGCGAGCCTCCAGAAAGATTCTCTGGCACTTTCTGGAGATCTCAAGTGT 1404

Db 1321 TGTGGGAAAGCGAGCTTCCAGAAAGATTCTCTGGCACTTTCTGGAGATCTCAAGTGT 1380

QY 1405 CATAGACCATCCTGTGCATCTGAAATTCAATGTGTCTCTGGGAAAGGCAGCCCTGGTTGG 1464

Db 1381 CATAGACCATCCTGTGCATCTGAAATTCAATGTGTCTCTGGGAAAGGCAGCCCTGGTTGG 1440

QY 1465 CATTTATGGCAGAAAGGCCCTCCCTCCATTACATACAGATTTGACTTTTGTGGAGCTGCT 1524

Db 1441 CATTTATGGCAGAAAGGCCCTCCCTCCATTACATACAGATTTGACTTTTGTGGAGCTGCT 1500

QY 1525 GGATGGCAGGAGGCTCCTAACCCAGGAGCGCGGAGCCTAGAGGGGACCCCGCGCCAGTC 1584

Db 1501 GGATGGCAGGAGGCTCCTAACCCAGGAGCGCGGAGCCTAGAGGGGACCCCGCGCCAGTC 1560

QY 1585 TCGGGGAACGTGCCCCCCTCCAGCCCATGAGACAGGCTTCATCCAGTATTTGGATTTCAGG 1644

Db 1561 TCGGGGAACGTGCCCCCCTCCAGCCCATGAGACAGGCTTCATCCAGTATTTGGATTTCAGG 1620

QY 1645 AATCTGGCACTTGGCTTTTACAAATGACGGAAAGGAGTCAGAAAGTGTTTCTCTTCTCAC 1704

Db 1621 AATCTGGCACTTGGCTTTTACAAATGACGGAAAGGAGTCAGAAAGTGTTTCTCTTCTCAC 1680

QY 1705 CACTGCCATTGAGTCGGTGGATAACTGCCCCAGCAACTGCTATGGCAATGGTACTGCAT 1764

Db 1681 CACTGCCATT-----CTTGATTCTGGGCTCTCTGTTGGGTGATGGAGAAATGCGT 1731

QY 1765 CTCTGGGACCTGCCACTGCTTCCTGGGTTTCTTGGGCCCGCACTGTGGCAGAGCCTCCTG 1824

Db 1732 TTCTGGAACTTGCCATTGTTTTCCAGGATTTCTGGGTCCGGATTGTTCAAGAGCCGCCTG 1791

QY 1825 CCCCCTGCTCTGTAGCGGAAATGGCCAAATACATGAAGGCAGATGCTTTGTGCCACAGTGG 1884

Db 1792 TCCAGTGTATGTAGTGGCAACGGGCAGTACTCCAAGGGCCGCTGCCCTGTGTTTCAGCGG 1851

QY 1885 CTGGAAAGCGCTGAGTGCATGTGCCCAACCAACCAAGTGTATCGATGTGGCTGCAGCAA 1944

Db 1852 CTGGAAGGCAACGAGTGTATGTGCCGACTACCCAGTGTATTGACCAAGTGTGGGG 1911

QY 1945 CCATGGCACCTGCATCAGGGCACCTGCATCTGCAACCTTGCTACAAAGGCGAGAGCTG 2004

Db 1912 TCGTGGGATTTGTATCATGGGCTCCTGTGCTTGCAACTCAGGATACAAAGGAGAAAAGTTG 1971

QY 2005 TGAGGAAGTGGACTGCATGGACCCCAACATGTTTCAGGCCGGGGTGTCTGCTGAGAGGCGA 2064

Db 1972 TGAAGAAGCTGACTGTATAGACCCCTGGGTGTTCTAATCATGGTGTGTATCCACGGGA 2031

QY 2065 ATGCCATTGCTTTGTGGGATGGGAGGCCAACAACTGCGAGACCCCCAGGGCCACATGCTT 2124

Db 2032 ATGTCACTGCACTCCAGGATGGGAGGTAGCAATTGTGAAATACTGAAGACCATGTGTCC 2091

QY 2125 AGACCAGTGTTCAGGCCACGGAACTTCTCTCCGGACACCGGGCTTTTGACGTGTGACCC 2184

Db 2092 AGACCAGTGTTCGGCCACGGAACTATCTTCAAGAAAGTGGTCTCTGCACGTGTGACCC 2151

QY 2185 AAGCTGGACTGGACACGACTGTTCTATCGAGATCTGTGTCGCGACTGTGTGGCCATGG 2244

Db 2152 TAACTGGACTGSCCCAGACTGCTCAAACGAAATATGTTCTGTGGACTGTGGCTCACACGG 2211

QY 2245 CGTGTGCTAGGGGSCACCTGCCGCTGCGAGGATGGATGGATGGGGGCGAGCTGCGACCA 2304

Db 2212 CGTTTGCAATGGGGGACGTGTGCTGTGAAGAGGCTGGAACGGGCCAGCCTGTAATCA 2271

QY 2305 GCGGGCCTGCCACCCCGCTGTGCCGAGCATGGGACCTGCCCGCAGCGGCAAGTGCAGTG 2364

Db 2272 GAGAGCCTGCCACCCCGCTGTGCCGAGCACGGGACCTGCCCGCAGCGGCAAGTGCAGTG 2331

QY 2365 CAGCCCTGGCTGGAATGGCGAAACACTGCACCATC-----GCTCACTATCTGGATAGGGT 2418

Db 2332 CAGCCCTGGCTGGAATGGCGAAACACTGCACCATCTCCCTAGCTCACTATCTGGATAGGGT 2391

QY 2419 AGTTAA-----AGAGGGTTGCCCTGGGTTGTGCAATGGCAACGGCAGATGTACTTAGA 2472

Db 2392 AGTTAACTTTTCAGAGGGTTGCCCTGGGTTGTGCAATGGCAACGGCAGATGTACTTAGA 2451

QY 2473 CCTGAATGGTTGGCACTGCGTCTGCCAGCTGGCTGGAGAGGAGCTGGCTGTGACACTTC 2532

Db 2452 CCTGAATGGTTGGCACTGCGTCTGCCAGCTGGGCTGGAGAGGAGCTGGCTGTGACACTTC 2511

QY 2533 CATGGAGACTGCCCTGCGGTGACAGCAAAAGCAATGATGGAGATGGCCCTGGTGGACTGCAT 2592

Db 2512 CATGGAGACTGCCCTGCGGTGACAGCAAAAGCAATGATGGAGATGGCCCTGGTGGACTGCAT 2571

QY 2593 GGACCTGACTGCTGCCCTCCAGCCCTGTGCCATATCAACCCGCTGTGCCCTTGGCTCCCC 2652

Db 2572 GGACCTGACTGCTGCCCTCCAGCCCTGTGCCATATCAACCCGCTGTGCCCTTGGCTCCCC 2631

QY 2653 TAAACCTCTTGACATCATCCAGGAGACACAGGTCCCTGTGTCAAGCAGAACTTACACTC 2712

Db 2632 TAAACCTCTTGACATCATCCAGGAGACACAGGTCCCTGTGTCAAGCAGAACTTACACTC 2691

QY 2713 CTTCTATGACCAGCATCAAGTTCTCTGTTGGGAGGAGCAGCAGCAATAATCCCCGGGGA 2772

Db 2692 CTTCTATGACCAGCATCAAGTTCTCTGTTGGGAGGAGCAGCAGCAATAATCCCCGGGGA 2751

QY 2773 GAAACCCCTTTGATGGAGGGCATGCTTGTGTTATTCTGTGGCCCAAGTATGACATCAGATGG 2832

Db 2752 GAAACCCCTTTGATGGAGGGCATGCTTGTGTTATTCTGTGGCCCAAGTATGACATCAGATGG 2811

QY 2833 AACCCCCCTGGTTGGTGTGAACATCAGTTTTGTCAATACCCCTCTCTTTGGATATACAAT 2892

Db 2812 AACCCCCCTGGTTGGTGTGAACATCAGTTTTGTCAATACCCCTCTCTTTGGATATACAAT 2871



Qy	2893	CAGCAGGCAAGATGGCAGCTTTGACTTGGTGACAAATGGCGGCATCTCCATCATCCTGCG	2952	Qy	3964	GGTGAAGGACCTTGTCAAGAACTCTGAGGTGGTTGCGGGGACAGGTGACCAGTGCCTCCC	4023
Db	2872	CAGCAGGCAAGATGGCAGCTTTGACTTGGTGACAAATGGCGGCATCTCCATCATCCTGCG	2931	Db	3952	GGTGAAGGACCTTGTCAAGAACTCTGAGGTGGTTGCGGGGACAGGTGACCAGTGCCTCCC	4011
Qy	2953	GTTTCGAGCGGCACCTTTTCATCACACAGGAGCACACCCCTGTGGTGCCATGGGATCGCTT	3012	Qy	4024	CTTTGATGACACTCGCTGCGGGGATGGTGGGAAGGCCACAGAAGCCACACTCACCAATCC	4083
Db	2932	GTTTCGAGCGGCACCTTTTCATCACACAGGAGCACACCCCTGTGGTGCCATGGGATCGCTT	2991	Db	4012	CTTTGATGACACTCGCTGCGGGGATGGTGGGAAGGCCACAGAAGCCACACTCACCAATCC	4071
Qy	3013	CTTTGTCAATGGAACCATCATGAGACATGAGGAGAATGAGATTCCCAGCTGTGACCT	3072	Qy	4084	CAGGGT-----ATTACAGTGGACAAAGTTTGGGCTGATCTACTTTCGTGGATGGCAC	4134
Db	2992	CTTTGTCAATGGAACCATCATGAGACATGAGGAGAATGAGATTCCCAGCTGTGACCT	3051	Db	4072	CAGGGTCCCCCAGGCATTACAGTGGACAAAGTTTGGGCTGATCTACTTTCGTGGATGGCAC	4131
Qy	3073	GAGCAATTTTGGCCGCCCCAACCCAGTCGTCTCTCCATCCCCACTGACGTCCTTCGCCAG	3132	Qy	4135	CATGATCAGACGCAATCGATCAGAAATGGGATCATCTCCACCCTGCTCGGCTCTAAATGATCT	4194
Db	3052	GAGCAATTTTGGCCGCCCCAACCCAGTCGTCTCTCCATCCCCACTGACGTCCTTCGCCAG	3111	Db	4132	CATGATCAGACGCAATCGATCAGAAATGGGATCATCTCCACCCTGCTCGGCTCTAAATGATCT	4191
Qy	3133	CTCCTGTGCAGAGAAAGGCCCATTTGTGCCGGAATTCAGGCTTTCAGGAGGAAATCTC	3192	Qy	4195	CACATCAGCCCCGCCACTCAGCTGTGATTCTGTCTCATGGATATTTTCCCAGGTAAGA-----	4249
Db	3112	CTCCTGTGCAGAGAAAGGCCCATTTGTGCCGGAATTCAGGCTTTCAGGAGGAAATCTC	3171	Db	4192	CACATCAGCCCCGCCACTCAGCTGTGATTCTGTCTCATGGATATTTTCCCAGGTAAGACAGGT	4251
Qy	3193	TATCTCTGGCTGCAAGATGAGGCTGAGCTACCTGAGCAGCGCGGACCCCTGGCTACAAATC	3252	Qy	4250	----CTGGAGTGGCCCCACAGACTTAGCCATCAACCCCAATGGACAACTCACTTTATGTCT	4305
Db	3172	TATCTCTGGCTGCAAGATGAGGCTGAGCTACCTGAGCAGCGCGGACCCCTGGCTACAAATC	3231	Db	4252	TCACCTGGAGTGGCCCCACAGACTTAGCCATCAACCCCAATGGACAACTCACTTTATGTCT	4311
Qy	3253	TGTCTGAGGATCAGCCTCACCCACCCGACCATCCCTTCAACCTCATGAAGTGCACCT	3312	Qy	4306	CGACAACAATGTGCTCCTGCAAACTCTCTGAAAACCAACAGGTGGCATTTGTCGCCGGAG	4365
Db	3232	TGTCTGAGGATCAGCCTCACCCACCCGACCATCCCTTCAACCTCATGAAGTGCACCT	3291	Db	4312	CGACAACAATGTGCTCCTGCAAACTCTCTGAAAACCAACAGGTGGCATTTGTCGCCGGAG	4371
Qy	3313	CATGGTAGCGGTGAGGGCGGCTCTTCAGGAAGTGGTTCGCTGAGCAGCCCCAGACCTGTC	3372	Qy	4366	GCCCATGCACTGCCAGGTCCCTGGCATTTGACCACTTCTCTGTAAGCAAGGTGGCCATCCA	4425
Db	3292	CATGGTAGCGGTGAGGGCGGCTCTTCAGGAAGTGGTTCGCTGAGCAGCCCCAGACCTGTC	3351	Db	4372	GCCCATGCACTGCCAGGTCCCTGGCATTTGACCACTTCTCTGTAAGCAAGGTGGCCATCCA	4431
Qy	3373	CTATTATTTCAATTTGGACAAGACAGACGCTCTACAACCAGAAAGTGTTTGGGCTTTCAGA	3432	Qy	4426	CGAACCCCTGGAGTCAGCCACCGCTTTTGGCTGTTTACACAAATGGSGTCTGTATATTGC	4485
Db	3352	CTATTATTTCAATTTGGACAAGACAGACGCTCTACAACCAGAAAGTGTTTGGGCTTTCAGA	3411	Db	4432	CGAACCCCTGGAGTCAGCCACCGCTTTTGGCTGTTTACACAAATGGSGTCTGTATATTGC	4491
Qy	3433	AGCCTTTGTTTCCGTGGGTTATGAATATGAATCCTGCCAGATCTAATCCTGTGGGAAAA	3492	Qy	4486	TGAGACTGATGAGAAAAAGATCAACCGCATCAGGCAGGTCAACCACTAGTGGAGAGATCTC	4545
Db	3412	AGCCTTTGTTTCCGTGGGTTATGAATATGAATCCTGCCAGATCTAATCCTGTGGGAAAA	3471	Db	4492	TGAGACTGATGAGAAAAAGATCAACCGCATCAGGCAGGTCAACCACTAGTGGAGAGATCTC	4551
Qy	3493	AAGAACACAGTGTGCAGGGCTATGAATTTGACGGTCCAAGCTTGAGGATGGAGCCT	3552	Qy	4546	ACTCGTTGCTGGGGCCCCCAGTGGCTGTGACTGTAAAAATGATGCCAACTGTGATTGTTT	4605
Db	3472	AAGAACACAGTGTGCAGGGCTATGAATTTGACGGTCCAAGCTTGAGGATGGAGCCT	3531	Db	4552	ACTCGTTGCTGGGGCCCCCAGTGGCTGTGACTGTAAAAATGATGCCAACTGTGATTGTTT	4611
Qy	3553	AGACAAACATCATGCCCTCAACATTCAAAGTGGT--ATCCTGCACAAAGGGAATGGGGA	3609	Qy	4606	TTCTGGAGACGATGGTTATGCCAAGGATGCAAAAGTTAAATACCCCATCTTCTTGGCTGT	4665
Db	3532	AGACAAACATCATGCCCTCAACATTCAAAGTGGTGGCATCCTGCACAAAGGGAATGGGGA	3591	Db	4612	TTCTGGAGACGATGGTTATGCCAAGGATGCAAAAGTTAAATACCCCATCTTCTTGGCTGT	4671
Qy	3610	GAACCAAGTTGTGTCTCAGCAGCCTCCTGTCAATGGGAGCATATGGGCAATGGGCGCG	3669	Qy	4666	GTGTGCTGATGGGGAGCTCTACGTGGCCGACCTTGGGAACATCCGAAATTCGGTTTATCCG	4725
Db	3592	GAACCAAGTTGTGTCTCAGCAGCCTCCTGTCAATGGGAGCATATGGGCAATGGGCGCG	3651	Db	4672	GTGTGCTGATGGGGAGCTCTACGTGGCCGACCTTGGGAACATCCGAAATTCGGTTTATCCG	4731
Qy	3670	GAGAAGCATCTCTGCCCCAGCTGCAACGGCCTTGCTGACGGCAACAAGCTCCTGGCCCC	3729	Qy	4726	GAAGAACAAAGCCTTCTCTCAACACCCAGAACATGTATGAGCTGTCTTCAACCAATTGACCA	4785
Db	3652	GAGAAGCATCTCTGCCCCAGCTGCAACGGCCTTGCTGACGGCAACAAGCTCCTGGCCCC	3711	Db	4732	GAAGAACAAAGCCTTCTCTCAACACCCAGAACATGTATGAGCTGTCTTCAACCAATTGACCA	4791
Qy	3730	AGTGGCCCTCACCTGTGGCTCTGACGGGAGCCTCTATGTGGGTGATTTCAACTACATTAG	3789	Qy	4786	GGAGCTCTATCTGTTTGATACCCACCGGCAAGCACCTGTACACCCAAAAGCCTGCCACAGG	4845
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Qy	3844	TTTTCACATAGTCACAGTCCAGCACAAAATACTACTGGCCACAGACCCCATGAGTGG	3903	Qy	4906	CAATGGCAACATGGTAAATGTCCGCCGAGACTCTACTGGGATGCCCTCTGGCTGGTGGT	4965
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RESULT 6  
US-10-723-860-3169  
; Sequence 3169, Application US/10723860  
; Publication No. US20040253606A1  
; GENERAL INFORMATION:  
; APPLICANT: Aziz, Natasha  
; APPLICANT: Ginsburg, Wendy M.  
; APPLICANT: Zlotnik, Albert  
; TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &  
; TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators  
; FILE REFERENCE: 05882.0193.NPUS01  
; CURRENT APPLICATION NUMBER: US/10/723,860  
; CURRENT FILING DATE: 2003-11-26  
; PRIOR APPLICATION NUMBER: 60/429,739  
; PRIOR FILING DATE: 2002-11-26  
; NUMBER OF SEQ ID NOS: 8393  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 3169  
; LENGTH: 8624  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
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RESULT 7  
US-10-756-149-2959  
; Sequence 2959, Application US/10756149  
; Publication No. US20050181375A1  
; GENERAL INFORMATION:  
; APPLICANT: Aziz, Natasha  
; APPLICANT: Zlotnik, Albert  
; TITLE OF INVENTION: NOVEL METHODS OF DIAGNOSIS OF METASTATIC CANCER, COMPOSITIONS AND  
; TITLE OF INVENTION: METHODS OF SCREENING FOR MODULATORS OF METASTATIC CANCER  
; FILE REFERENCE: file  
; CURRENT APPLICATION NUMBER: US/10/756,149  
; CURRENT FILING DATE: 2004-01-12  
; NUMBER OF SEQ ID NOS: 5818  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 2959  
; LENGTH: 8624  
; TYPE: DNA  
; ORGANISM: Homo Sapiens  
US-10-756-149-2959

Query Match 44.1%; Score 3680.8; DB 9; Length 8624;  
Best Local Similarity 97.8%; Pred. No. 0;  
Matches 3775; Conservative 0; Mismatches 2; Indels 83; Gaps 1;

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601 ATTAGATAACAAGCCTGAAACCCACACGGTACGACAGCTTTTGGCCGCTGACAAATGTGAC 660



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QY	5275	CTTCTACACACTGCTGCAAGACCAAGTCCGGAACAGCTACTACATCGGGGCCGATGGCTC	5334
Db	781	CTTCTACACACTGCTGCAAGACCAAGTCCGGAACAGCTACTACATCGGGGCCGATGGCTC	840
QY	5335	CTTGCGGCTGCTGGCCAAACGGCATGGAGTGGCGCTGCAGACTGAGCCCACTTGCT	5394
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QY	5395	GGCTGGCACCGTCAACCCACCGTGGGCAAGAGGAATGTCACGCTGCCCATCGACAACGG	5454
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QY	5455	CCTCAACCTGGTGGAGTGGCGCCAGCGCAAGAGCAGGCTCGGGGCCAGGTCACTGTCTT	5514
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QY	5515	TGGCGCCGGCTGGCGGTGCACAACCCGAAATCTCTATCTCTGGACTTTGATCGCGTAAC	5574
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QY	5635	GGCGGGCGGCCAGCCTCTGGTCACCCAGCAGCAGGCTGAATGGTGTCAACGTGACATA	5694
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QY	5755	CGACCAGCGGGCCGCATCACATCCAGGATCTTCGCTGATGGGAAGACATGGAGCTACAC	5814
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QY	5815	ATACTTAGAAGTCCATGGTGTCTACTACACAGCCAGAGGCAGTATATCTTTGAGTT	5874
Db	1321	ATACTTAGAAGTCCATGGTGTCTACTACACAGCCAGAGGCAGTATATCTTTGAGTT	1380
QY	5875	CGACAAGAAATGACCGCTCTCTTCTGTGACGATGCCCAACGTGGCGCGGACACTAGA	5934
Db	1381	CGACAAGAAATGACCGCTCTCTTCTGTGACGATGCCCAACGTGGCGCGGACACTAGA	1440
QY	5935	GACCATCCGCTCAGTGGCTACTACAGAAACATCTATCAGCCCCCTGAGGGCAATGCCTC	5994
Db	1441	GACCATCCGCTCAGTGGCTACTACAGAAACATCTATCAGCCCCCTGAGGGCAATGCCTC	1500
QY	5995	AGTCATACAGGACTTCACTGAGGATGGGCCACCTCCTTCACACCTTCTACCTGGGCACTGG	6054
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QY	6175	GAATGAGGGCTTCACTGCACCATCCGCTACCGTACAGATTGGGCCCCCTGATTGACCGACA	6234
Db	1681	GAATGAGGGCTTCACTGCACCATCCGCTACCGTACAGATTGGGCCCCCTGATTGACCGACA	1740
QY	6235	GATCTTCCGCTTCACTGAGGAAGGCATGGTCAACGCCCGTTTTTGACTACAACTATGACAA	6294

Db	1741	GATCTTCGGCTTCACTGAGGAAGSCATGGTCAACGCCCGTTTTTGACTACAACATA TGACAA 1800
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Qy	6355	CTATCGCTATGATGATGTGT CAGGCAAGACAGAGCAGTTTGGGAAGTTTGGTGTCAATTA 6414
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Qy	6475	ATATGSCAGGATGAAGGAAGTGCAGTATGAGATCTTCCGCTCGCTCATGTACTGGATGAC 6534
Db	1981	ATATGSCAGGATGAAGGAAGTGCAGTATGAGATCTTCCGCTCGCTCATGTACTGGATGAC 2040
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Db	2281	GCTGGTGACGTGCAATACAAGATGGATGAGGATGGCTTCTTGAGGCAGCGGGCGGTGA 2340
Qy	6835	TATCTTTGAGTACAACTCAGCTGGCCTGCTCATCAAGGCCTACAACCGGGCTGGCAGCTG 6894
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Qy	7195	GATCTACATGGATACCAACCCCAACTTTCAGATCATCATAGGCTACCATGGTGGCCTCTA 7254
Db	2701	GATCTACATGGATACCAACCCCAACTTTCAGATCATCATAGGCTACCATGGTGGCCTCTA 2760
Qy	7255	TGATCCACTCACCAAGCTTGTCCACATGGSGCGGCGAGATTATGATGTGCTGGSCGGACG 7314
Db	2761	TGATCCACTCACCAAGCTTGTCCACATGGSGCGGCGAGATTATGATGTGCTGGSCGGACG 2820
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Db 3841 CCGGAGGTGACAGAGAGGAC 3860

; Sequence 7176, Application US/10723860  
; Publication No. US20040253606A1  
; GENERAL INFORMATION:  
; APPLICANT: Aziz, Natasha  
; APPLICANT: Ginsburg, Wendy M.  
; APPLICANT: Zlotnik, Albert  
; TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &  
; TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators  
; FILE REFERENCE: 05882.0193.NPUS01  
; CURRENT APPLICATION NUMBER: US/10/723,860  
; CURRENT FILING DATE: 2003-11-26  
; PRIOR APPLICATION NUMBER: 60/429,739  
; PRIOR FILING DATE: 2002-11-26  
; NUMBER OF SEQ ID NOS: 8393  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 7176  
; LENGTH: 8774  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (4015)..(4029)  
; OTHER INFORMATION: n is a, c, g, or t  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (6561)..(6580)  
; OTHER INFORMATION: n is a, c, g, or t  
US-10-723-860-7176

Query Match 43.4%; Score 3621.6; DB 8; Length 8774;  
Best Local Similarity 97.4%; Pred. No. 0;  
Matches 3758; Conservative 0; Mismatches 14; Indels 88; Gaps 4;

QY 4578 GTAAAAATGATGCCAACTGTGATTGTTTTTCTGGAGACGATGGTTATGCCAAGGATGCAA 4637

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QY 5155 CTTCCCTACTGGCCAGGTGAGCAGTTTCCGAAGTGATACAGACAGTTTCAGTGCATGTCCA 5214  
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Db 1796 CCAGCTCCGGGTGACCAGCATGCAGGCTGTGATCAACGAGACCCCACTGCGCCATGATCT 1855  
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QY 7195 GATCTACATGGATACCAACCCCAACTTTTCAGATCATATAGGCTACCATGGTGGCCTCTA 7254  
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Db 151 ATGGATGTGAAAGAACGCAGGCCTTACTGCTCCCTGACCAAGAGCAGACGAGAGAAGGAA 210  
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Qy 326 ACAGACATTTGGCTGCCCCCAATGCGGCTACTCCATGGGGCTGGCTCTGATGCCGACATG 385  
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Qy 1286 GAAGGAAAGCCAGTAGTTTCTTTCCAGAGGACAGTTTCATAGATTCTGGAGAAATTGAT 1345  
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Qy 1946 CATGGCACCTGTCATCACGGGCACCTGCATCTGCAACCTTGGCTACAAAGGCGAGAGCTGT 2005  
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Qy 2006 GAGGAAGTGGACTGCATGGACCCCACTGTTCAGGCCGGGGTGTCTGCTGAGAGGCGAA 2065  
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Qy 2066 TGCCATTGCTTTGTGGGATGGGAGGCCAACCAACTGCGAGACCCCGAGGCCACATGCTTA 2125  
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Qy 2126 GACCAGTGTTCAGGCCACGGAACCTTCTCTCCGGACACCGGGCTTTTGACGTGTGACCCA 2185  
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Db 6535 GATAACATGGGTGGGTAAACCAAGAGAGAGATTAAAAATAGGGCCCTTTGCCAACACCAACC 6594





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TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same  
FILE REFERENCE: 21402-230  
CURRENT APPLICATION NUMBER: US/10/038,854  
CURRENT FILING DATE: 2003-01-22  
PRIOR APPLICATION NUMBER: 60/258,928  
PRIOR FILING DATE: 2000-12-29  
PRIOR APPLICATION NUMBER: 60/259,415  
PRIOR FILING DATE: 2001-01-02  
PRIOR APPLICATION NUMBER: 60/259,785  
PRIOR FILING DATE: 2001-01-04  
PRIOR APPLICATION NUMBER: 60/269,814  
PRIOR FILING DATE: 2001-02-20  
PRIOR APPLICATION NUMBER: 60/279,832  
PRIOR FILING DATE: 2001-03-29  
PRIOR APPLICATION NUMBER: 60/279,833  
PRIOR FILING DATE: 2001-03-29  
PRIOR APPLICATION NUMBER: 60/279,863  
PRIOR FILING DATE: 2001-03-29  
PRIOR APPLICATION NUMBER: 60/283,889  
PRIOR FILING DATE: 2001-04-13  
PRIOR APPLICATION NUMBER: 60/284,447  
PRIOR FILING DATE: 2001-04-18  
PRIOR APPLICATION NUMBER: 60/286,683  
PRIOR FILING DATE: 2001-04-25  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 411  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 35  
LENGTH: 8675  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-038-854-35

Query Match 41.6%; Score 3473.8; DB 7; Length 8675;  
Best Local Similarity 65.2%; Pred. No. 0;  
Matches 5445; Conservative 0; Mismatches 2692; Indels 216; Gaps 14;

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Dd 211 CGGCGCTACACAAATTCCTCCGAGACAAATGAGGAGTGCGGGGTACCCACACAGAAGTCC 270  
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QY 266 TTCACCCCTGCGGGAGCTGGGGTGAAGAAGTAACGCCCCCTTACGGGACCCCTGATCCGG 325  
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Dd 511 GAAATGAAGCAGTGTATGTCACAGAGCATGCCATGAGACTTTGGGGCAGGGGGTCAAA 570  
QY 446 TCAGGGCGCAGCTCCTGCCTGTCCAGCCGGGCCAATTCCAAATCTCACACTCACCGACACC 505

Dd 571 TCAGGCCGCGAGCTCCTGCCTGTCAAGTCGGTCCAACTCAGCCCTCACCTGACAGATAAG 630  
QY 506 GAGCATGAAAAACACTGAGACTGATCATCCGGCGGCTGCAGAACCAACGCGCGCTCCGG 565  
Dd 631 GAGCAGGAAAAACAAGTCCGACAGTGAGAAATGAGCAACCTGCAAGCAATCAAGGCCAGTCT 690  
QY 566 ACGCCGCGCGCGCTCTCGCACGCGCCACACCCCAACCAACGAGCACCACGCGCGCTCCATT 625  
Dd 691 ACCCTGAGCCCTTGCCTTCCCATAGCAGCACTCTGCACAGCATCATCCATCCATC 750  
QY 626 AACTCCCTGAACCGGGGCAACTTCACGCCGAGGAGCAACCCAGCCCGCCACCGGAC 685  
Dd 751 ACTTCTCTCAACAGAAACTCCCTGACCAATAGAAGAACAGAGTCCGGCCCGCGCGCT 810  
QY 686 CACTCGCTCTCCGAGAGCCCCCTGCGCGCGCGCCAGGAGCTGCCCAACGCGCCAGGAG 745  
Dd 811 GCTTTGCCCGCGAGCTGCAAAAC-----CACACCCGAGTCCGTCCAGCTGAGGAC 861  
QY 746 AACTGGCTGTCAACAGCAACATCCCCCTGGAGACCAAGAACCTAGGCAAGCAGCCATT 805  
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Dd 906 -----CCTATTCAAAACAGGAACAGGTACAACGCCACTGTTCAAT 945  
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Dd 946 ACTGCAACCCCGAGTACACAATGGCATCTGGCTCTGTTTATTACCACCTACTCGGCCA 1005  
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QY 1166 CAGATGTATGAGATCACGGAGGACACAGCCAGCAAGTTGGCCCTGTGCCAACCGACGTCTCC 1225  
Dd 1186 GACACATTTGAGA-----ATGGAAGAGTGAAATCTGATACCATGCCAACAAACACTGTG 1239  
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QY 1406 ATAGACCATCCTGTGATCTGAAATTCAAATGTGTCTCTGGGAAAGGAGCCCTGGTTGGC 1465  
Dd 1378 ATTGATCAGCCACAGTTTCTTAAATTCAAATATCTCTCTTCAAGGATGCAATTGATTGA 1437  
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Qy 1634 TTGGATTACAGGAATCTGGCACTTGCGCTTTTACAATGACGSAAGAGTCAAGAAGTGT 1693

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Db 2038 ATCCACGGGGAATGTCACTGCAGTCCAGGATGGGAGGTAGCAATTGTGAATACTGAAG 2097

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Db 2998 ATTCATGGAATGTCTTTTATGTGATGGATACCTAGTATCCCAATCCCATCATTTGTGTACCT 3117

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QY 7553 CAGATGAAAAACGAGGAGTGGGCAACAGCAAGTCTATCCTCGGGGTACAGTGTGAAGTA 7612

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QY 7913 GGTGACCTGGCCATCTTGGCCCTCAGTGGGGGGCGGCAACCTTGGAGAAATGGGGTCAAC 7972

Db 7897 AGCGACCTGGGCACGCTGCGGTTGACCAGCGGCGCAAGGCGCTGGAGAACCGGCATCAAC 7956

QY 7973 GTCACTGTGCCAGATCAACACAGTACTTAATGGCAGGACTAGACGCTACACAGACATC 8032

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QY 8033 CAGCTCCAGTACGGGGCACTGTGCTTGAACACACACGCTACGGGACAACTTGGATGAGGAG 8092

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Dbb 3677 CAAACCAGCTCATAGATACTACCTTGTCAAACGGATCCAGTCACGGGAGATCTGTACGTTTC 3736  
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QY 4039 CTGCGGGGATGGTGGGAAGGCCACAGAAAGCCACACTCACCAATCCCAGGGGTATTACAGT 4098  
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QY 4159 TGGGATCATCTCCACCCTGCTCGGCTCTAATGATCTACATCAGCCCGGCACCTCAGCTG 4218  
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QY 5896 TTCTGTGCGATGCCCAACGCTGGCGCGGAGACACTAGAGACCATCCGCTCAGTGGGCTA 5955  
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Dbb 5774 CTACCGCAACATATACAAACCCCCCGGAAAGCAACGCCTCCATCATCACGGACTACAACGA 5833  
QY 6016 GGATGGGCACCTCCTTCAACCTTCTACCTGGGCACTGGCCGAGGGTGATATACAAAGTA 6075  
Dbb 5834 GGAAGGGCTGCTTCTACAAACAGCTTTTCTTGGGTACAAGTCCGAGGGTCTTATTCAAATA 5893







Db 8036 GCAGGGCTACGACGGGTACTACGTACTCTCGGTGGAGCAGTACCCCGAGCTGGCCGACAG 8095  
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Db 8096 CGCCAACAACATCCAGTTCTCTGCGGCAGAGCGAGATCGGCAGGAGGTAAC 8145

RESULT 12  
US-10-038-854-41  
; Sequence 41, Application US/10038854  
; Publication No. US20040022781A1  
; GENERAL INFORMATION:  
; APPLICANT: Spytek, Kimberly A  
; APPLICANT: Li, Li  
; APPLICANT: Wolenc, Adam R  
; APPLICANT: Vernet, Corine  
; APPLICANT: Eisen, Andrew J  
; APPLICANT: Liu, Xiaohong  
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; APPLICANT: Tchernev, Velizar  
; APPLICANT: Spaderna, Steven K  
; APPLICANT: Gorman, Linda  
; APPLICANT: Kekuda, Ramesh  
; APPLICANT: Patturajan, Meera  
; APPLICANT: Gusev, Vladimир Y  
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; APPLICANT: Guo, Xiaojia S  
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; APPLICANT: Smithson, Glenda  
; APPLICANT: Millet, Isabelle  
; APPLICANT: MacDougall, John R  
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same  
; FILE REFERENCE: 21402-230  
; CURRENT APPLICATION NUMBER: US/10/038,854  
; CURRENT FILING DATE: 2003-01-22  
; PRIOR APPLICATION NUMBER: 60/258,928  
; PRIOR FILING DATE: 2000-12-29  
; PRIOR APPLICATION NUMBER: 60/259,415  
; PRIOR FILING DATE: 2001-01-02  
; PRIOR APPLICATION NUMBER: 60/259,785  
; PRIOR FILING DATE: 2001-01-04  
; PRIOR APPLICATION NUMBER: 60/269,814  
; PRIOR FILING DATE: 2001-02-20  
; PRIOR APPLICATION NUMBER: 60/279,832  
; PRIOR FILING DATE: 2001-03-29  
; PRIOR APPLICATION NUMBER: 60/279,833  
; PRIOR FILING DATE: 2001-03-29  
; PRIOR APPLICATION NUMBER: 60/279,863  
; PRIOR FILING DATE: 2001-03-29  
; PRIOR APPLICATION NUMBER: 60/283,889  
; PRIOR FILING DATE: 2001-04-13  
; PRIOR APPLICATION NUMBER: 60/284,447  
; PRIOR FILING DATE: 2001-04-18  
; PRIOR APPLICATION NUMBER: 60/286,683  
; PRIOR FILING DATE: 2001-04-25  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 411  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 41  
; LENGTH: 8487  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-038-854-41

Query Match 40.7%; . Score 3398.8; DB 7; Length 8487;

Best Local Similarity 67.0%; Pred. No. 0;  
Matches 5008; Conservative 0; Mismatches 2362; Indels 102; Gaps 9;  
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QY 937 AGGTATCCCACTGACGTCCAGCACAGTGTACTCTCTCCGCCCGACCCCTGCCCCGAG 996  
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Db 1120 TGGAGACA-----ATGGAAAATT 1137  
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Db	1738	CGAGTGTGATGTGCCGACTACCCAGTGTATTGACCCACAGTGTGGGGTCTGTGGGATTG	1797
QY	1957	CATCAGGGCACCTGCATCTGCAACCCCTGGCTACAAAGGCGAGAGCTGTGAGGAAGTGA	2016
Db	1798	TATCATGGGCTCCTGTGCTTGCAACTCAGGATACAAAGGAGAAAGTTGTGAAGAAGCTGA	1857
QY	2017	CTGCATGGACCCACATGTTCAGGCCCGGGTGTCTGCGTGAGAGGCGGAATGCCATTGCTT	2076
Db	1858	CTGTATAGACCTTGGGTGTTCTTAATCATGGTGTGTATCCACGGGGAATGTCACTGCAG	1917
QY	2077	TGTGGGATGGGAGGCACCAACTGCGAGACCCCCAGGGCCACATGCTTAGACCAAGTGTTC	2136
Db	1918	TCCAGGATGGGAGGTAGCAATGTGTGAATACTGAAGACCATGTGTCCAGACCAGTGCTC	1977
QY	2137	AGGSCACGGAACCTTCCTCCGGACACCGGGCTTTGCAGCTGTGACCCAAAGCTGGACTGG	2196
Db	1978	CGGCCACGGAACGTATCTTCAAGAAAGTGGCTCCTGCACGTGTGACCCCTAACTGGACTGG	2037
QY	2197	ACACGACTGTTCTATCGAGATCTGTGCTGCCGACTGTGSGTGCCATGGCGTGTGCGTAGG	2256
Db	2038	CCCAGACTGCTCAACCGAAATATGTTCTGTGGACTGTGCTGCACACGGCGTTTGCATGGG	2097
QY	2257	GGSCACCTGCCGCTGCGAGGATGGCTGGATGGGGGCGAGCTTGCAGACCAGCGGGCCTGCCA	2316
Db	2098	GGGACGTGTGCTGTGAAGAGGCTGGACGGGCCCAACCTGTAATCAGAGAGCCTGCCA	2157
QY	2317	CCCGCGCTGTCCGAGCATGGACCTGCCGCGACGGGCAAGTGCAGCTGCAGCCCTGGCTG	2376
Db	2158	CCCCCGCTGTCCGAGCACCGGACCTGCAAGGATGGCAAGTGTGAATGCAGCCATGGCTG	2217
QY	2377	GAATGGCGAACACTGCACCATCGCTCACTATCTGGATAGGGTAGTTAAAGAGGGTTGCCCC	2436
Db	2218	GAATGGAGAGCACTGCACTATC-----GAGGGTTGTCC	2250
QY	2437	TGGGTTGTGCAATGGCAACCGCAGATGTACCTTAGACCTGAATGGTTGGCACTGGCTCTG	2496
Db	2251	TGGTCTGTGCAACAGCAATGGAAGATGTACCCCTGGACCAAAATGGCTGGCAATTGTGTGTG	2310
QY	2497	CCAGCTGGCTGGAGAGGAGCTGGCTGTGACACTTCCATGGAGACTGCCCTGCGGTGACAG	2556
Db	2311	CCAGCTGGATGGAGAGGAGCAGGCTGTGACGTAGCCATGGAGACTCTTTGCAACAGATAG	2370
QY	2557	CAAGACAAATGATGGAGATGGCCTGGTGACTGTCATGGACCCCTGACTGCTGCCCTCCAGCC	2616
Db	2371	CAAGGACAAATGAAGGAGATGGACTCATTTGACTGCAATGGATCCCGATTGCTGCCCTACAG	2430
QY	2617	CCTGTGCCATATCAACCCGCTGTGCTTGGCTCCQCTAACCCCTCTGGACATCATCCAGGA	2676
Db	2431	TTCTGCCAGAAATCAGCCCTATTGTGGGGACTGCCCGGATCTCAGGACATCATTAGCCA	2490
QY	2677	GACACAGGTCCCCTGTGTACAGCAGAACTTACACTCCTCTTATGACCGCATCAAGTTCCT	2736
Db	2491	AAGCCTTCAATCGCCTTCTCAGCAAGCTGCCAAATCCTTTTATGATCGAATCAGTTTCCT	2550
QY	2737	CGTGGCAGGGACAGCACGCACATAATCCCGGGGAGAACCCCTTTGATGGAGGGCATGC	2796
Db	2551	TATAGGATCTGATAGCACCCCATGTTATACCTGGAGAAAGTCCCTTCAATAAGAGSCCTTGC	2610
QY	2797	TTGTGTTATTCTGTGGCCAAAGTGATGACATCAGATGGAAACCCCCCTGGTTGGTGTGAACAT	2856
Db	2611	ATCTGTATCAGAGGCCCAAGTACTGACTGCTGATGGAACTCCACTTATTGGAGTAATGT	2670
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Db	2671	CTCGTTTTTCCATTACCCAGAAATATGGATATACTATTACCGCCAGGACGGAATGTTTGA	2730
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Db	2731	CTTGGTGGCAAAATGGTGGGCCTCTCTAACTTTTGGTATTTGAACGATCCCCATTCCTCAC	2790
QY	2977	ACAGGAGCACACCCTGTGGCTGCCATGGGATCGCTTCTTTGTFCATGGAAACCATCATCAT	3036
Db	2791	TCAGTATCATACTGTGTGGATTCCATGGAATGTCTTTTATGTGATGGATACCCCTAGTCAT	2850

QY	3037	GAGACATGAGGAGAAATGAGATTCCCAGCTGTGACCTTGACCAATTTTGGCCGCCCAACCC	3096
Db	2851	GGAGAAAGAGAGAAATGACATTCCCAGCTGTGATCTGAGTGGATTCTGTGAGGCCAAATCC	2910
QY	3097	AGTCGTCTCTCCATCCCCACTGACGTCCTTCGCCAGACTCCTGTGCAGAGAAAGGCCCCCAT	3156
Db	2911	CATCATTTGTGTCACTACCTTTATCCACCTTTTTCAGATCTTCTCCTGAAGACAGTCCCAT	2970
QY	3157	TGTGCCGGAATTCAGGCTTTGCAGGAGGAAATCTCTATCTCTGGCTGCAAGATGAGGCT	3216
Db	2971	CATTCCCAGAAACACAGGTACTCCACGAGGAAACTACAATTCAGGAACAGATTGAAACT	3030
QY	3217	GAGCTACCTGAGCAGCCGGACCCCTGGCTACAAATCTGTCTCCTGAGGATCAGCCTCACCCA	3276
Db	3031	CTCCTACTTGTAGTTCAGAGCTGCAGGGTATAAGTCAGTTCTCAAGATCACCATGACCCA	3090
QY	3277	CCCGACCATCCCCTTCAACCTCATGAAGGTGCACCTCATGGTAGCGGTGGAGGCCGCT	3336
Db	3091	GTCTATTATTCCATTTAATTTAATGAAGGTTTCATCTTATGGTAGCTGTAGTAGGAAGACT	3150
QY	3337	CTTCAGGAAGTGGTTCGCTGCAGCCCCCAGACCTGTCTCTATTATTTCATTTTGGACAAGAC	3396
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QY	3397	AGACGTCTACAAACAGAAAGGTGTTTGGGCTTTCAGAAGCCTTTGTTTCCGTGGGTATGA	3456
Db	3211	AGATGCATATAATCAGAAAAGTCTATGGTCTATCTGGAAGCTGTTGTGTAGTTGGATATGA	3270
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Db	3271	GTATGAGTCGTGTTGGACCTGACTCTGTGGGAAAAAGGAGACTGCCATTCTGCAGGGCTA	3330
QY	3517	TGAAATTGACGCGTCCAAAGCTTTGAGGATGGAGCTTAGACAAACATCATGCCCTCAACAT	3576
Db	3331	TGAATTGGATGCGTCCAACATGGGTGGCTGGACATTAGATAAACATCACGTGCTGGATGT	3390
QY	3577	TCAAAGTGGTATCCTGCAAAAAGGGAATGGGGGAACCCAGTTTGTGTCTCAGCAGCCTCC	3636
Db	3391	ACAGAACGGTATACTGTACAAGGGAACCGGGGAAAAACAGTTTCATCTCCCAGCAGCCTCC	3450
QY	3637	TGTCATTGGGAGCATCATGGGCAATGGGGCGCGGAGAAAGCATCTCCTGCCCCAGCTGCAA	3696
Db	3451	AGTCGTGATGATGATGGGCAATGGGCGAAGGCGCAGCATTTCTCTGCCCCAGTTGCAA	3510
QY	3697	CGGCCCTTGTGACGGCAACAAAGCTCCTGGCCCCAGTGGCCCTCACCTGTGGCTCTGACGG	3756
Db	3511	TGGTCAAGCTGATGGTAAACAAAGTTACTTGGCCCCAGTGGCGCTAGCTTGTGGATCGATGG	3570
QY	3757	GAGCCTCTATGTGGGTGATTTCAACTACATTAGAAGGATCTTCCCCTCTGGAAATGTTCAC	3816
Db	3571	CAGTCTGTACGTAGCGGATTTCAACTACGTGCGGCGGATATTCCCTTCTGGAATGTAAAC	3630
QY	3817	CAACATCCTTAGAGCTGAGGAATAAAGATTTTCAGACATAGTTCACAGTCCAGCACACAATA	3876
Db	3631	AAGTGTCTTAGAACTAAGAAATAAAGATTTTAGACATAGCAGCAACCCAGCTCATAGATA	3690
QY	3877	CTACCTGGCCACAGACCCCATGAGTGGGGCCGTCTTCTCTTCTGACAGCAACAGCCGCGG	3936
Db	3691	CTACCTTGCAACGGATCCAGTCACGGGAGATCTGTACGTTTCTGACACAAACACCCGAG	3750
QY	3937	GGTCTTTAAATCAAAGTCCACTGTGTGGTGGTGAAGGACCTTGTCAAGAACTCTGAGGTGGT	3996
Db	3751	AATTATCGCCCAAAGTCACTTACGGGGGCAAAAGACTTGACTAAAAATGCAGAAAGTCGT	3810
QY	3997	TGCGGGGACAGGTGACAGTGCCCTCCCCTTTTGTATGACACTCGCTGCGGGGATGTTGGGAA	4056
Db	3811	CGCAGGGACAGGGGAGCAATGCCCTTCCGTTTTCAGCAGGCGAGATGTGGGGATGGAGGAA	3870
QY	4057	GGCCACAGAAAGCCACACTCACCAATCCCAGGGGTATTACAGTGGACAAAGTTTGGGCTGAT	4116
Db	3871	GGCCGTGGAAGCCACACTCATGAGTCCCAAAAGGAATGGCAGTTGATAAGAATGGATTAAAT	3930







Db 6088 ATTTGACTATAGCTATGACAAACAGCTTTCGAGTGACCAGCATGCAGGGTGTGATCAATGA 6147

QY 6334 GACCCCACTGCCCATTTGATCTCTATCGCTATGATGATGTGTCAGGCAAGACAGAGCAGTT 6393

Db 6148 AACGCCACTGCCATTTGATCTGTATCAGTTTGATGACATTTCTGGCAAAGTTGAGCAGTT 6207

QY 6394 TGGGAAGTTTGGTGTCAATTTACTATGACATTAACCCAGATCAATCACCAACAGCTGTCTGAC 6453

Db 6208 TGGAAAGTTTGGAGTTATATATTTATGATATTAACCCAGATCAATTTCTACAGCTGTAATGAC 6267

QY 6454 CCACACCAAGCATTTTGTATGATATGCGAGGATGAAGGAAGTGCAGTATGAGATCTTCCG 6513

Db 6268 CTATACGAAGCACTTTGTATGCTCATGGCCGTATCAAGGAGATTCATATGAGATATTCAG 6327

QY 6514 CTCGCTCATGTACTGGATGACCGTCCAGTATGATAACATGGGGCGAGTAGTGAAGAAGGA 6573

Db 6328 GTCGCTCATGTACTGGATTTACAATTCAGTATGATAACATGGGTCCGGTAAACCAAGAGAGA 6387

QY 6574 GCTGAAGGTAGGACCTTACGCCAATPACCACCTCGTACTCCTATGAGTATGATGCTGACGG 6633

Db 6388 GATTAAATAGGGCCCTTTGCCAACACCACCAAAATATGCTTATGAATATGATGTTGATGG 6447

QY 6634 CCAGCTGCAGACAGTCTCCATCAATGACAAGCCACTCTGCGCTACAGCTACGACCTCAA 6693

Db 6448 ACAGCTCCAACAGTTTACCTCAATGAAGAATAATGTGSCGGTACAACACTACGATCTGAA 6507

QY 6694 TGGGAACCTGCACCTTACTGAGCCCTGGGAACAGTGCACGGCTCACACCACACTACGGTATGA 6753

Db 6508 TGGAAACCTCCATTTACTGAACCCAAGTAACAGTGGCGTCTGACACCCCTTCGCTATGA 6567

QY 6754 CATCCGCGACCGCATCACTCGGCTGGGTGACGTGCAATACAAGATGGATGAGGATGGCTT 6813

Db 6568 CCTGCAGACAGAATCACTCGACTGGGTGATGTTCAATATACGGTTGGATGAAGATGGTTT 6627

QY 6814 CCTGAGGAGCGGGCGGTGATFATCTTTGAGTACAACCTCAGCTGGCCTGCTCATCAAGGC 6873

Db 6628 CCTACGTCAAAGGGGCACGGAAATCTTTGAATATAGCTCCAAGGGGCTTCTAACTCGAGT 6687

QY 6874 CTACAACGGGCTGGCAGCTGGAGTGTGAGTACCGCTACGATGGCCTGGGCGGCGGT 6933

Db 6688 TTACAGTAAAGGCAGTGGCTGGACAGTGATCTACCGTTATGACGGCCTGGGAAGGCGTGT 6747

QY 6934 GTCCAGCAAGAGCAGCCACAGCCACCACTGCAGTTCCTTATGACAGCCTGACCAACCC 6993

Db 6748 TTCTAGCAAAACCAAGTCTAGGACAGCACCTGCAGTTTTTTTATGCTGACTTAACCTATCC 6807

QY 6994 CACCAAGGTCACCCACCTGTACAAACCACCTCCAGCTCTGAGATCACCTCCCTCTACTACGA 7053

Db 6808 CACTAGATTAATCATGTCTACAACCATTCGAGTTCAGAAATTAACCTCCCTGTATTATGA 6867

QY 7054 CTTGCAAGGACACCTCTTTGCCATGGAGCTGAGCAGTGGTGAACAGGTTTGATGATCAAGCAAAT 7113

Db 6868 TCTCCAAGGACATCTTTTGGCCATGGAAATCAGCAGTGGGATGAATTCATATTGCAATC 6927

QY 7114 TGACAAATCGGGACCCCTCTTGTGTCTTTAGTGGAAACAGGTTTGATGATCAAGCAAAT 7173

Db 6928 GGATAACACAGGGACACCACTGSGCTGTGTTCAGTAGCAATGGGCTTATGCTGAACAGAT 6987

QY 7174 CCTGTACACAGCCCTATGGGGAGATCTACATGGAATACCAACCCCAACTTTCAGATCATCAT 7233

Db 6988 TCAGTACACTGCATATGGGGAATCTATTTTGACTCTAATATGACTTTCAACTGGTAAT 7047

QY 7234 AGGCTACCATGGTGGCCTCTATGATCCACTCACCAAGCTTGTCCACATGGGCGCGGAGAGA 7293

Db 7048 TGGATTTCAATGGTGGCCTGTATGACCCCACTCACCAAAATTAATCCACTTTGGAGAAAGAGA 7107

QY 7294 TTATGATGTGCTGGCCGACGCTGGACTAGCCCAAGACCAAGCTGTGGAAGCACTTAG 7353

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QY 7354 TAGCAGCAACGTCATGCCCTTTTAATCTCTATATGTTCAAAAAACAACAACCCCATCAGCAA 7413

Db 7165 TGGGAAGGACCCAGCTCCTTTTAACTTGTAATGTAATGTTTAGGAATAACAACCCCTGCAAGCAA 7224

QY 7414 CTCCCAGGACATCAAGTGCTTTCATGACAGATGTTTAAACAGCTGGCTGCTCACCCTTTGGATT 7473

Db 7225 AATCCATGACGTGAAAGATTACATCAAGATGTTTAAACAGCTGGCTGGTGACATTTGGTTT 7284

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QY 7534 CTACGAGCTCATCCACACACAGATGAAAACGAGGAGTGGGACAAACAGCAAGTCTATCCT 7593

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QY 7594 CGGGTACAGTGTGAAGTACAGAAAGCAGCTCAAGGCCTTTGTACCTTTAGAACGGTTTGA 7653

Db 7393 CGGAGTCCAGCAAGTGGCGCGCAGGCCCAAGGCCTTCTGTGCTGSGGAAGATGGC 7452

QY 7654 CCAGCTCTATGGCTCCACAATCACCAGCTGCCAGCAGGCTCCAAAGACCAAGAAAGTTTGC 7713

Db 7453 CGAGGTGCAGGTGAGCCGGCGCCGGGCCGCGC---GGCGCGCAGTCCCTGGCTGTGGTTGCG 7509

QY 7714 ATCCAGCGGCTCAGTCTTTGGCAAGGGGTCAAGTTTGCCTTGAAGGATGGCCGAGTGAC 7773

Db 7510 CACGGTCAAGTCCGTGATCGCAAGGGCGTCACTGTGGCCGTCAGCCAGGCGCGGTGCA 7569

QY 7774 CACAGACATCATCAGTGTGGCCAATGAGGATGGGCGGAAGGTTGCTGCCATCTTTGAACCA 7833

Db 7570 GACCAACGTGCTCAACATCGCCAACGAGGACTGCATCAAGGTGGCGCGGTGCTCAACAA 7629

QY 7834 TGCCCACTACCTTAGAGAACTTGCACCTTCAACATTTATGGGTGGATACCCATTAATTGT 7893

Db 7630 CGCCTTCTACCTGGAGAACCTGCACCTTCAACCATCGAGGGCAAGGACACGCACTACTTCA 7689

QY 7894 GAAACCAAGCACCTTCAGAAAGGTGACCTGGCCATCTTGGCCCTCAGTGGSGGCGGCGAAC 7953

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QY 8014 TAGACGCTACACAGACATCCAGCTCCAGTACGGGGCACTGTGCTTTGAACACACGCTACGG 8073

Db 7810 GCGCAGGTTCCGCGACGTGGAGATGCAAGTTCGGCGCGCTGGCGCTGCACTGCGCTACGG 7869

QY 8074 GACAAACGTTGGATGAGGAGAAAGGCACGGGTCTTGAGCTGGCCCGGAGAGAGCCGTGCG 8133

Db 7870 CATGACCCCTGGACGAGGAGAAAGCGCGCATCCTGGAGCAGGCGCGGAGCGCGCGCTCGC 7929

QY 8134 CCAAGCGTGGCCCGCAGCAGCAGAGACTTCGGGGAAGGGAGGAAAGCCTGCGGGCCTG 8193

Db 7930 CCGGGCCTGGSCGCGAGCAGCAGCGCGCTGCGCGACGGCGAGGAGGCGCGCGCTCTG 7989

QY 8194 GACAGAGGGGAGAAAGCAGCAGGTGCTGAGCACAGGGCGGGTGCAGGCTACGACGGCTT 8253

Db 7990 GACGAGGGCGAGAAAGCGGACGCTGCTGAGCGCCGGCAAGGTGCAGGCTACGACGGTA 8049

QY 8254 TTTCTGTGATCTGTGAGCAGTACCCAGAACTGTGAGACAGCGGCCCAACAACATCCACTT 8313

Db 8050 CTACGTACTCTCGTGGAGCAGTACCCCGAGCTGGCCGACAGCGCCCAACAACATCCAGTT 8109

QY 8314 CATGAGACAGAGCGAGATGGGCCGGAGGTGAC 8345

Db 8110 CCTGCGGCAGAGCGAGATCGGCAGGAGGTAAC 8141

RESULT 13  
US-09-808-602-78  
; Sequence 78, Application US/09808602  
; Patent No. US20020155115A1  
; GENERAL INFORMATION:  
; APPLICANT: Vernet, Corine A  
; APPLICANT: Fernandes, Elma

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; APPLICANT: Majumder, Kumud
; APPLICANT: Mishra, Vishnu
; APPLICANT: Mezes, Peter S
; APPLICANT: MacDougall, John
; TITLE OF INVENTION: No. US20020155115A1el Proteins and Nuclec Acids Encoding Same
; FILE REFERENCE: 15966-697 CIP
; CURRENT APPLICATION NUMBER: US/09/808,602
; CURRENT FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 09/800,198
; PRIOR FILING DATE: 2001-03-05
; PRIOR APPLICATION NUMBER: 60/186,596
; PRIOR FILING DATE: 2000-03-03
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 78
; LENGTH: 8689
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; US-09-808-602-78

Query Match 40.7%; Score 3397.8; DB 3; Length 8689;
Best Local Similarity 64.8%; Pred. No. 0;
Matches 5469; Conservative 0; Mismatches 2712; Indels 254; Gaps 19;

QY	35	ATGGACGTGAAGGAGAGAACCTTACCGCTCGCTGACCCCGCGCGCGAGCGCGC	94
Db	133	ATGGATGTGAAGGATCGCGACATCGCTCTTTGACCAGGGGACGGTGTGGCAAGGAGTGT	192
QY	95	CGGTACACCAGTCTGTCGCGGACAGCGAGGAGGGCAAG---CCCCGCAAGAAATCGTAC	151
Db	193	CGCTACACCAGTCTCTCTGGACAGTGAAGTGTGCGGTGTCCTGACGAGGAGTCTCTAC	252
QY	152	AGCTCCAGCGAGACCTGAAGGCCTACGACCGACGCGCCCGCTAGCCTATGGCAGCCGC	211
Db	253	AGTTCAGTGAGACCTGAAGGCTTATGACCATGACAGCAGAATGCACATATGGAACCGA	312
QY	212	GTCAAGGACATTGTGCCGAGGAGGCGGAGGAATTTCTGCCGCAAGGTGCCAACTTCACC	271
Db	313	GTCACAGACCTGGTGCACCGGAGTCCGATGAGTTTCTAGACAAGGGGCTAATTTCAAC	372
QY	272	CTGCGGGAGCTGGGGCTGAAGAAGTAACGCCCCCTCACGGGACCCCTGTACCGGACAGAC	331
Db	373	CTGGCAGAATTGGGAATCTGCGAG---CCCTCCCCACACCGAAGTGGTTACTGTTCGAC	429
QY	332	ATTGGCTGCCCCAATGCGGCTACTCCATGGGGGTGGCTCTGTATGCCGACATGGAGGCT	391
Db	430	ATGGGGATCCTCCACCAGGGCTACTCCTGAGCACTGGGTCTGATCGGACTTCGGACACC	489
QY	392	GACACGGTGTGTCCCTGAGCACCCCCTGCGTGTGTGGGGCCGGAGCACACGGTCAAGG	451
Db	490	GAGGGAGGATGTCTCCAGAACATGCCATCAGACTGTGGGACGAGGGATAAATCGAGG	549
QY	452	CGCAGCTCCTGCTGCCAGCGGGCCCAATTCCAAATCTCACACTCACCGACACCGAGCAT	511
Db	550	CGCAGCTCTGGCTTGTCCAGCGCGAGAACTCAGCCCTTACTCTGACTGATTCAGCAAT	609
QY	512	GAAGAACACTGAGACTGATCATCCGGGCGGCC---TGAGAAACCACGCGGGCTCCGGAC	567
Db	610	GAAGATAAATCGGATGACGACAATGGTCGACCCCAATCCACCTACATCTCTGCTAGCCTC	669
QY	568	GCCGCGCGCGCTCTCGACGCCCCACACCCCAACAGCACACCGGGCCTCCATTAA	627
Db	670	CTCCCATCTGCTCAGCTGCTAGCTCCCATATCTCTCCACCAAGTTAGTGCC-AGATGCC	728
QY	628	CTCCCTGAACCGGGGCACTTCACGCCGAGGAGCAACCCAGCCCGG-----674	
Db	729	ATTGCTAGACAGCAACACCTCCCATCAGATCATGGACACCAACCCCGATGAGGAATTC	788
QY	675	-----CCCCCACGACCACCTCGCTCTCCGGAGAGCCCCCTGCCGGCGGCGCC	722
Db	789	CCCTAATTCATACCTGCTCAGAGCATGCTCAGGGGCCCCCAGCAAGCCTCCAGTAGTGGCCC	848

QY	723	AGGAGCCTGCCACGCCCAGGAGAACTGSGCTGCTCAACAGCAACAATCCCTCGGAGACCA	782
Db	849	TCCGAACCAACACAGCCAGTCAACGCTGAGGCCCCCTCTGCCACCTCCTCATAAACACAC	908
QY	783	GGAACCTAGCAAGCAGCCATTTCCTAGGACATTCGAGGACAACCTCATTTGAGATGGACA	842
Db	909	CCTGTCCCAACCACTCCTCTGCCAACTCCCTCAACAGAAACTCACTGACCAATCGCG	968
QY	843	TTCTCGGCGCTCCCGCCA-----861	
Db	969	GAGTCAAATCCAGCCCCCAGCTCCTGCAACCAATGACCTGGCCACCACCGCGGAGTCCGT	1028
QY	862	-----TGATGGGGCTTACAGTGACGGGCACCTTCCT	891
Db	1029	TCAGTCCAGGACAGTGGGTGCTGAACAGTAACGTGCCGTGGAGACGCGGCACCTTCCT	1088
QY	892	CTTCAA---GCCTGGAGGCACCTCCCGCTCTTCTGCACCACATCACAGGGGTACCCACT	948
Db	1089	CTTCAAGACGTCCTCCGGAAGCACACCCCTGTTTTCAGCAGCTCTTCTCCAGGATACCCCTT	1148
QY	949	GACGTCCAGCACAGTGTACTCTCTCCGCCCGGACCCCTGCCCGCAGACCTTCGCCCG	1008
Db	1149	GACCTCAGGACCGTTTATACACCACACCCCGCTGCTGCCACGGAATACATTTCTCTAG	1208
QY	1009	GCCGGCCTTTAACTCAAGAAGCCCTCCAACTACTGTAACTGGAAGTGCAGCCCTGAG	1068
Db	1209	GAAGGCTTCAAGCTGAAGAAACCTCCAAATACTGCAGTTGGAATGCGCCGCTGTC	1268
QY	1069	CGCATCGTCACTCTCAGCCACTCTGGTCACTCTGCTGGCATACTTTGTGGCCATGCACCT	1128
Db	1269	TGCCATTGCCGCTGCCCTCCTTCTGGCCATTTTGTGGCCTATTTTCATAGCAATGCATCT	1328
QY	1129	GTTTGGCTTAACTGGCACCTGCAGCCGATGAGGGGCGAGATGTATGAGATCACGGAGGA	1188
Db	1329	GCTCGGACTCAATTGGCAACTCCAGCCGCGAGATGGACACACCTTTAACA-----ATGG	1382
QY	1189	CACAGCCAGCAGTTGGCCTGTGCCAACCGACGCTCTCCCTATACCCCTCAGGGGGCACTGG	1248
Db	1383	CGTAAGGACCGGCTTACCAGGAACGATGATGTGGCAACAGTGCCATCTCGAGGCAAAAT	1442
QY	1249	CTTAGAGACCCCTGACAGGAAGGCAAGGAACCAAGAACACAGAAAGCCAGTAGTTTCTT	1308
Db	1443	GCCCTGGTCTGAAAA-----1459	
QY	1309	TCCAGAGGACAGTTTCATAGATTCTGGAGAAATTGATGTGGGAAGGCGAGCTCCAGAA	1368
Db	1460	-----ACAGCAGCATAGACAGCGCGGAGGAGCAAGTCCGTGACGGGTGACACAGGA	1511
QY	1369	GATTCTCTCGCACTTTCTGGAGATCTCAAGTGTTCATAGACCATCTCTGTGTCATCTGAA	1428
Db	1512	AGTCCCAACAGGGGTGTTTGGAGGTCCCAAGATTCACATCAGTCAGCCTCAGTTCTTAA	1571
QY	1429	ATTCAAATGTGTCTCTGGGAAAGGACGCCCTGGTTGGCATTTATGGCAGAAAAGGCTCCC	1488
Db	1572	GTTCAACATCTCCCTGGGAAGGATGCCCTCTTCGGCGTCTACATAAGAAGAGGACTGCC	1631
QY	1489	TCCTTCACATACAGATTGACTTTGTGGAGCTGCTGGATGGCAGGAGGCTCCTAAACCCA	1548
Db	1632	ACCATCTCATGCACAGTATGACTTCATGGAACGCTGGACGGAA-----A	1676
QY	1549	GGAGGCGGGAGCTAGAGGGGACCCCGGCCAGTCTCGGGGAACTGTGCCCCCTCCAG	1608
Db	1677	GGAGAAGTGGAGTGTGGTTCAGTCCACCCAGGGAAACGCGGAGCATCCAGACCCCTGGTGA	1736
QY	1609	CCATGAGACAGGCTTCATCCAGTATTTGGATTGAGGAATCTGGCACTTGGCTTTTACAA	1668
Db	1737	GAACGAGGCTGTGTTCGTGCAGTACTTGGATGTGGGCTGTGGCACCTCGCCTTCTACAA	1796
QY	1669	TGACGGAAAGGAGTCAGAAAGTGGTTTCTCTTCTCACCACCTGCCATTGAGTCGGTGGATAA	1728
Db	1797	TGACGGCAAGGACAGGAGATGGTCTCTCTTCAATACGGTTGTCTTAGATTTCAGTGCAGGA	1856







Db 3984 GGACCCCTGTGACTGGCTCGTCTATGTCCTTGACACCAACAGTCGCCGGATCTACCGAGT 4043

Qy 3949 CAAGTCCACTGTGGTGAAGGACCTTGTCAAGAACTCTGAGGTGGTTGCGGGGACAGG 4008

Db 4044 CAAGTCTCTAAGCGGAGCCAAAGACCTTGGCTGGGAATTCGGAAGTTGTGGCCGGACTGG 4103

Qy 4009 TGACCAAGTGCCTCCCTTTGATGACACTCGCTGCGGGGATGGTGGGAAGGCCACAGAAGC 4068

Db 4104 CGAACAAATGTCTACCCCTTTGATGAAGCCCGCTGTGGGGATGGCGGAAGGCTGTGGATGC 4163

Qy 4069 CACACTCACCAATCCCAGGGGTATTACAGTGGACAAAGTTTGGGCTGATCTACTTTCGTGGA 4128

Db 4164 CACCCTGATGAGCCCTAGAGGTATTGCAGTAGACAAAGACGGGCTTATGTATTGTGGA 4223

Qy 4129 TGGCACCATGATCAGACGCATCGATCAGAATGGGATCATCTCCACCCCTGCTCGGCTCTAA 4188

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Qy 4189 TGATCTCACATCAGCCCGGCCACTCAGCTGTGATCTGTCTCATGGATATTTCACAGGTAAG 4248

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Qy 4249 ACTGGAGTGGCCACAGACTTAGCCATCAACCCCAATGGACAACTCACTTTATGTCTCTGA 4308

Db 4344 TCTAGAATGGCCGACAGACCTTGGGTC AACCCCATGGACAAATTCCTGTACGTCTCTGA 4403

Qy 4309 CAACAATGTGGTCCCTGCAAAATCTCTGAAAAACCACAGGTGCGCATTTGTCGCCGGAGGCC 4368

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Qy 4369 CATGCACCTGCCAGGTCCCTGGGCATTGACCACTTCTCTGCTAAGCAAGGTGGCCATCCACGC 4428

Db 4464 CATGCACCTGCCAGGTTCCCGGCATCGACTACT---CGCTCAGCAAGCTCGCCATCCACTC 4520

Qy 4429 AACCCCTGGAGTCAGCCACCGCTTTGGCTGTTTCACACAATGGGGTCCCTGTATATTGCTGA 4488

Db 4521 TGCTCTGGAGTCAGCCAGCGCCATCGCCATTTCTCACACCGGGTGCTCTACATCACCGA 4580

Qy 4489 GACTGATGAGAAAAAGATCAACCCGCATCAGGCAAGTCAACCACTAGTGGAGAGATCTCACT 4548

Db 4581 GACGGACGAGAAGATCAACCGCCTACGCCAGGTCAACCAACCGAGAGATCTGCCT 4640

Qy 4549 CGTTGCTGGGGCCCCAGTGGCTGTGACTGTAAAAATGATGCCAACTGTGATGTTTTC 4608

Db 4641 CTTAGCCGGGCAGCCTCAGACTGTGACTGTCAAAAAATGACGTCAACTGCATCTGCTATTTC 4700

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Qy 4669 TGCTGATGGGAGCTCTACGTGGCCGACCTTGGGAACATCCGAATTCGGTTTATCCGGAA 4728

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Db 5541 GGAGAACGGCCTGAACTCCATCGAGTGGCGCCTGAGGAAGGAACAGATTAAAGGCAAGT 5600

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Db 5601 CACCATCTTTGGGAGGAAGCTTCGGGTCCACGGAAGGAACCTCCTGTCCATTGATTATGA 5660

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Db 5781 TGTCTCCTACTTCTTCAAACGGGCGCCTGGCCGCGCTCCAGCGGGGCCATGAGCGAGAG 5840

Qy 5746 AATGGAATACGACAGGCGGCGCGCATCAATCCAGGATCTTCGCTGATGGGAAGACATG 5805

Db 5841 GACAGACATTGACAAGCAAGGCCGGAATTGTGTCCCGAATGTTTCGCCGACGGGAAGTCTG 5900

Qy 5806 GAGCTACACATACTTAGAGAAGTCCATGGTGTGCTACTACACAGCCAGAGGAGTATAT 5865

Db 5901 GAGCTATTCTCTACCTTGACAAGTCCATGGTCTCTCTGTCAGAGCCAGCGTCAGTACAT 5960

Qy 5866 CTTTGAGTTCGACAAGAAATGACCCGCTCTCTTCTGTGACGATGCCCAACGTTGGCGGCA 5925

Db 5961 ATTTGAATATGACTCCTCTGACCGCCTCCACGAGTCACCATGCCCAGTGTGCGCCGCA 6020

Qy 5926 GACACTAGAGACCATCCGCTCAGTGGGCTACTACAGAAACATCTATCAGCCCCCTGAGGG 5985

Db 6021 CAGCATGTCCACGACACCTCCATTGGCTACATCCGGAACATTTACAACCCACCGGAAG 6080

Qy 5986 CAATGCCTCAGTCAATACAGGACTTCACTGAGGATGGGCACCTCCTTCACACCTTCTACCT 6045

Db 6081 CAACGCCCTCGGTCACTTTGACTACAGTATGACGGCCGATCCTGAAGACGTCCTTCTCT 6140

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Db 6141 GGGCACCGGGCGCCAGGTGTTCTATAAGTACGGA AAACTGTCCAAGTTATCGGAGATCGT 6200





Db 8340 TTACGTGCTTCCGGTGGAACAGTACCCAGAGCTGGCAGACAGTAGCAGCAACATCCAGTT 8399

QY 8314 CATGAGACAGACGAGATGGGCCGAGGTGACAGA 8348

Db 8400 CTTAAGACAGAATGAGATGGGAAAGAGGTAACAAA 8434

RESULT 14

US-09-800-198-66

; Sequence 66, Application US/09800198

; Publication No. US20030087816A1

; GENERAL INFORMATION:

; APPLICANT: Vernet, Cornie AM

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; APPLICANT: Majumder, Kumud

; APPLICANT: Mishra, Vishna

; APPLICANT: Mezes, Peter S

; APPLICANT: Rastelli, Luca

; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME

; FILE REFERENCE: 15966-697

; CURRENT APPLICATION NUMBER: US/09/800,198

; CURRENT FILING DATE: 2001-03-05

; PRIOR APPLICATION NUMBER: 60/186,596

; PRIOR FILING DATE: 2000-03-03

; NUMBER OF SEQ ID NOS: 98

; SOFTWARE: PatentIn ver. 2.1

; SEQ ID NO 66

; LENGTH: 8689

; TYPE: DNA

; ORGANISM: Rattus norvegicus

US-09-800-198-66

Query Match 40.7%; Score 3397.8; DB 3; Length 8689;

Best Local Similarity 64.8%; Pred. No. 0;

Matches 5469; Conservative 0; Mismatches 2712; Indels 254; Gaps 19;

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Db 193 CGCTACACACGCTCCTCTCTGGACAGTGAGGACTGCCGTGTGCCACGCAGAACTCCTAC 252

QY 152 AGCTCCAGCGAGACCCCTGAAGCCCTACGACACGAGGACGCCCGCCTAGCCCTATGGCAGCCGC 211

Db 253 AGTTCAGTGAGACCCCTGAAGCCTTATGACCATGACAGCAGAATGCATATGGAAACCGA 312

QY 212 GTCAAGGACATTTGTCCGCGAGGAGGCCGAGGAATTTGCGCGCACAGGTGCCAACTTCACC 271

Db 313 GTCACAGACCTGGTGCACCGGAGTCCGATGAGTTTTCTAGACAAGGGGCTAATTTCAAC 372

QY 272 CTGCGGGAGCTGGGCTGGAAGAAGTAAACGCCCCCTCACGGGACCCCTGTACCCGACAGAC 331

Db 373 CTGGCAGAATTGGGAATCTGGAG---CCCTCCCCACACCGAAGTGTTACTGTTCCGAC 429

QY 332 ATTGGCCTGCCCCCAATGCGGCTACTCCATGCGGGCTGGCTCTGATGCCGACATGAGGCT 391

Db 430 ATGGGGATCCTCCACCAAGGCTACTCCCTGAGCACTGGGTCTGATCGGACTCGACACC 489

QY 392 GACACGGTGTCTCCCTGAGCACCCCGTGGCTCTGTGGGGCCGGAGCACACGTCAGGG 451

Db 490 GAGGGAGGGATGTCTCCAGAAACATGCCATCAGACTGTGGGACGAGGGATAAATCGAGG 549

QY 452 CGCAGCTCCTGCCTGTCCAGCGGGCCCAATTCCAATCTCACACTCACCGACACCGAGCAT 511

Db 550 CGCAGCTCTGGCTTGTCCAGCGCGAGAACTCAGCCCTTACTCTGACTGATTTCTGACAA 609

QY 512 GAAACACACTGAGACTGATCATCCGGGGCGGC-----TGAGAAACACCGCGGCTCCGGAC 567

Db 610 GAAATAAATCGGATGACGACAATGGTCGACCCCAATTCACCTACATCCTCGTCTAGCCTC 669

QY 568 GCCGCCGCCGCGCTCTCGCAGCGCCACACCCCCAACCCAGCACCCAGCGGCTCCATTAA 627

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QY 628 CTCCTGAACCGGGGCAACTTCACGCCGAGGAGCAACCCAGCCCCG----- 674

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QY 675 -----CCCCACGGACCACTCGCTCTCCGGAGAGCCCCCTGCCGGCGGCGCCC 722

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QY 843 TTCTCGGCGCCTCCCGCCA----- 861

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QY 1489 TCCTTCACATACACAGTTTGACTTTGTGGAGCTGTGGATGGCAGGAGGCTCTTAACCCA 1548

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RESULT 15

US-09-808-602-7

; Sequence 7, Application US/09808602

; Patent No. US20020155115A1

; GENERAL INFORMATION:

; APPLICANT: Vernet, Corine A

; APPLICANT: Fernandes, Elma

; APPLICANT: Shimkets, Richard A

; APPLICANT: Herxman, John L

; APPLICANT: Majumder, Kumud

; APPLICANT: Mishra, Vishnu

; APPLICANT: Mezes, Peter S

; APPLICANT: MacDougall, John

; TITLE OF INVENTION: No. US20020155115A1el Proteins and Nuclec Acids Encoding Same

; FILE REFERENCE: 15966-697 CIP

; CURRENT APPLICATION NUMBER: US/09/808,602

; PRIOR FILING DATE: 2001-03-14

; PRIOR APPLICATION NUMBER: 09/800,198

; PRIOR FILING DATE: 2001-03-05

; PRIOR APPLICATION NUMBER: 60/186,596

; PRIOR FILING DATE: 2000-03-03

; NUMBER OF SEQ ID NOS: 114

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 7

; LENGTH: 9826

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (280)..(8478)

US-09-808-602-7

Query Match 40.5%; Score 3385; DB 3; Length 9826;

Best Local Similarity 64.7%; Pred. No. 0;

Matches 5393; Conservative 0; Mismatches 2790; Indels 154; Gaps 18;

QY 35 ATGGACGTGAAGGAGAGGAAGCCTTACCGCTCGCTGACCCCGCGCCGCGACGCGCAGCGC 94

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QY 1347 TGGGAAGGCGAGCCTCCAGAAGATTCTCTGGCACTTTCTGGAGATCTCAAGTGTTCAC 1406

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Db	1919	CCGGGGTGTCACTGTTTCCAGGATTTCTAGGAGCAGACTGTGCTAAAGCTGCCTGCC	1978
QY	1827	CCGTGCTCTGTAGCGGAAATGGCCAATACATGAAAGGCAGATGCTTGTGCCACAGTGGCT	1886
Db	1979	CTGTCTGTGCAGTGGGAATGGACAATATTCTAAAGGGACGTGCCAGTGCTACAGCGGCT	2038
QY	1887	GGAAAGGCGCTGAGTGCAGTGTGCCACCAACCAAGTGTATCGATGTGGCCTGCAGCAACC	1946
Db	2039	GGAAAGGTGCAGAGTGCAGCGTGGCCATGAAATCAGTGCATCGATCCTTCTTCCGGGGGCC	2098
QY	1947	ATGGCACCTGTCATCAGGGCACCTGTCATCTGCAAACCTGGCTACAAGGGCGAGAGCTGTG	2006
Db	2099	ACGGCTCCTGCATTGATGGGAATGTGTCTGTCTGTCTGTGGCTACAAAGGCGAGCACTGTG	2158
QY	2007	AGGAAGTGGACTGCATGGACCCCCACATGTTCAGGCCGGGTGTCTGCGTGAGAGCGCAAT	2066
Db	2159	AGGAAGTTGATTGCTTGATCCCCACCTGCTCCAGCCACGGAGTCTGTGTGAATGGAGAAT	2218
QY	2067	GCCATTGCTTTGTGGGATGGGAGGCGACCAACTGCGAGACCCCGGGCTTTGCAGCTGTGACCCAA	2126
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QY	2127	ACCAGTGTTCAGGCCACGGAACCTTCTCTCCGGACACCGGGCTTTGCAGCTGTGACCCCA	2186
Db	2279	ACCAGTGCAGTGGGCATGGCACGTACCTGCCTGACACGGGCCCTGCGAGCTGCGATCCCA	2338
QY	2187	GCTGGACTGGACACGACTGTTCTATCGAGATCTGTGCTGCCGACTGTGGTGGCCATGGCG	2246
Db	2339	ACTGGATGGGTCCCGACTGCTCTGTTGAAAGTGTGCTCAGTAGACTGTGGCACTCACGGCG	2398
QY	2247	TGTGCGTAGGGGCACCTGCCGTGCGAGGATGGCTGGATGGGGGAGCCTGCGACCCAGC	2306
Db	2399	TCTGCATCGGGGAGCCTGCCGCTGTGAAGAGGGCTGGACAGGCGCAGCGTGTGACCCAGC	2458
QY	2307	GGGCCCTGCCACCGCGCTGTGCCGAGCATGGACCTGCCGCGACGGCAAGTGCAGTGCA	2366
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QY	2367	GCCCTGGCTGGAATGGCGAACACTGCACCATCGCTCACTATCTGGAFAGGGTAGTTAAAG	2426
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QY	2427	AGGGTTGCCCTGGGTTGTGCAATGGCAACGGCAGATGTACCTTAGACCTGAATGGTTGGC	2486
Db	2579	ATGGCTGCCCTGACTTGTGCAACGGTAACGGGAGATGCACACTGSGGTGAGAACAGCTGGC	2638

QY	2487	ACTGCGTCTGCCAGCTGGGCTGGAGAGGAGCTGGCTGTGACACTTCCATGGAGACTGCCT	2546
Db	2639	AGTGTGTCTGCCAGACCCGCTGGAGAGGGCCCCGATGCAACGTTGCCATGGAAACTTCCT	2698
QY	2547	GCGGTGACAGCAAAAGACAAATGATGGAGATGGCCTGGTGGACTGATGGAACCCCTGACTGCT	2606
Db	2699	GTGCTGATAACAAGGATAATGAGGAGATGGCCTGGTGGAATTGTTGGACCCCTGACTGCT	2758
QY	2607	GCCITCCAGCCCTGTGCCATATCAACCCGCTGTGCCCTTGGCTCCCTTAACCCCTCTTGACA	2666
Db	2759	GCCTGCAGTCAGCCTGTCAAGAACAGCCTGCTCTCCCGGGGTCCCGGACCCACTGGACA	2818
QY	2667	TCATCCAGGAGACACAGGTCCCTGTGTACAGCAGAAACCTACACTCCTTCTATGACCCGCA	2726
Db	2819	TCATTTCAG-----CAGGGCCAGACGGATTGGCCCCGAGTGAAGTCTTCTATGACCCGTA	2872
QY	2727	TCAAGTTCTCGTGGGCAGGACAGCACGACATAATCCCCGGGGAGAACCCCTTTTGATG	2786
Db	2873	TCAAGCTCTTGGCAGGCAAGGATAGCACCCACATCATTCCTGGAGAGAACCCCTTCAACA	2932
QY	2787	GAGGGCATGCTTGTGTTATTCTGTGGCCAAAGTGATGACATCAGATGGAACCCCTGGTTG	2846
Db	2933	GCAGCTTGGTTTCTCTCATCCGAGGCCAAGTAGTAACACAGATGGAATCCCTGGTCG	2992
QY	2847	GTGTGAACATCAGTTTGTCAAATAACCTCTCTCTTTGGATATACAATCAGCAGGCAAGATG	2906
Db	2993	GTGTGAACGTGTCTTTGTCAAGTACCCAAATAACGGCTACACCATCACCCGCCAGGATG	3052
QY	2907	GCAGCTTTGACTTGGTGACAAATGGCGGCATCTCCATCATCCTGCGGTTTCAGCGGGCAC	2966
Db	3053	GCACGTTCGACCTGATCGAAATGGAGGTGCTTCTTGACTCTACACTTGTAGCGAGCCC	3112
QY	2967	CTTTTCATCACACAGGAGCACACCCCTGTGGCTGCATGGGATCGCTTCTTTGTCATGGAAA	3026
Db	3113	CGTTCATGAGCCAGAGCGCACTGTGTGGCTGCGTGGAAACAGCTTTTACGCCATGGACA	3172
QY	3027	CCATCATCATGAGACATGAGGAGAATGAGATTCCCAGCTGTGACCTGAGCAATTTTGCCC	3086
Db	3173	CCCTGGTGATGAAGACCGAGGAGAACTCCCATCCCGAGCTGTGACCTCAGTGGCTTTGTCC	3232
QY	3087	GCCCCAACCCAGTCTCTCTCCATCCCCACTGACGCTCCTTCGCCAGCTCCTGTGCAGAGA	3146
Db	3233	GGCCTGATCCAAATCATCTCTCTCCCCACTGTCCACCTTCTTTAGTGTGCCCTGGGC	3292
QY	3147	AAGCCCCCATTTGTCCGGAAATTCAGGCTTTGAGGAGGAAATCTCTATCTCTGGGTGCA	3206
Db	3293	AGAAATCCCATCGTGCCTGAGACCCAGGTTCTTCATGAAGAAATCGAGCTCCCTGGTTCCA	3352
QY	3207	AGATGAGGCTGAGCTACCTACCTGAGCAGCCGACCCCTGGCTACAAATCTGTCTGAGGATCA	3266
Db	3353	ATGTGAAACTTCGCTATCTGAGCTCTAGAACTGCAAGGTTCAGGGTACAGGTCACTGCTGAAGATCA	3412
QY	3267	GCCTCACCCACCCGACCATCCCTTCAACCTTCATGAAGGTGCACCTCATGGTAGCGGTGG	3326
Db	3413	CCATGACCCAGTCCACAGTGCCTTGAACCTCATTTAGGCTTCACCTGATGGTGGCTGTGG	3472
QY	3327	AGGGCCGCTCTTCAGGAAGTGGTTTCGCTGCAGCCCCCAGACCTGTCTCTATTATTTCATTT	3386
Db	3473	AGGGGCATCTCTTCCAGAAAGTCATTCAGGCTTCTCCCAACCTGGCCTCCACCTTCATCT	3532
QY	3387	GGACAAGACAGACGTCTACAAACAGAAAGGTGTTTGGGCTTTTCAGAAAGCCTTTGTTTCCG	3446
Db	3533	GGGAAGAAGACAGATGCGTATGGCCAAAGGTGTATGGACTCTCAGATGCTGTGTGTCTG	3592
QY	3447	TGGGTATGAATATGAATCTGCCCCAGATCTAATCTGTGGGAAAAAAGAACACAGTGC	3506
Db	3593	TCGGSTTGAATATGAGACCTGTCTCCAGTCTAAATCTCTGGGAGAAAGGACAGCCCTCC	3652
QY	3507	TGCAGGGCTATGAAATTGACGGTCCAAAGCTTGGAGGATGGAGCCTAGACAAACATCATG	3566
Db	3653	TTCAGGGATTTCGAGCTGGACCCCTCAAACCTCGGTGGCTGGTCCCTAGACAAACACCACA	3712
QY	3567	CCCTCAACATTCAAAGTGGTATCTCTGCACAAAGGGAATGGGGAGAACCAAGTTTGTGTCTC	3626



Db 3713 TCCTCAATGTTAAAGTGAATCCTACACAAAGGCACCTGGGAAACCAGTTCCTGACCC 3772  
QY 3627 AGCAGCCTCCTGTANTGGGAGCATCATGGGCAATGGGCGCCGGAGAGCAGCATCTCCTGCC 3686  
Db 3773 AGCAGCCTGCCATCATACCAGCATCATGGGCAATGGTCGCCCGCGGAGCATTTCTGTGTC 3832  
QY 3687 CCAGCTGCAACGGCCTTGCTGACGGCAACAAGTCCTGGCCCCCAGTGGCCCTCACCTGTG 3746  
Db 3833 CCAGCTGCAACGGCCTTGCTGAAGGCAACAAGTCGTGGCCCCCAGTGGCTCTGGCTGTTG 3892  
QY 3747 GCTCTGACGGGAGCCTCTATGTGGGTGAATTTCAACTACATTAGAAGGATCTTCCCCTCTG 3806  
Db 3893 GAATCGATGGGAGCCTCTATGTGGGTGACTTCAATTACATCCGACGCATCTTCCCTCTC 3952  
QY 3807 GAAATGTCACCAACATCCTAGAGCTGAGGAATAAAGATTTTCAGACATAGTCACAGTCCAG 3866  
Db 3953 GAAATGTGACCAGCATCTTGGAGTTACGAATAAAGAGTTTAAACATAGCAACAACCCAG 4012  
QY 3867 CACACAAATACTACTGGCCACAGACCCCATGAGTGGGGCCGCTCTTCCCTTCTTGACAGCA 3926  
Db 4013 CACACAAGTACTACTTGGCAGTGGACCCCGTGTCCGGCTCGCTCTACGTGCCGACACCA 4072  
QY 3927 ACAGCCGGCGGTCTTTAAAAATCAAGTCCACTGTGGTGGTGAAGGACCTTGTCAAGAACT 3986  
Db 4073 ACAGCAGGAGAAATCTACCGCGTCAAGTCTCTGAGTGGAAACCAAGACCTGGTGGGAATT 4132  
QY 3987 CTGAGGTGGTTGCGGGGACAGGTGACCAGTGCCCTCCCTTTGATGACACTCGCTGCGGGG 4046  
Db 4133 CGGAAGTTGTGGCAGGACGGGAGAGCAGTGTCTACCCCTTTGATGAAGCCCGCTGCGGGG 4192  
QY 4047 ATGGTGGGAAGCCACAGAACCCACACTCACCAATCCCAGGGGTATTACAGTGGACAAGT 4106  
Db 4193 ATGGAGGGAAGGCCATAGATGCAACCCCTGATGAGCCCGAGAGGTATTGCGAGTAGACAAGA 4252  
QY 4107 TTGGGCTGATCTACTTCGTGGATGGCACCATGATCAGACGCATCGATCAGAAATGGGATCA 4166  
Db 4253 ATGGGCTCATGTACTTTGTCGATGCCACCATGATCCGGAAGGTTGACCAGAAATGGAATCA 4312  
QY 4167 TCTCCACCCTGCTCGGCTCTAATGATCTCACATCAGCCCGGCCACTCAGCTGTGATTTCTG 4226  
Db 4313 TCTCCACCCTGCTGGGCTCCAATGACCTCACGTCCGCTCCGGCCGCTGAGCTGTGATTCCA 4372  
QY 4227 TCATGGATATTTCCAGGTPAAGACTGGAGTGGCCACAGACTTAGCCATCAACCCAAATGG 4286  
Db 4373 GCATGGATGTAGCCCAAGTTCGTCTGGAGTGGCCAAACAGACCTTGTCTCAATCCCATGG 4432  
QY 4287 ACAACTCACTTTATGTCTCGACAACAATGTGGTCTCTGCAAAATCTCTGAAACACCACAGG 4346  
Db 4433 ATAACTCCTTGATGTTCTAGAGAACAAATGTCTATCTTCTGAAATCACCGAGAACCCCAAG 4492  
QY 4347 TGGCGATTGTGCGCGGAGGCCCATGCACTGCCAGTCCCTGGCATTTGACCACTTCCCTGC 4406  
Db 4493 TCAGCATCATTTGCGGGACGCCCATGCACTGCCAAGTTCCTGGCATTGACTACT--CAC 4549  
QY 4407 TAAGCAAGGTGGCCATCCAGCAACCCCTGGAGTCAGCACCCGCTTTGGCTGTTTCACACA 4466  
Db 4550 TCAGCAAACTAGCCATTCACTCTGCCCTGGAGTCAGCCAGTGCCATTGCCATTTCTCACA 4609  
QY 4467 ATGGGGTCTGTATATTGTGTGAGACTGATGAGAAAAGATCAACCCGCATCAGGCAGGTCA 4526  
Db 4610 CTGGGGTCTCTACATCACTGAGACAGATGAGAAGAAAGATTAACCGTCTACGCCAGGTAA 4669  
QY 4527 CCACTAGTGGAGAGATCTCACTCGTTGCTGGGGCCCCCAGTGGCTGTGACTGTAAAAATG 4586  
Db 4670 CAACCAACGGGGAGATCTGCGCTTTTAGCTGGGGCAGCCTCGGACTCGGACTGCAAAAACG 4729  
QY 4587 ATGCCAACTGTGATTTTCTGGAGACGATGGTTATGCCAAGGATGCAAAATTAATA 4646  
Db 4730 ATGTCAATTGCAACTGCTATTTCAGGAGATGATGCCCTACGCGACTGATGCCATCTTGAATT 4789  
QY 4647 CCCCATCTTCCCTTGGCTGTGTGCTGATGGGGAGCTCTACGTGGCCGACCTTGGGAACA 4706

Db 4790 CCCCATCATCTTAGCTGTAGCTCCAGATGGTACCATTTACATTCAGACCTTGGAAATA 4849  
QY 4707 TCCGAATTCGGTTTATCCGGAAGAACAAAGCCTTTTCTCAACACCCAGAACATGTATGAGC 4766  
Db 4850 TTCGGATCAGGGCGGTGAGCAAGAACAAAGCCTGTTCTTAATGCGCTTCAACCAGTATGAGG 4909  
QY 4767 TGTCTTCAACAATTGACCAGGAGCTCTATCTGTTTGTATACCAACCGCAAGCACCTGTACA 4826  
Db 4910 CTGCATCCCCCGGAGAGCAGGAGTTATATGTTTCAACGCTGATGGCATCCACCAATACA 4969  
QY 4827 CCCAAAGCCTGCCACAGGAGACTACCTGTACAACTTCACCTACACTGGGACGGCGACA 4886  
Db 4970 CTGTGAGCCTGGTGACAGGGGAGTACTTGTACAAATTTACATATAGTACTGACAATGATG 5029  
QY 4887 TCACACTCATCAGACACAACAATGGCAACATGGTAAATGTCCGCCGAGACTCTTACTTGGGA 4946  
Db 5030 TCACTGAATTGATTGACAATAATGGGAATTCCTTGAAGATCCGTCGGGACAGCAGTGGCA 5089  
QY 4947 TGCCCCCTCTGGCTGGTGGTCCCAGATGGCCAGGTGTACTGGGTGACCATGGGCACCAACA 5006  
Db 5090 TGCCCCGTCACTGCTCATGCCGTGACAACCCAGATCATCCCTCACCCGTGGGCACCAATG 5149  
QY 5007 GTGCACTCAAGAGTGTGACCACACAAAGGACAGCAGATTGGCCATGATGACATACCATGGCA 5066  
Db 5150 GAGGCCCTCAAAAGTCGTGCCACACAGAACCTGGAGCTTGGTCTCATGACCTATGATGGCA 5209  
QY 5067 ATTCCGGCCTTCTGGCAACCAAAAGCAATGAAACCGGATGGACAAACATTTTATGAGTACG 5126  
Db 5210 AACTGGGCTCTTGGCCACCAAGAGCGGATGAAACAGGATGGACGACTTCTTATGACTATG 5269  
QY 5127 ACAGCTTTGGCCCTTGACAAATGTGACCTTCCCTACTTGGCCAGGTGAGCAGTTTCCGAA 5186  
Db 5270 ACCACGAAGGCCGCTGACCAACGTGACGGCGCCACCGGGGTGGTAACCAAGTCTGCACC 5329  
QY 5187 GTGATACAGACAGTTTCAAGTGCAATGTCAGGTAGAGACCTCCA--GCAAGGATGATGTCA 5243  
Db 5330 GGGAAATGGAGAAATCTATTACCATTTGACATTGAGAACTCCAACCGTGTATGATGACGTCA 5389  
QY 5244 CCATAACCAACCACTGTCTGCCTCAGGCGCCTTCTACACACTGCTGCAAGACCAAGTCC 5303  
Db 5390 CTGTCAATCACCACCTCTCTTCAGTAGAGGSCCTCTACACAGTGGTACAGATCAAGTTTC 5449  
QY 5304 GGAACAGCTACTACATCGGGGCCGATGGCTCCTTGGGCTGCTGCTGGCCAACGGCATGG 5363  
Db 5450 GGAACAGCTACCAGCTCTGTAATAATGGTACCTGAGGGTGATGTATGCTAATGGGATGG 5509  
QY 5364 AGGTGGCGCTGCAGACTGAGCCCCACCTTGTGCTGGCACCCTCAACCCACCCTGGGCA 5423  
Db 5510 GTATCAGCTTCCACAGCGAGCCCCATGTCTTAGCGGGCACCATCACCCCCACCATTGGAC 5569  
QY 5424 AGAGGAATGTACGCTGCCCATCGACAACGGCCTCAACCTGGTGGAGTGGCGCCAGCGCA 5483  
Db 5570 GCTGCAACATCTCCTGCTCTATGGAGAAATGGCTTAAACTCCATTGAGTGGCGCTTAAGAA 5629  
QY 5484 AAGAGCAGGCTCGGGGCCAGGTCACTGTCTTTGGGCGCCGGCTGCGGGTGCAACACCGAA 5543  
Db 5630 AGGAACAGATTAAAGGCAAAAGTCACCATCTTTGGCAGGAAGCTCCGGGTCCATGGGAAGAA 5689  
QY 5544 ATCTCCTATCTTGGACTTTGATCGCGTAAACAGCACAGAGAAGATCTATGATGACCACC 5603  
Db 5690 ATCTCTTGTCCATTGACTATGATCGAAATATTTCGGAATGAAAGATCTATGATGACCACC 5749  
QY 5604 GCAAGTTCACCCCTCGGATTTGTACGACCAGCGGGGGCGGCCAGCCCTCTGTGTACCCCA 5663  
Db 5750 GGAAGTTTCACCCCTGAGGATCATTTATGACCAGGTGGGGCGCCCTTCTCTTGGCTGCCCA 5809  
QY 5664 GCAGCAGGCTGAATGGTGTCAACGTGACATACTCCCTGGGGTTACATTGCTGGCATCC 5723  
Db 5810 GCAGCGGGCTGGCAGCTGTCAACGTGTCTACTACTTCTTCAATGGGCGCCTGGCTGGCTTC 5869  
QY 5724 AGAGGGGCATCATGTCTGAAAGAAATGGAATACGACCAGGCGGGCCGCTCATCATCCAGGA 5783  
Db 5870 AGCGTGGGGCCATGAGCGGAGGACAGACATCGACAAGCAAGCGCCGCTCGTGTCCCGCA 5929



Qy	5784	TCTTCGCTGATGGGAAGACATGGAGCTACACATACCTTAGAGAAAGTCCATGGTGTCTGTAC	5843	6861	TGCTCATCAAGGCTACAAACCGGGCTGGCAGCTGGAGTGTCCAGGTACCGCTACGATGGCC	6920
Dd	5930	TGTTTCGCTGACGGGAAAGTGTGGAGCTACTCCTACCTTGACAAAGTCCATGGTCCCTCTGC	5989	7010	TCCTAAACAAGAGCTACAAACAAGGCCAGCGGTGGAGTGTCCAGTACCCTATGATGGCG	7069
Qy	5844	TACACAGCCAGAGGCAGTATATCTTTTGAGTTCGACAAAGATGACCGCCTCTCTTCTGTGA	5903	6921	TGGGGCGGCGGTCTCCAGCAAGAGCAGCCACAGCCACCACCTGCAGTTCGAGTTCCTCTATGCAG	6980
Dd	5990	TTCAGAGCCAAACGTTCAGTATATATTTGAGTATGACTCCTCTGACCGCCTCCTTGGCCGTCA	6049	7070	TAGGACGGCGGGCTTCCTACAAGACCAACCTGGGCCAACACCTGCAGTACTTCTACTCTG	7129
Qy	5904	CGATGCCCAAACGTGGCGGCGAGACACTAGAGACCAATCCGCTCAGTGGGTACTACAGAA	5963	6981	ACCTGACCAAACCCACCAAGGTCAACCCACCTCTGTACAAACCACTCCAGCTCTGAGATCACCT	7040
Dd	6050	CCATGCCAGCGTGGCCCGCACAGCATGTCCACACACACACCTCCATCGGCTACATCCGTA	6109	7130	ACCTCCACAACCCGACGGCATCACCCCATGTCTACAATCACTCCAACCTCGGAGATTACCT	7189
Qy	5964	ACATCTATCAGCCCCCTTGAGGCAATGCCTCAGTCAATACAGGACTTCACCTGAGGATGGC	6023	7041	CCCTCTACTACGACTTGCAAGGACACCTCTTTGGCCATGGAGCTGAGCAGTGGTGATGAGT	7100
Dd	6110	ATATTTACAACCCGCTGAAAGCAATGCTTCGGTCACTTTTGACTACAGTGAAGCGCC	6169	7190	CACTGTACTACGACCTCCAGGGCCACCTCTTTGCCATGGAGAGCAGCAGTGGGAGGAGT	7249
Qy	6024	ACCTCCTTACACCTTCTACCTTGGGCACCTGGCCGACGTGGCCGACGGTGATATACAAGTATGSCAAAC	6083	7101	TTTACATAGCTTGTGACAAACATCGGGACCCCTCTTTGCTGTCTTTTAGTGGAAACAGTTTGA	7160
Dd	6170	GCATCCTGAAGACCTCCTTTTGGGCACCGGACGCCAGGTGTTCTACAAAGTATGGGAAC	6229	7250	ACTATGTTGCCCTCTGATAAACACAGGGACTCCTCTGGCTGTGTTCAGCATCAACGGCCTCA	7309
Qy	6084	TGTCAAAGCTGGCAGAGACGCTCTATGACACCAACCAAGGTCACTTTACCTATGACGAGA	6143	7161	TGATCAAGCAAAATCCTGTACACAGCCTATGGGAGATCTACATGGATACCAACCCCAACT	7220
Dd	6230	TCTCCAAGTTATCAGAGATTGTCTACGACAGTACCGCCGTCACTTCGGGTATGACGAGA	6289	7310	TGATCAAAACAGCTGCAGTACACGGCCTATGGGAGATTATATGACTCCAACCCCGACT	7369
Qy	6144	CGCAGGCATGCTGAAGACCAATCAACCTACAGAAATGAGGCTTCACCTGCACCATCCGCT	6203	7221	TTCAGATCATATAGGCTACCATGGTGGCCTCTATGATCCACTACCAAGCTTGTCCACA	7280
Dd	6290	CCACTGGTGTCTTGNAGATGGTCAACCTCCAAAGTGGGGCTTCTCCTGCACCATCAGGT	6349	7370	TCCAGATGGTCAATTGGCTTCATGGGGACTCTATGACCCCTGACCAAGCTGGTCCACT	7429
Qy	6204	ACCGTCAGATTGGGCCCCCTGAATTGACCGGACAGATCTTCCGCTTCACTGAGGAAGGCATGG	6263	7281	TGGCCGGCGAGATTATGATGTGCTGGCCGAGCGCTGGACTAGCCCAGACCAAGAGCTGT	7340
Dd	6350	ACCGAAAGATTGGCCCCCTGGTGGACAAGCAGATCTACAGGTTCCTCCGAGGAAGGCATGG	6409	7430	TCACTCAGCGTGATTATGATGTGCTGGCAGGACGATGGACCTCCCCAGACTATACCATGT	7489
Qy	6264	TCAACGCCCGTTTTTGACTACAACT--ATGACAAACAGCTTCCGGGTGACCAGCATGCAGG	6320	7341	GGAAACACCTTAGTAGCAGCAACGTCAATGCCTTTTAATCTCTATATGTTCAAAAACAACA	7400
Dd	6410	TCAATGCCAGGTTTGACTACACCTATCATGACAAACAGCTTCGCGATCGCAAGCATCAAGC	6469	7490	GGAAAAACGT---GGCAAGGAGCCGGCCCCCTTTAACTGTATATGTTCAAGAGCAACA	7546
Qy	6321	CTGTGATCAACGAGACCCCACTGCCCATTTGATCTCTATCGCTATGATGATGTGTCAAGCA	6380	7401	ACCCCATCAGCAATCCCAGGACATCAAGTGTCTCATGACAGATGTTAAACAGCTGCTGC	7460
Dd	6470	CCGTCAAGTGAGACTCCCCCTCCCGTTGACCTCTACCGGTATGATGAGATTTCTTGGCA	6529	7547	ATCCTCTCAGCAGTGAGCTAGATTTTGAAGAACTACGTGACAGATGTGAAAAGCTGGCTTG	7606
Qy	6381	AGACAGAGCAGTTTGGGAAGTTTGGTGTCAATTTACTATGACATTAACCAGATCATCACCA	6440	7461	TCACCTTTTGATTCCAGCTACACAACGATGATCCCTGGTTATCCCAACAGACATGGATG	7520
Dd	6530	AGGTGAAACACTTTTGGTAAGTTTGGAGTCACTATTATGACATCAACCAGATCATCACCA	6589	7607	TGATGTTTGATTTCAGCTTAGCAACATCAATTCCTGGCTTCCGAGAGCCAAATGTATT	7666
Qy	6441	CAGCTGTCAATGACCCACACCAAGCATTTTGATGCATATGGCAGGATGAAGGAAGTGCAGT	6500	7521	CCATGGAAACCTCTCTACGAGCTCATCCACACACAGATGAAAAACGAGGATGGGACAACA	7580
Dd	6590	CTGCCGTGATGACCTCAGCAAAACACTTCGACACCCCATGGCGGATCAAGGAGGTCCAGT	6649	7667	TCGTGCCCTCCTCCCTATGA-----ATTGTCAGAGAGTCAAGCAAGTGAGAAATG	7714
Qy	6501	ATGAGATCTTCCGTCGCTCATGTACTGTGATGACCGTCCAGTATGATAACATGGGCGAG	6560	7581	GCAAGTCTATCCTCGGGTACAGTGTGAAGTACAGAAGCAGCTCAAGGCCCTTTGTACCT	7640
Dd	6650	ATGAGATGTTCCGGTCCCTCATGTACTGTGATGACGGTGCAATATGACAGCATGGGCGAGG	6709	7715	GACAGCTCATTACAGGTGTCCAACAGACAACAGAGAGACATAACCAGGCCTTCATGGCTC	7774
Qy	6561	TAGTGAAGAAGGAGCTGAAGGTAGGACCTTACGCCAATACCACTCGCTACTCCTATGAGT	6620	7641	TAGAACGGTTTGACCAAGCTCTATGGCTCCCAATCACCAGCTGCCAGCAGGCTCCAAAGA	7700
Dd	6710	TGATCAAGAGGGAGCTAAAACCTGGGGCCCTATGCCAATACCAAGATACACCTATGACT	6769	7775	TGGAA-----GGACAGGTCAATTACTAAAAAGCTCCACGCCAGCATCCGAGAGAAAGCAG	7828
Qy	6621	ATGATGCTGACGGCCAGCTGCAGACAGTCTCCATCAATGACAGCCCACTCTGGCGCTACA	6680	7701	CCAAGAAAGTTTGCAATCCAGCGGCTCAGTCTTTGGCAAGGGGGTCAAGTTTGCCTTGAAGG	7760
Dd	6770	ACGATGGGACGGGCAGCTCCAGAGCGTGGCCGTCAATGACCGCCGACCTTGGCGCTACA	6829	7829	GTCACTGGTTTGCCACCAACCAACGCCCATCATTTGGCAAAGGCATCATGTTTGCCATCAAG	7888
Qy	6681	GCTACGACCTCAATGGGAACCTTGCACTTACTGAGCCCTGGGAACAGTGCACGGCTCACAC	6740	7761	ATGGCCGAGTGAACCAAGACATCATCAGTGTGGCCAAATGAGGATGGCGAAGGGTTGCTG	7820
Dd	6830	GCTATGACCTTAATGGGAATCTCCAATTAAGTAAACCCAGGCAACAGTGTGCGCCTCATGC	6889	7889	AAGGGCGGTGACCACGGGCGTGTCCAGCATCGCCAGCAAGATAGCCGCAAGGTGGCAT	7948
Qy	6741	CACCTACGTPATGACATCCGCGACCGGCATCACTCGGCTGGGTGACGTGCAATACAAGATGG	6800	7821	CCATCTTGAACCATGCCCACTACCTTAGAGAACCTGCACCTTCAACATTGATGGGGTGGATA	7880
Dd	6890	CCTTGGCTATGACCTCCGGGATCGGATAACAGACTCGGGGATGTGCAGTACAATAATTG	6949	7949	CTGTGCTGAACAACGCCTACTACCTTGACAAGATGCACTACAGCATCGAGGGCAAGGACA	8008
Qy	6801	ATGAGGATGGCTTCTGAGGCAGCGGGCGGTGATATCTTTGAGTACAACCTCAGCTGGCC	6860	7881	CCCATTACTTTGTGTAACCAAGGACCTTCAGAAGGTGACTGGCCCATCTCTGGCCTCAGTG	7940
Dd	6950	ACGACGATGGCTATCTGTGCCAGAGAGGGTCTGACATCTTCCGAATACAATTCGAAGGCC	7009	8009	CCCACTACTTTGTGAAGATTGGCTCAGCCGATGGCGACTGGTCACTAGGCACCA	8068

Db	8069	TCGGCCGCAAGGTGCTAGAGAGCGGGTGAACGTGACCGTGTCCAGCCCAAGCTGCTGG	8128
Qy	8001	TTAATGGCAGGACTAGACGCTACACAGACATCCAGCTCCAGTACGGGGCACTGTGCTTGA	8060
Db	8129	TCAACGGCAGGACTCGAAGGTTACGAACTTGAGTTCAGTACTCCACGCTGCTGCTCA	8188
Qy	8061	ACACACGCTACGG-----GACAAAGTTGGATGAGGAGAAGGCACGGGTCTCTGGAGC	8111
Db	8189	GCATCCGCTATGGCCTCACCCCCGACACCCCTGGACGAAGAGAAGGCCCGCTCCTGGACC	8248
Qy	8112	TGGCCCGGCAGAGCCGTGCGCCCAAGCGTGGGCCCGCGAGCAGACAGACTGCGGGAAG	8171
Db	8249	AGGCGAGACAGAGGGCCCTGGGCACCGGCTGGGCCAAGGAGCAGCAGAAAGCCAGGGACG	8308
Qy	8172	GGGAGGAAGCCTGCGGGCCTGGACAGAGGGGGAAGCAGCAGGTGCTGAGCACAGGGC	8231
Db	8309	GGAGAGAGGGGAGCGCCTGTGGACTGAGGGCGAGAAGCAGCAGCTTCTGAGCACCGGGC	8368
Qy	8232	GGGTGCAAGGCTACGACGGCTTTTTCGTGATCTGTGTCGAGCAGTACCCAGAACTGTCAG	8291
Db	8369	GCGTGCAAGGGTACGAGGGATATTACGTGCTTCCCGTGGAGCAATACCCAGAGCTTGCA	8428
Qy	8292	ACAGCGCCAAACAATCCACTTCATGAGACAGACCGAGATGGGCCGGAGGTGACAGA	8348
Db	8429	ACAGTAGCAGCAACATCCAGTTTAAAGACAGAAATGAGATGGGAAAGAGGTAACAAA	8485

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OM nucleic - nucleic search, using sw model

Run on: December 9, 2005, 19:05:23 ; Search time 1303 Seconds  
(without alignments)  
11396.585 Million cell updates/sec

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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents NA:\*  
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9: /cgn2\_6/ptodata/1/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	1708.8	20.5	3111	3	US-08-891-845-1	Sequence 1, Appli
2	1708.8	20.5	3111	3	US-09-514-573-1	Sequence 1, Appli
3	1708.8	20.5	3111	3	US-10-290-578-1	Sequence 1, Appli
4	1673.6	20.0	1680	3	US-08-891-845-3	Sequence 3, Appli
5	1673.6	20.0	1680	3	US-09-514-573-3	Sequence 3, Appli
6	1673.6	20.0	1680	3	US-10-290-578-3	Sequence 3, Appli
7	1185.6	14.2	2387	3	US-08-891-845-11	Sequence 11, Appl
8	1185.6	14.2	2387	3	US-09-514-573-11	Sequence 11, Appl
9	1185.6	14.2	2387	3	US-10-290-578-11	Sequence 11, Appl
C 10	208.6	2.5	2007	3	US-09-976-594-407	Sequence 407, App
11	109	1.3	6763	3	US-09-949-016-3399	Sequence 3399, Ap
12	109	1.3	13857	3	US-09-620-312D-75	Sequence 75, Appl
13	109	1.3	34534	3	US-09-949-016-15141	Sequence 15141, A
14	96.4	1.2	399	3	US-09-861-893-29	Sequence 29, Appl
C 15	93.2	1.1	601	3	US-09-949-016-121669	Sequence 121669
16	92.2	1.1	6049	3	US-08-793-273C-3	Sequence 3, Appli
17	92.2	1.1	6049	6	PCT-US95-11684-3	Sequence 3, Appli
18	84	1.0	7286	3	US-08-793-273C-1	Sequence 1, Appli
19	84	1.0	7286	6	PCT-US95-11684-1	Sequence 1, Appli
20	84	1.0	7346	3	US-09-554-267-1	Sequence 1, Appli
C 21	82.8	1.0	601	3	US-09-949-016-121670	Sequence 121670,
C 22	65.8	0.8	601	3	US-09-949-016-121671	Sequence 121671,
C 23	64.4	0.8	601	3	US-09-949-016-121668	Sequence 121668,
C 24	58.4	0.7	7218	2	US-08-232-463-14	Sequence 14, Appl

25	57	0.7	4716	3	US-09-949-002-67	Sequence 67, Appl
26	57	0.7	4716	3	US-09-949-002-145	Sequence 145, App
27	57	0.7	4724	2	US-08-404-665-3	Sequence 3, Appli
28	57	0.7	4724	2	US-08-404-671-3	Sequence 3, Appli
29	57	0.7	4724	2	US-08-404-781-3	Sequence 3, Appli
30	57	0.7	88002	3	US-09-949-002-639	Sequence 639, App
31	57	0.7	88002	3	US-09-949-002-717	Sequence 717, App
C 32	56	0.7	4403765	3	US-09-103-840A-2	Sequence 2, Appli
C 33	56	0.7	4411529	3	US-09-103-840A-1	Sequence 1, Appli
34	54.2	0.6	4411529	3	US-09-103-840A-1	Sequence 1, Appli
C 35	52.6	0.6	2183	3	US-10-104-047-1064	Sequence 1064, Ap
36	52.6	0.6	4403765	3	US-09-103-840A-2	Sequence 2, Appli
C 37	51.4	0.6	324	3	US-09-902-540-4979	Sequence 4979, Ap
C 38	51.4	0.6	23951	3	US-09-902-540-1245	Sequence 1245, Ap
C 39	49.8	0.6	690	3	US-09-252-991A-3288	Sequence 3288, Ap
40	49.8	0.6	1173	3	US-09-252-991A-3422	Sequence 3422, Ap
C 41	49.8	0.6	1434	3	US-09-252-991A-3260	Sequence 3260, Ap
42	49.6	0.6	293	3	US-09-313-294A-6760	Sequence 6760, Ap
C 43	49.6	0.6	3489	2	US-08-728-323A-1	Sequence 1, Appli
C 44	49.6	0.6	3489	3	US-09-298-568-1	Sequence 1, Appli
C 45	49.6	0.6	3489	3	US-09-410-399-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1  
US-08-891-845-1  
; Sequence 1, Application US/08891845  
; Patent No. 6096873  
; GENERAL INFORMATION:  
; APPLICANT: Schaefer, Gabriele M.  
; APPLICANT: Sliwowski, Mark  
; TITLE OF INVENTION: Gamma-Heregulin  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 460 Point San Bruno Blvd  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPatIn (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/891,845  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/021640  
; FILING DATE: 07/12/96  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Lee, Wendy M.  
; REGISTRATION NUMBER: 40,378  
; REFERENCE/DOCKET NUMBER: P1043  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415/225-1994  
; TELEFAX: 415/952-9881  
; TELEX: 910/371-7168  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 3111 base pairs  
; TYPE: Nucleic Acid  
; STRANDEDNESS: Single  
; TOPOLOGY: Linear  
US-08-891-845-1

Query Match 20.5%; Score 1708.8; DB 3; Length 3111;  
Best Local Similarity 99.6%; Pred. No. 0;  
Matches 1713; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 GTTTGTGATGTGGAGGAGCGCGGCGGAGGCCATGGACGTGAAGGAGAGAAAGCCTTA 60  
Db |||||  
300 GTTTGTGATGTGGAGGAGCGCGGCGGAGGCCATGGACGTGAAGGAGAGAAAGCCTTA 359  
QY 61 CCGTCTCGTGACCCGGCGCGCGAGCGCGGAGCGCGCTACACGAGCTCGTCCGCGGACAG 120  
Db |||||  
360 CCGTCTCGTGACCCGGCGCGCGAGCGCGGAGCGCGCTACACGAGCTCGTCCGCGGACAG 419  
QY 121 CGAGGAGGCAAAAGCCCCGAGAAATCGTACAGCTCCAGGAGACCCCTGAAGGCTACGA 180  
Db |||||  
420 CGAGGAGGCAAAAGCCCCGAGAAATCGTACAGCTCCAGGAGACCCCTGAAGGCTACGA 479  
QY 181 CCAGGACGCGCGCCTAGCCTATGGCAGCCGCGTCAAGGACATTTGTCCCGCAGGAGGCCGA 240  
Db |||||  
480 CCAGGACGCGCGCCTAGCCTATGGCAGCCGCGTCAAGGACATTTGTCCCGCAGGAGGCCGA 539  
QY 241 GGAATTTCTGCGGCACAGGTGCCAACTTCACCCCTGCGGGAGCTGGGGCTGGAAGATTAAC 300  
Db |||||  
540 GGAATTTCTGCGGCACAGGTGCCAACTTCACCCCTGCGGGAGCTGGGGCTGGAAGATTAAC 599  
QY 301 GCCCCTCACGGGACCTGTATCCGGACAGACATTTGGCCCTGCCCCAAATGCGGCTACTCCAT 360  
Db |||||  
600 GCCCCTCACGGGACCTGTATCCGGACAGACATTTGGCCCTCCCCACTGCGGCTACTCCAT 659  
QY 361 GGGGCTGGCTCTGATGCCGACATGGAGGCTGACACGGTGTCTCCCTGAGCACCCCGT 420  
Db |||||  
660 GGGGCTGGCTCTGATGCCGACATGGAGGCTGACACGGTGTCTCCCTGAGCACCCCGT 719  
QY 421 GCGTCTGTGGGCGGAGCACACGCTCAGGGCGCAGCTCTGCCTGTCCAGCCGSGCAA 480  
Db |||||  
720 GCGTCTGTGGGCGGAGCACACGCTCAGGGCGCAGCTCTGCCTGTCCAGCCGSGCAA 779  
QY 481 TTCCAATCTCACACTCACCGACACCGAGCATGAAAACACTGAGACTGATCATCCGGCGG 540  
Db |||||  
780 TTCCAATCTCACACTCACCGACACCGAGCATGAAAACACTGAGACTGATCATCCGGCGG 839  
QY 541 CCTGCAGAACACGCGCGCTCCGAGCGCCGCGCGCTCTGCACGCCCCACACCCC 600  
Db |||||  
840 CCTGCAGAACACGCGCGCTCCGAGCGCCGCGCGCTCTGCACGCCCCACACCCC 899  
QY 601 CAACGAGCACACGCGGCTCCATTAACCTCCCTGAACCGGGCAACTTCACGCCGAGGAG 660  
Db |||||  
900 CAACGAGCACACGCGGCTCCATTAACCTCCCTGAACCGGGCAACTTCACGCCGAGGAG 959  
QY 661 CAACCCAGCCCGGCCCCACGGACCACTCGCTCTCCGAGAGCCCCCTGCGGCGGCGC 720  
Db |||||  
960 CAACCCAGCCCGGCCCCACGGACCACTCGCTCTCCGAGAGCCCCCTGCGGCGGCGC 1019  
QY 721 CCAGGAGCCTGCCACGCGCCAGGAGAACTGGCTGCTCAACAGCAACATCCCCCTGGAGAC 780  
Db |||||  
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QY 781 CAGGAACCTAGGCAAGCAGCCATTCTAGGGACATTGCAGGACAACTCATTTGAGATGGA 840  
Db |||||  
1080 CAGGAACCTAGGCAAGCAGCCATTCTAGGGACATTGCAGGACAACTCATTTGAGATGGA 1139  
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1140 CATTCTGGGCGCCTCCGCGCATGATGGGGCTTACAGTGACGGGCACTTCCTCTTCAAGCC 1199  
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Db |||||  
1200 TGGAGGACCTCCCCGCTCTTCTGCAACCACATCACAGGGTACCCACTGACGTCCAGCAC 1259  
QY 961 AGTGACTCTCTCCGCCCCGACCCCTGCCCGCAGCACTTCGCCCGGCGCGCCTTTAA 1020  
Db |||||  
1260 AGTGACTCTCTCCGCCCCGACCCCTGCCCGCAGCACTTCGCCCGGCGCGCCTTTAA 1319  
QY 1021 CCTCAAGAAGCCCTCCAAGTACTGTAAGTGCGAGCCCTTGAGCGCCATCGTCAAT 1080  
Db |||||  
1320 CCTCAAGAAGCCCTCCAAGTACTGTAAGTGCGAGCCCTTGAGCGCCATCGTCAAT 1379

QY 1081 CTCAGCCACTCTGCTCATCTGCTGGCATACTTTGTGGCCATGCACCTGTTGGCCTAAA 1140  
Db |||||  
1380 CTCAGCCACTCTGGTCACTCTGCTGGCATACTTTGTGGCCATGCACCTGTTGGCCTAAA 1439  
QY 1141 CTGGCACCTGCAGCCGATGGAGGGGCAGATGTATGAGATCACGGAGGACACAGCCAGCAG 1200  
Db |||||  
1440 CTGGCACCTGCAGCCGATGGAGGGGCAGATGTATGAGATCACGGAGGACACAGCCAGCAG 1499  
QY 1201 TTGGCCTGTGCCAACCGACGTCTCCCTATACCCCTCAGGGGGCACTGGCTTAGAGACCCC 1260  
Db |||||  
1500 TTGGCCTGTGCCAACCGACGTCTCCCTATACCCCTCAGGGGGCACTGGCTTAGAGACCCC 1559  
QY 1261 TGACAGGAAAGGCAAAAGGAACACACAGAAAGAACCCAGTAGTTTCTTCCAGAGGACAG 1320  
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1560 TGACAGGAAAGGCAAAAGGAACACACAGAAAGAACCCAGTAGTTTCTTCCAGAGGACAG 1619  
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Db |||||  
1620 TTTCATAGATTCTGGAGAAATTGATGTGGAAAGCGAGCTTCCAGAAAGATTCTCTCTGG 1679  
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1680 CACTTTCTGGAGATCTCAAGTGTTCATAGACCATCTGTGCATCTGAAATTCAATGTGTC 1739  
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Db |||||  
1740 TCTGGAAAGGCAGCCCTCGTTGGCATTTATGGCAGAAAGGCCCTCCCTCCTTCACATAC 1799  
QY 1501 ACAGTTTGACTTTGTGGAGCTGTGATGGCAGGAGGCTCTTAACCCAGGAGGCGGGAG 1560  
Db |||||  
1800 ACAGTTTGACTTTGTGGAGCTGTGATGGCAGGAGGCTCTTAACCCAGGAGGCGGGAG 1859  
QY 1561 CCTAGAGGGAGCCCCCGCCAGTCTCGGGGAACTGTGCCCCCTCCAGCCCATGAGACAGG 1620  
Db |||||  
1860 CCTAGAGGGAGCCCCCGCCAGTCTCGGGGAACTGTGCCCCCTCCAGCCCATGAGACAGG 1919  
QY 1621 CTTTCATCCAGTATTTGGATTTCAGGAATCTGGCACTTGGCTTTTACAATGACGGAAGGA 1680  
Db |||||  
1920 CTTTCATCCAGTATTTGGATTTCAGGAATCTGGCACTTGGCTTTTACAATGACGGAAGGA 1979  
QY 1681 GTCAGAAGTGGTTTCTTTCTCACCACCTGCCATTGAGTCG 1720  
Db |||||  
1980 GTCAGAAGTGGTTTCTTTCTCACCACCTGCCATTGCTCTG 2019

RESULT 2

US-09-514-573-1  
; Sequence 1, Application US/09514573  
; Patent No. 6500941  
; GENERAL INFORMATION:  
; APPLICANT: Schaefer, Gabriele M.  
; APPLICANT: Sliwowski, Mark  
; TITLE OF INVENTION: Gamma-Herregulin  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 460 Point San Bruno Blvd  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPatin (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/514,573  
; FILING DATE: 28 FEB 2000  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/891845  
; FILING DATE: 10 JULY 1997

; APPLICATION NUMBER: 60/021640
; FILING DATE: 07/12/96
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P1043
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3111 base pairs
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
;
US-09-514-573-1
Query Match 20.5%; Score 1708.8; DB 3; Length 3111;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1713; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 GTTGTGGATGTGGAGAGCGCGGGCCGGAGGCCATGGACGTGAAGGAGAGAGCCCTTA 60
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QY 61 CCGCTCGCTGACCCCGCGCGGACGCGCGCGCTACACCAGCTCGTCCGGGACAG 120
Db |||||
QY 121 CGAGGAGGGCAAAGCCCGCAGAAATCGTACAGCTCCAGCGAGACCCTGAAGGCCTACGA 180
Db |||||
QY 181 CCAGGACGCCCGCTAGCCTATGGCAGCCGCGTCAAGGACATTGTGCCGCGAGGCCGA 240
Db |||||
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Db |||||
QY 540 GGAATTCTGCCGCACAGGTGCCAACTTCAACCCTGCGGAGCTGGGGCTGGAAGAGTAAC 599
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QY 600 GCCCCCTCACGGGACCCTGTACCGGACAGACATTGSGCTCCCCCACTGCGGCTACTCCAT 659
QY 361 GGGGGCTGGCTCTGATGCCGACATGGAGGCTGACACGGTGTCTCCCTGAGCACCCCGT 420
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QY 421 GCGTCTGTGGGGCCGGAGCACACGGTCAAGGCGCAGTCTCGCTGTCCAGCCGGGCCAA 480
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QY 720 GCGTCTGTGGGGCCGGAGCACACGGTCAAGGCGCAGTCTCGCTGTCCAGCCGGGCCAA 779
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QY 780 TTCCAATCTCACACTCACCGACACCGAGCATGAAACACTGAGACTGATCATCCGGGCGG 839
QY 541 CCTGCAGAACCAACGCGGCTCCGGACGCGCGCGCGCTCTCGCACGCCCCACACCCCC 600
Db |||||
QY 840 CCTGCAGAACCAACGCGGCTCCGGACGCGCGCGCGCGCTCTCGCACGCCCCACACCCCC 899
QY 601 CAACACGACCAACGCGGCTCCATTAACTCCCTGAACCGGGGCAACTTCAACGCCGAGGAG 660
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QY 900 CAACACGACCAACGCGGCTCCATTAACTCCCTGAACCGGGGCAACTTCAACGCCGAGGAG 959
QY 661 CAACCCCGAGCCCGCCCCCAGGACCACTCGCTCTCCGGAGAGCCCCCTGCCGGCGGCGC 720
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QY 960 CAACCCCGAGCCCGCCCCCAGGACCACTCGCTCTCCGGAGAGCCCCCTGCCGGCGGCGC 1019
QY 721 CCAGGAGCCTGCCCCACGCCCGCAGGAGAACTGGTGTCTCAACAGCAACATCCCCCTGGAGAC 780
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QY 1020 CCAGGAGCCTGCCCCACGCCCGCAGGAGAACTGGTGTCTCAACAGCAACATCCCCCTGGAGAC 1079

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QY 841 CATTCCTCGGCGCTCCCGCCATGATGGSGTTACAGTGACGGGCACCTTCTCTTCAAGCC 900
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QY 1440 CTGGCACCTGCAGCCGATGGAGGGGCGAGATGTATGAGATCACGGAGGACACAGCCAGCAG 1499
QY 1201 TTGGCCTGTGCCAAACCGACGTCTCCCTATACCCCTCAGGGGCACTGGCTTAGAGACCCC 1260
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QY 1500 TTGGCCTGTGCCAAACCGACGTCTCCCTATACCCCTCAGGGGCACTGGCTTAGAGACCCC 1559
QY 1261 TGACAGGAAAGGCAAAAGGAACCCACAGAAAGGAAGCCAGTAGTTTCTTTCCAGAGGACAG 1320
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QY 1560 TGACAGGAAAGGCAAAAGGAACCCACAGAAAGGAAGCCAGTAGTTTCTTTCCAGAGGACAG 1619
QY 1321 TTTTCATAGATTCTGGAGAAATTGATGTGGGAAGGCGAGCCTCCAGAAAGATTCTCTCTGG 1380
Db |||||
QY 1620 TTTTCATAGATTCTGGAGAAATTGATGTGGGAAGGCGAGCTTCCCAGAAAGATTCTCTCTGG 1679
QY 1381 CACTTTCTGGAGATCTCAAGTGTTCATAGACCATTCTGTGCATCTGAAATTCATATGTGC 1440
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QY 1680 CACTTTCTGGAGATCTCAAGTGTTCATAGACCATTCTGTGCATCTGAAATTCATATGTGC 1739
QY 1441 TCTGGAAAGGCGAGCCCTGGTTGGCATTTATGGCAGAAAGGCCCTCCCTCTCACATAC 1500
Db |||||
QY 1740 TCTGGAAAGGCGAGCCCTGGTTGGCATTTATGGCAGAAAGGCCCTCCCTCTCACATAC 1799
QY 1501 ACAGTTTGACTTTGTGGAGCTGCTGGATGGCAGGAGGCTCCTAACCCAGAGGCGCGGAG 1560
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QY 1800 ACAGTTTGACTTTGTGGAGCTGCTGGATGGCAGGAGGCTCCTAACCCAGAGGCGCGGAG 1859
QY 1561 CCTAGAGGGGAGCCCGCGCCAGTCTCGGGAACTGTGCCCCCTCCAGCCATGAGACAGG 1620
Db |||||
QY 1860 CCTAGAGGGGAGCCCGCGCCAGTCTCGGGAACTGTGCCCCCTCCAGCCATGAGACAGG 1919
QY 1621 CTTTCATCCAGTATTGGATTTCAGGAATCTGGCACTTGGCTTTTACAAATGACGGAAGGA 1680
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QY 1920 CTTTCATCCAGTATTGGATTTCAGGAATCTGGCACTTGGCTTTTACAAATGACGGAAGGA 1979
QY 1681 GTCAGAAAGTGGTTTCTTCTCACCACCTGCCATTGAGTCG 1720
Db |||||
QY 1980 GTCAGAAAGTGGTTTCTTCTCACCACCTGCCATTGCTTG 2019

RESULT 3
US-10-290-578-1
; Sequence 1, Application US/10290578
; Patent No. 6916624
; GENERAL INFORMATION:
; APPLICANT: Schaefer, Gabriele M.
; Sliwkowski, Mark



;;  
;; TITLE OF INVENTION: Gamma-Herregulin  
;; NUMBER OF SEQUENCES: 11  
;; CORRESPONDENCE ADDRESS:  
;;   ADDRESSEE: Genentech, Inc.  
;;   STREET: 460 Point San Bruno Blvd  
;;   CITY: South San Francisco  
;;   STATE: California  
;;   COUNTRY: USA  
;;   ZIP: 94080  
;;  
;; COMPUTER READABLE FORM:  
;;   MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
;;   COMPUTER: IBM PC compatible  
;;   OPERATING SYSTEM: PC-DOS/MS-DOS  
;;   SOFTWARE: Winpatin (Genentech)  
;;  
;; CURRENT APPLICATION DATA:  
;;   APPLICATION NUMBER: US/10/290,578  
;;   FILING DATE: 08-No. 6916624-2002  
;;   CLASSIFICATION: <Unknown>  
;;  
;; PRIOR APPLICATION DATA:  
;;   APPLICATION NUMBER: US/08/891,845  
;;   FILING DATE: <Unknown>  
;;   APPLICATION NUMBER: 60/021640  
;;   FILING DATE: 12-Jul-96  
;;  
;; ATTORNEY/AGENT INFORMATION:  
;;   NAME: Lee, Wendy M.  
;;   REGISTRATION NUMBER: 40,378  
;;   REFERENCE/DOCKET NUMBER: P1043  
;;  
;; TELECOMMUNICATION INFORMATION:  
;;   TELEPHONE: 415/225-1994  
;;   TELEFAX: 415/952-9881  
;;   TELEX: 910/371-7168  
;;  
;; INFORMATION FOR SEQ ID NO: 1:  
;;   SEQUENCE CHARACTERISTICS:  
;;     LENGTH: 3111 base pairs  
;;     TYPE: Nucleic Acid  
;;     STRANDEDNESS: Single  
;;     TOPOLOGY: Linear  
;;  
;;   SEQUENCE DESCRIPTION: SEQ ID NO: 1:

US-10-290-578-1

Query Match           20.5%;   Score 1708.8;   DB 3;   Length 3111;  
Best Local Similarity   99.6%;   Pred. No. 0;  
Matches 1713;   Conservative   0;   Mismatches   7;   Indels   0;   Gaps   0;

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Db	360	CCGCTCGTGAACCCGCGCGCGGACCGCGGAGCGCGCTACACCAAGCTCGTCCGCGGACAG	419
QY	121	CGAGGAGGCAAAAGCCCCCGCAGAAATCGTACAGCTCCAGGAGACCCCTGAAGGCCTACGA	180
Db	420	CGAGGAGGCAAAAGCCCCCGCAGAAATCGTACAGCTCCAGGAGACCCCTGAAGGCCTACGA	479
QY	181	CCAGGACGCGCCGCTAGCCTATGGCAGCCGCGTCAAGGACATTTGCCGAGGAGGCCCGA	240
Db	480	CCAGGACGCGCCGCTAGCCTATGGCAGCCGCGTCAAGGACATTTGCCGAGGAGGCCCGA	539
QY	241	GGAAATTCGCGCACAGGTGCCAACTTCACCCCTGCGGGAGCTGGGGCTGGAAGAAGTAAC	300
Db	540	GGAAATTCGCGCACAGGTGCCAACTTCACCCCTGCGGGAGCTGGGGCTGGAAGAAGTAAC	599
QY	301	GCCCCCTCAGGGGACCCCTGTACCGGACAGACATTGGCCCTGCCCCCAATGCGGCTACTCCAT	360
Db	600	GCCCCCTCAGGGGACCCCTGTACCGGACAGACATTGGCCCTGCCCCCAATGCGGCTACTCCAT	659
QY	361	GGGGCTGGGCTCTGATGCCGACATGGAGGCTGACACGGTGCTGTCCCCTGAGCACCCCGT	420
Db	660	GGGGCTGGGCTCTGATGCCGACATGGAGGCTGACACGGTGCTGTCCCCTGAGCACCCCGT	719
QY	421	GCGTCTGTGGGGCCGGAGCACACGGTCAAGGGCGCAGCTCCTGCTGTCCAGCCGGGCAAA	480

Db	720	GCGTCTGTGGGGCCGGAGCACACGGTCAAGGGCGAGCTCCTGCCTGTCCAGCCGGGCAAA	779
QY	481	TTCCAATCTCACTCACTCAACCGACACCGAGCATGAAAAACACTGAGACTGATCATCCGGGCGG	540
Db	780	TTCCAATCTCACTCACTCAACCGACACCGAGCATGAAAAACACTGAGACTGATCATCCGGGCGG	839
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Db	840	CCTGCAGAACCAACGCGGGCTCCGGACGCGCGCGCGCTCTCGACGCCCCACACCCC	899
QY	601	CAACCAGCACCAACGCGGGCTCCATTAACTCCCTGAAACCGGGGCAACTTCACGCGCGAGGAG	660
Db	900	CAACCAGCACCAACGCGGGCTCCATTAACTCCCTGAAACCGGGGCAACTTCACGCGCGAGGAG	959
QY	661	CAACCCCGAGCCCCCGCCCCACGGACCACTCGCTCTCCGGAGAGCCCCCTGCGCGGCGCGC	720
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QY	721	CCAGGAGCCTGCCACGCCACGCCAGGAGAACTGGCTGCTCAACAGCAACATCCCCCTGGAGAC	780
Db	1020	CCAGGAGCCTGCCACGCCACGCCAGGAGAACTGGCTGCTCAACAGCAACATCCCCCTGGAGAC	1079
QY	781	CAGGAACCTAGGCAAGCAGCCATTCTTAGGACATTGACGAGCAACCTCATTTAGATGGA	840
Db	1080	CAGGAACCTAGGCAAGCAGCCATTCTTAGGACATTGACGAGCAACCTCATTTAGATGGA	1139
QY	841	CATTCTCGGCGCTCCCGCCATGATGGGCTTACAGTGACGGGCACTTCTCTTCAAGCC	900
Db	1140	CATTCTCGGCGCTCCCGCCATGATGGGCTTACAGTGACGGGCACTTCTCTTCAAGCC	1199
QY	901	TGGAGGCACCTCCCGCTCTTCTGCACCAATCACCAGGCTACCCACTGACGTCAGCAC	960
Db	1200	TGGAGGCACCTCCCGCTCTTCTGCACCAATCACCAGGCTACCCACTGACGTCAGCAC	1259
QY	961	AGTGTAATCTCTCGGCCCCGACCCCTTGCCCCCGCAGCACCTTCGCCCCGGCGCCTTTAA	1020
Db	1260	AGTGTAATCTCTCGGCCCCGACCCCTTGCCCCCGCAGCACCTTCGCCCCGGCGCCTTTAA	1319
QY	1021	CCTCAAGAACCCCTCCAAGTACTGTAACTGGAAGTGCAGCCCTGAGCGCCATCGTCAT	1080
Db	1320	CCTCAAGAACCCCTCCAAGTACTGTAACTGGAAGTGCAGCCCTGAGCGCCATCGTCAT	1379
QY	1081	CTCAGCCACTCTGGTTCATCCTGTGGCATACTTTGTGGCCATGCACCTGTGGCCTAAA	1140
Db	1380	CTCAGCCACTCTGGTTCATCCTGTGGCATACTTTGTGGCCATGCACCTGTGGCCTAAA	1439
QY	1141	CTGGCACCTGCAGCCGATGGAGGGCAGATGTATGAGATCACGGAGGACACAGCCAGCAG	1200
Db	1440	CTGGCACCTGCAGCCGATGGAGGGCAGATGTATGAGATCACGGAGGACACAGCCAGCAG	1499
QY	1201	TTGGCCTGTGCAACCGACGCTCTCCCTATACCCCTCAGGGGGCACTGGCTTAGAGACCCC	1260
Db	1500	TTGGCCTGTGCAACCGACGCTCTCCCTATACCCCTCAGGGGGCACTGGCTTAGAGACCCC	1559
QY	1261	TGACAGGAAGGCAAGGAACCAACAGAAAGCCCACTAGTTTCTTTCCAGAGGACAG	1320
Db	1560	TGACAGGAAGGCAAGGAACCAACAGAAAGCCCACTAGTTTCTTTCCAGAGGACAG	1619
QY	1321	TTTCATAGATTCTGGAGAAATTGATGTGGAAAGGCGAGCCTCCAGAAATTCCTCCTGG	1380
Db	1620	TTTCATAGATTCTGGAGAAATTGATGTGGAAAGGCGAGCTTCCAGAAATTCCTCCTGG	1679
QY	1381	CACCTTCTGGAGATCTCAAGTGTTCATAGACCATCTCTGTGCATCTGAAATTCATGTGTC	1440
Db	1680	CACCTTCTGGAGATCTCAAGTGTTCATAGACCATCTCTGTGCATCTGAAATTCATGTGTC	1739
QY	1441	TCTGGGAAAGGCGAGCCCTGGTTGGCATTTATGGCAGAAAAGGCCCTCCCTTACATAC	1500
Db	1740	TCTGGGAAAGGCGAGCCCTGGTTGGCATTTATGGCAGAAAAGGCCCTCCCTTACATAC	1799
QY	1501	ACAGTTTGACTTTGTGGAGCTGCTGGATGGCAGGAGGCTCCTAACCCAGGAGGCGGAG	1560

Db 1800 ACAGTTTGACTTTGTGAGCTGCTGGATGGCAGGAGGCTCTAAACCCAGGAGGCGGGAG 1859  
QY 1561 CCTAGAGGGGACCCCGCCAGTCTCGGGGAACGTGTGCCCCCCTCCAGCCATGAGACAGG 1620  
Db 1860 CCTAGAGGGGACCCCGCCAGTCTCGGGGAACGTGTGCCCCCCTCCAGCCATGAGACAGG 1919  
QY 1621 CTTTCATCCAGTATTTGGATTGAGGAATCTGGCACTTGGCTTTTACAAATGACGGAAGGA 1680  
Db 1920 CTTTCATCCAGTATTTGGATTGAGGAATCTGGCACTTGGCTTTTACAAATGACGGAAGGA 1979  
QY 1681 GTCAGAAAGTGGTTTCCTTCTCACCACCTGCCATTGAGTCG 1720  
Db 1980 GTCAGAAAGTGGTTTCCTTCTCACCACCTGCCATTGCTTG 2019

RESULT 4  
US-08-891-845-3  
; Sequence 3, Application US/08891845  
; Patent No. 6096873  
; GENERAL INFORMATION:  
; APPLICANT: Schaefer, Gabriele M.  
; APPLICANT: Sliwowski, Mark  
; TITLE OF INVENTION: Gamma-Heregulin  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 460 Point San Bruno Blvd  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPatin (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/891,845  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/021640  
; FILING DATE: 07/12/96  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Lee, Wendy M.  
; REGISTRATION NUMBER: 40,378  
; REFERENCE/DOCKET NUMBER: P1043  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415/225-1994  
; TELEFAX: 415/952-9881  
; TELEX: 910/371-7168  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1680 base pairs  
; TYPE: Nucleic Acid  
; STRANDEDNESS: Single  
; TOPOLOGY: Linear  
US-08-891-845-3

Query Match 20.0%; Score 1673.6; DB 3; Length 1680;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 1676; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
QY 35 ATGACGTGAAGGAGAGAGCCTTACCGCTCGCTGACCCGGCGCCGCGACGCCGAGCGC 94  
Db 1 ATGACGTGAAGGAGAGAGCCTTACCGCTCGCTGACCCGGCGCCGCGACGCCGAGCGC 60  
QY 95 CGGTACACCAAGCTCGTCCGGGACAGCGAGGAGGGCAAGCCCCCGCAGAAATCGTACAGC 154  
Db 61 CGGTACACCAAGCTCGTCCGGGACAGCGAGGAGGGCAAGCCCCCGCAGAAATCGTACAGC 120  
QY 155 TCAGCGAGACCCTGAAGGCTTACGACCAGGACGCCCGCTAGCCTATGGCAGCGCGTC 214

Db 121 TCCAGCGAGACCCTGAAGGCCTACGACCAGGACGCCCGCCTAGCCTATGGCAGCGCGTC 180  
QY 215 AAGGACATTTGTCCCGCAGAGGCGCGAGGAATTTCTCCGCACAGGTGCCAACTTCACCCCTG 274  
Db 181 AAGGACATTTGTCCCGCAGAGGCGCGAGGAATTTCTCCGCACAGGTGCCAACTTCACCCCTG 240  
QY 275 CGGAGCTGGGGCTGGAAGAAGTAACGCCCCCTCACGGGACCCCTGTACCGGACAGACATT 334  
Db 241 CGGAGCTGGGGCTGGAAGAAGTAACGCCCCCTCACGGGACCCCTGTACCGGACAGACATT 300  
QY 335 GGCCTGCCCCAATGCGGCTACTCCATGSGGGCTGGCTCTGATGCCGACATGGAGGCTGAC 394  
Db 301 GGCCTCCCCCACTGCGGCTACTCCATGSGGGCTGGCTCTGATGCCGACATGGAGGCTGAC 360  
QY 395 ACGTGTCTGTCCCCTGAGCACCCCGTGCCTCTGTGGGGCCGGAGCACACGGTCAGGGCGC 454  
Db 361 ACGTGTCTGTCCCCTGAGCACCCCGTGCCTCTGTGGGGCCGGAGCACACGGTCAGGGCGC 420  
QY 455 AGTCTCCTGCTGTCCAGCCGGGCCAATTCCAATCTCACACTCACCGACACCCGAGCATGAA 514  
Db 421 AGTCTCCTGCTGTCCAGCCGGGCCAATTCCAATCTCACACTCACCGACACCCGAGCATGAA 480  
QY 515 AACACTGAGACTGATCATCCGGGGCGCTGACAGAACCCACGCGCGCTCCATTAATCCCTG 634  
Db 481 AACACTGAGACTGATCATCCGGGGCGCTGACAGAACCCACGCGCGCTCCATTAATCCCTG 540  
QY 575 CCGCCGCTCTCGCACGCCCCACACCCCAACCCAGCACACCGCGCTCCATTAATCCCTG 634  
Db 541 CCGCCGCTCTCGCACGCCCCACACCCCAACCCAGCACACCGCGCTCCATTAATCCCTG 600  
QY 635 AACCGGGGCAACTTCAGCCGAGGAGCAACCCAGCCCGCCCCCACGGACCACCTCGCTC 694  
Db 601 AACCGGGGCAACTTCAGCCGAGGAGCAACCCAGCCCGCCCCCACGGACCACCTCGCTC 660  
QY 695 TCCGAGAGCCCCCTGCCGGCGGCCAGGAGCCTGCCACGCCCGAGGAACTGGCTG 754  
Db 661 TCCGAGAGCCCCCTGCCGGCGGCCAGGAGCCTGCCACGCCCGAGGAACTGGCTG 720  
QY 755 CTCAACAGCAACATCCCCCTGGAGACCAGGAACCTTAGGCAAGCAGCCTTCCTAGGGACA 814  
Db 721 CTCAACAGCAACATCCCCCTGGAGACCAGGAACCTTAGGCAAGCAGCCTTCCTAGGGACA 780  
QY 815 TTGCAGGACAACCTCATTTGAGATGGACATTTCTGGCGCCTCCCGCCTATGATGGGCTTAC 874  
Db 781 TTGCAGGACAACCTCATTTGAGATGGACATTTCTGGCGCCTCCCGCCTATGATGGGCTTAC 840  
QY 875 AGTGACGGGCACTTCCTCTTCAAGCCTGGAGGCACCTCCCGCTCTTCTGCACCACATCA 934  
Db 841 AGTGACGGGCACTTCCTCTTCAAGCCTGGAGGCACCTCCCGCTCTTCTGCACCACATCA 900  
QY 935 CCAGGTATCCCACTGACGTCCAGCACAGTGTACTCTCTCCGCCCGCCGACCCCTGCCCGC 994  
Db 901 CCAGGTATCCCACTGACGTCCAGCACAGTGTACTCTCTCCGCCCGCCGACCCCTGCCCGC 960  
QY 995 AGCACCTTCGCCCGCGCCGCTTTAACTCAAGAACCCCTCAAGAGCCCTCCAAGTACTGTAAG 1054  
Db 961 AGCACCTTCGCCCGCGCGCTTTAACTCAAGAACCCCTCCAAGTACTGTAAGTGGAAAG 1020  
QY 1055 TGCGCAGCCCTGAGCGCCCATCGTCATCTCAGCACCTTGGTCATCTCTGTCATCTTGGCATACTTT 1114  
Db 1021 TGCGCAGCCCTGAGCGCCCATCGTCATCTCAGCACCTTGGTCATCTCTGTCATCTTGGCATACTTT 1080  
QY 1115 GTGGCCATGCACCTGTTTGGCCTAAACTGGCACCTTGACCCGATGGAGGGGCGAGATGTAT 1174  
Db 1081 GTGGCCATGCACCTGTTTGGCCTAAACTGGCACCTTGACCCGATGGAGGGGCGAGATGTAT 1140  
QY 1175 GAGATCACGGAGGACACAGCCAGCAGTTTGGCTGTGCCAACCGACGCTCTCCCTATACCCC 1234  
Db 1141 GAGATCACGGAGGACACAGCCAGCAGTTTGGCTGTGCCAACCGACGCTCTCCCTATACCCC 1200  
QY 1235 TCAGGGGCACTGGCTTAGAGACCCCTGACAGGAAGGCAAGGAACCCAGAGGAAAG 1294  
Db 1201 TCAGGGGCACTGGCTTAGAGACCCCTGACAGGAAGGCAAGGAACCCAGAGGAAAG 1260

QY 1295 CCCAGTAGTTCTTCCAGAGGACAGTTTCATAGATTCTGGAGAAATTGATGTGGGAAGG 1354  
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Db 1261 CCCAGTAGTTCTTCCAGAGGACAGTTTCATAGATTCTGGAGAAATTGATGTGGGAAGG 1320  
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QY 1355 CGAGCCTCCAGAGAATTCCCTCCTGGCAGCTTTCTGGAGATCTCAAGTGTTCATAGACCAT 1414  
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Db 1321 CGAGCTTCCAGAGAATTCCCTCCTGGCAGCTTTCTGGAGATCTCAAGTGTTCATAGACCAT 1380  
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QY 1415 CCTGTGATCTGAAATTCAATGTGTCTCTGGGAAAGGACGCCCTGGTTGGCATTTATGGC 1474  
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QY 1475 AGAAAGGCTCCCTCCTTCACATACACAGTTTGTGAGCTGTGGATGGCAGG 1534  
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Db 1441 AGAAAGGCTCCCTCCTTCACATACACAGTTTGTGAGCTGTGGATGGCAGG 1500  
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QY 1535 AGGCTCCTAAACCCAGGAGCGCGGAGCCTAGAGGGACCCCGCCAGTCTCGGGGAACT 1594  
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QY 1595 GTGCCCCCTCCAGCCATGAGACAGGCTTCATCCAGTATTTGGATTTCAGGAATCTGSCAC 1654  
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Db 1561 GTGCCCCCTCCAGCCATGAGACAGGCTTCATCCAGTATTTGGATTTCAGGAATCTGSCAC 1620  
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QY 1655 TTGGCTTTTACAATGACGGAAAGGAGTCAGAAAGTGTTTCTCACCACCTGCCATT 1714  
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Db 1621 TTGGCTTTTACAATGACGGAAAGGAGTCAGAAAGTGTTTCTCACCACCTGCCATT 1680  
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RESULT 5

US-09-514-573-3  
; Sequence 3, Application US/09514573  
; Patent No. 6500941  
; GENERAL INFORMATION:  
; APPLICANT: Schaefer, Gabriele M.  
; APPLICANT: Slikowski, Mark  
; TITLE OF INVENTION: Gamma-Herregulin  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 460 Point San Bruno Blvd  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPatIn (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/514,573  
; FILING DATE: 28 FEB 2000  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/891845  
; FILING DATE: 10 JULY 1997  
; APPLICATION NUMBER: 60/021640  
; FILING DATE: 07/12/96  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Lee, Wendy M.  
; REGISTRATION NUMBER: 40,378  
; REFERENCE/DOCKET NUMBER: P1043  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415/225-1994  
; TELEFAX: 415/952-9881  
; TELEX: 910/371-7168  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1680 base pairs  
; TYPE: Nucleic Acid  
; STRANDEDNESS: Single

; TOPOLOGY: Linear  
US-09-514-573-3  
Query Match 20.0%; Score 1673.6; DB 3; Length 1680;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 1676; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
QY 35 ATGGACGTGAAGGAGAGGAAGCCTTACCGCTCGCTGACCCGGCGCCGCGAGCCGCGAGCGC 94  
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Db 1 ATGGACGTGAAGGAGAGGAAGCCTTACCGCTCGCTGACCCGGCGCCGCGAGCGC 60  
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QY 95 CGCTACACCAAGCTCGTCCGCGGACAGCGAGGAGGGCAAAGCCCCCGCAGAAATCGTACAGC 154  
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Db 61 CGCTACACCAAGCTCGTCCGCGGACAGCGAGGAGGGCAAAGCCCCCGCAGAAATCGTACAGC 120  
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QY 155 TCCAGCGAGACCCTGAAGGCCCTACGACCAGGACGCCCGCTAGCCTATGGCAGCCGCGTC 214  
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QY 215 AAGGACATTGTCCGCGCAGGAGGCCGAGGAATTTCTCCGCACAGGTGCCAACTTCACCCCTG 274  
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Db 181 AAGGACATTGTCCGCGCAGGAGGCCGAGGAATTTCTCCGCACAGGTGCCAACTTCACCCCTG 240  
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QY 275 CGGGAGCTGGGGCTGGAAGAAAGTAAACGCCCCCTCACGGGACCCCTGTACCCGACAGACATT 334  
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Db 241 CGGGAGCTGGGGCTGGAAGAAAGTAAACGCCCCCTCACGGGACCCCTGTACCCGACAGACATT 300  
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QY 335 GGCCTGCCCCCAATGCGGCTACTCCATGGGGGCTGGCTCTGATGCCGACATGGAGGCTGAC 394  
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Db 301 GGCCTCCCCCACTGCGGCTACTCCATGGGGGCTGGCTCTGATGCCGACATGGAGGCTGAC 360  
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QY 395 ACGGTGCTGTCCCTGAGCACCCCGTGCTGTGTGGGGCCGGAGCACACGGTCAGGGCGC 454  
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QY 455 AGCTCCTGCCTGTCCAGCCGGGCCAATTCCAATCTCACACTCACCGACACCGAGCATGAA 514  
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QY 515 AACACTGAGACTGATCATCCGGCGGCTTGAGAAACACACGCGGCTCCGAGCCGCGCG 574  
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QY 575 CCGCCGCTCTCGCACGCCCCACACCCCCAACACAGCACACACGCGGCTCCATTAACCTCCCTG 634  
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Db 541 CCGCCGCTCTCGCACGCCCCACACCCCCAACACAGCACACACGCGGCTCCATTAACCTCCCTG 600  
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QY 635 AACCAGGGCACTTCACGCGGAGGAGCAACCCAGCCCGCCGCGCCACCGACCACTCGCTC 694  
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QY 695 TCCGAGAGCCCTGCTCGGCGGCGCCAGGAGCCTGCCACGCGCCAGGAGAACTGGCTG 754  
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QY 755 CTCAACAGCAACATCCCTTGAGACCAGGAACCTTAGGCAAGCAGCCATTCTTAGGGACA 814  
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QY 815 TTGCAGGACAACCTCATTTGAGATGGACATTTCTGGCGCTCCCGCCCATGATGGGCTTAC 874  
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QY 875 AGTGACGGGCACTTCTCTTCAAGCCTTGAGGCACCTCCCGCTCTTCTGCACCACATCA 934  
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QY 935 CCAGGGTACCACTGACGTCCAGCACAGTGTACTCTCTCCGCGCCCGACCCCTGCCCGCGC 994  
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Db 901 CCAGGGTACCACTGACGTCCAGCACAGTGTACTCTCTCCGCGCCCGACCCCTGCCCGCGC 960  
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QY 995 AGCACCTTCGCGGCGCGGCTTTAACCTCAAGAAGCCCTCCAAAGTACTGTAACTGGAAG 1054  
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Db 961 AGCACCTTCGCCCGCGCCCTTTAACTCAAGAAAGCCCTCCAAAGTACTGTAACTGGAAG 1020

QY 1055 TGCGAGCCCTGAGCGCCATCGTCACTCTAGCCACTCTGGTCACTCCTGCTGGCATACTTT 1114

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Db 1081 GTGGCCATGCACCTGTTGGCCTAAACTGGCACTGCAGCCGATGGAGGGCAGATGTAT 1140

QY 1175 GAGATCACGGAGGACACAGCCAGCAGTGGCCCTGTGCCAACCGACGCTCCTCCCTATACCCC 1234

Db 1141 GAGATCACGGAGGACACAGCCAGCAGTGGCCCTGTGCCAACCGACGCTCCTCCCTATACCCC 1200

QY 1235 TCAGGGGGCACTGGCTTAGAGACCCCTGCAGGAAAGCAAGCAACCAAGGAAAG 1294

Db 1201 TCAGGGGGCACTGGCTTAGAGACCCCTGCAGGAAAGCAAGCAACCAAGGAAAG 1260

QY 1295 CCCAGTAGTTCTTTCCAGAGGACAGTCTTCTGGAGATCTCAAGTGTTCATAGACCAT 1354

Db 1261 CCCAGTAGTTCTTTCCAGAGGACAGTCTTCTGGAGATCTCAAGTGTTCATAGACCAT 1320

QY 1355 CGAGCCTCCAGAAAGATTCTCTGGCACTTTCTGGAGATCTCAAGTGTTCATAGACCAT 1414

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Db 1381 CCTGTGCATCTGAATTTCAATGTGTCTCTGGGAAAGGCAGCCCTGGTTGSCATTTATGGC 1440

QY 1475 AGAAAAGGCCTCCCTCTCACATACAGTTTGAATTTGAGAGCTGCTGGATGGCAGG 1534

Db 1441 AGAAAAGGCCTCCCTCTCACATACAGTTTGAATTTGAGAGCTGCTGGATGGCAGG 1500

QY 1535 AGGCTCCTAACCCAGGAGCGCGGAGCCTAGAGGGGACCCCGCCAGTCTCGGGGAACT 1594

Db 1501 AGGCTCCTAACCCAGGAGCGCGGAGCCTAGAGGGGACCCCGCCAGTCTCGGGGAACT 1560

QY 1595 GTGCCCCCTCCAGCCATGAGACAGGCTTCATCCAGTATTTGGATTTCAGGAATCTGGCAC 1654

Db 1561 GTGCCCCCTCCAGCCATGAGACAGGCTTCATCCAGTATTTGGATTTCAGGAATCTGGCAC 1620

QY 1655 TTGGCTTTTACAATGACGGAAGGAGTCAGAAAGTGTTTCCCTTCTCACCAGTCCCAT 1714

Db 1621 TTGGCTTTTACAATGACGGAAGGAGTCAGAAAGTGTTTCCCTTCTCACCAGTCCCAT 1680

RESULT 6

US-10-290-578-3  
; Sequence 3, Application US/10290578  
; Patent No. 6916624

GENERAL INFORMATION:

; APPLICANT: Schaefer, Gabriele M.  
; TITLE OF INVENTION: Gamma-Heregulin  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 460 Point San Bruno Blvd  
; City: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPatIn (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/290,578  
; FILING DATE: 08-No. 6916624-2002  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/891,845  
; FILING DATE: <Unknown>  
; APPLICATION NUMBER: 60/021640  
; FILING DATE: 12-Jul-96  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Lee, Wendy M.  
; REGISTRATION NUMBER: 40,378  
; REFERENCE/DOCKET NUMBER: P1043  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415/225-1994  
; TELEFAX: 415/952-9881  
; TELEX: 910/371-7168  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1680 base pairs  
; TYPE: Nucleic Acid  
; STRANDEDNESS: Single  
; TOPOLOGY: Linear  
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:  
US-10-290-578-3

Query Match 20.0%; Score 1673.6; DB 3; Length 1680;

Best Local Similarity 99.8%; Pred. No. 0;

Matches 1676; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 35 ATGGACGTGAAGGAGAGGAAGCCTTACCGCTCGCTGACCCCGCGCCGCGAGCGC 94

Db 1 ATGGACGTGAAGGAGAGGAAGCCTTACCGCTCGCTGACCCCGCGCGCGAGCGC 60

QY 95 CGTACACCAAGTCTCGCGGACAGCGAGGGGCAAGCCCCCGCAGAAATCGTACAGC 154

Db 61 CGTACACCAAGTCTCGCGGACAGCGAGGGGCAAGCCCCCGCAGAAATCGTACAGC 120

QY 155 TCCAGCGAGACCCCTGAAGGCCTACGACCAGGACGCCCGCTAGCCTATGGCAGCCGCGTC 214

Db 121 TCCAGCGAGACCCCTGAAGGCCTACGACCAGGACGCCCGCTAGCCTATGGCAGCCGCGTC 180

QY 215 AAGGACATTGTCCCGCAGGAGCGCGGAATTCTGCCGCACAGGTGCCAACTTCACCCCTG 274

Db 181 AAGGACATTGTCCCGCAGGAGCGCGGAATTCTGCCGCACAGGTGCCAACTTCACCCCTG 240

QY 275 CGGAGCTGGGCTGGAAGAAGTAACGCCCCCTCACGGGACCCCTGTACCGACAGACATT 334

Db 241 CGGAGCTGGGCTGGAAGAAGTAACGCCCCCTCACGGGACCCCTGTACCGACAGACATT 300

QY 335 GGCCTGCCCCAATCGCGCTACTCCATGGGGCTGGCTCTGATGCCGACATGGAGGCTGAC 394

Db 301 GGCCTGCCCCAATCGCGCTACTCCATGGGGCTGGCTCTGATGCCGACATGGAGGCTGAC 360

QY 395 ACGGTGCTGTCCCCTGAGCACCCCGTGCCTGTGTGGGCGCGAGCACACGGTCAGGGCGC 454

Db 361 ACGGTGCTGTCCCCTGAGCACCCCGTGCCTGTGTGGGCGCGAGCACACGGTCAGGGCGC 420

QY 455 AGCTCCTGCTGTCCAGCGGGCCCTGCAGAAACCACGCGCGGCTCCGAGCGCCGCGG 514

Db 421 AGCTCCTGCTGTCCAGCGGGCCCAATTCCAATCTCACACTCACCGACACCGAGCATGAA 480

QY 515 AACACTGAGACTGATCATCCGGGGCGGCTGCAGAAACCACGCGCGGCTCCGAGCGCCGCGG 574

Db 481 AACACTGAGACTGATCATCCGGGGCGGCTGCAGAAACCACGCGCGGCTCCGAGCGCCGCGG 540

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Db 541 CCGCCGCTCTCGCACGCCCCACACCCCCCAACAGGACACCGCGGCTCCCAATTAACCTCCCTG 600

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QY 695 TCCGGAGAGCCCCCTGCCGGCGCGCCAGGAGCCTGCCACGCCCCAGGAACTGGCTG 754

Db 661 TCCGGAGAGCCCCCTGCCGGCGCGCCAGGAGCCTGCCACGCCCCAGGAACTGGCTG 720

QY	755	CTCAACAGCAACATCCOCTGGAGACCAAGAACCTTAGGCAAGCAGCCATTCTTAGGGACA	814
Db	721	CTCAACAGCAACATCCOCTGGAGACCAAGAACCTTAGGCAAGCAGCCATTCTTAGGGACA	780
QY	815	TTGCAGGACAACCTCATTTGAGATGGACATTTCTCGGCGCTCCCGCCATGATGGGCTTAC	874
Db	781	TTGCAGGACAACCTCATTTGAGATGGACATTTCTCGGCGCTCCCGCCATGATGGGCTTAC	840
QY	875	AGTGACGGGCACCTTCCTTTCAAGCCTGGAGGCACCTCCCCGCTCTTCTGCACCACATCA	934
Db	841	AGTGACGGGCACCTTCCTTTCAAGCCTGGAGGCACCTCCCCGCTCTTCTGCACCACATCA	900
QY	935	CCAGGGTACCCACTGACGTCCAGCACAGTGTACTCTCTCCGCCCGACCCCTGCCCGCCG	994
Db	901	CCAGGGTACCCACTGACGTCCAGCACAGTGTACTCTCTCCGCCCGACCCCTGCCCGCCG	960
QY	995	AGCACCTTCGCCCGCGCGCCTTTAAACCTCAAGAACCCCTCCAAGTACTGTAACTGGAAG	1054
Db	961	AGCACCTTCGCCCGCGCGCCTTTAAACCTCAAGAACCCCTCCAAGTACTGTAACTGGAAG	1020
QY	1055	TGCGCAGCCCTGAGGSCATCGTCATCTCAGCCACTTGGTCATCTCTGCTGGCATACTTT	1114
Db	1021	TGCGCAGCCCTGAGGSCATCGTCATCTCAGCCACTTGGTCATCTCTGCTGGCATACTTT	1080
QY	1115	GTGGCCATGCACCTGTTGGCCTAAACTGGCACCTGCAGCCGATGGAGGGCAGATGTAT	1174
Db	1081	GTGGCCATGCACCTGTTGGCCTAAACTGGCACCTGCAGCCGATGGAGGGCAGATGTAT	1140
QY	1175	GAGATCACGGAGGACACAGCCAGCAGTTGGCCTGTGCGCAACCGACGTCCTCCCTATACCCC	1234
Db	1141	GAGATCACGGAGGACACAGCCAGCAGTTGGCCTGTGCGCAACCGACGTCCTCCCTATACCCC	1200
QY	1235	TCAGGGGGCACTGGCTTAGAGACCCCTGCACAGGAAGGCAAGGAACCAAGAGGAAAG	1294
Db	1201	TCAGGGGGCACTGGCTTAGAGACCCCTGCACAGGAAGGCAAGGAACCAAGAGGAAAG	1260
QY	1295	CCCAGTAGTTTCTTTCCAGAGGACAGTTTCAATGATTTCTGGAGAAATTGATGTGGGAAGG	1354
Db	1261	CCCAGTAGTTTCTTTCCAGAGGACAGTTTCAATGATTTCTGGAGAAATTGATGTGGGAAGG	1320
QY	1355	CGAGCCTCCCAGAAATTCCTCTCGGCACTTTCTGGAGATCTCAAGTGTTCATAGACCAT	1414
Db	1321	CGAGCCTCCCAGAAATTCCTCTCGGCACTTTCTGGAGATCTCAAGTGTTCATAGACCAT	1380
QY	1415	CCTGTGCATCTGAAATTCATGTGTCTCTGGGAAAGGCAGCCCTGGTTGGCATTTATGGC	1474
Db	1381	CCTGTGCATCTGAAATTCATGTGTCTCTGGGAAAGGCAGCCCTGGTTGGCATTTATGGC	1440
QY	1475	AGAAAGGCCTCCCTCCTTACATACACAGTTTGACTTTGTGGAGCTGCTGGATGGCAGG	1534
Db	1441	AGAAAGGCCTCCCTCCTTACATACACAGTTTGACTTTGTGGAGCTGCTGGATGGCAGG	1500
QY	1535	AGGCTCCTAACCCAGGAGGCGGAGCCTAGAGGGGACCCCGCCAGTCTCGGGGAACT	1594
Db	1501	AGGCTCCTAACCCAGGAGGCGGAGCCTAGAGGGGACCCCGCCAGTCTCGGGGAACT	1560
QY	1595	GTGCCCCCTCCAGCCATGAGACAGGCTTCATCCAGTATTTGGATTTCAGGAATCTGGCAC	1654
Db	1561	GTGCCCCCTCCAGCCATGAGACAGGCTTCATCCAGTATTTGGATTTCAGGAATCTGGCAC	1620
QY	1655	TTGGCTTTTACAAATGACGGAAAGGAGTCAGAAGTGGTTTCTTTCTCACCACTGCCATT	1714
Db	1621	TTGGCTTTTACAAATGACGGAAAGGAGTCAGAAGTGGTTTCTTTCTCACCACTGCCATT	1680

## RESULT 7

US-08-891-845-11  
; Sequence 11, Application US/08891845  
; Patent No. 6096873  
; GENERAL INFORMATION:  
; APPLICANT: Schaefer, Gabriele M.  
; APPLICANT: Sliwowski, Mark  
; TITLE OF INVENTION: Gamma-Herexulin

```

; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/891,845
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/021640
; FILING DATE: 07/12/96
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P1043
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2387 base pairs
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
;
US-08-891-845-11

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Query Match 14.2%; Score 1185.6; DB 3; Length 2387;  
Best Local Similarity 98.8%; Pred. No. 2.1e-279;  
Matches 1194; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY	530	CATCCGGGGCGCCTGCAGAAACACGCGCGCTCCGGACGCGCGCGCGCTCTTCGCAC	589
Db	1	CATCCGGGGCGCCTGCAGAAACACGCGCGCTCCGGACGCGCGCGCGCTCTTCGCAC	60
QY	590	GCCACACCCCCAACACGACACACGCGGCCTCCATTAACTCCCTGAACCGGGGCAACTTC	649
Db	61	GCCACACCCCCAACACGACACACGCGGCCTCCATTAACTCCCTGAACCGGGGCAACTTC	120
QY	650	ACGCCGAGGAGCAACCCACGACCCCGGCCCCCACGGACCACTCGCTCTCCGGAGAGCCCCCT	709
Db	121	ACGCCGAGGAGCAACCCACGACCCCGGCCCCCACGGACCACTCGCTCTCCGGAGAGCCCCCT	180
QY	710	GCCGGCGGGCCACGAGGCCTGCCACGCCACGGAGAACTGGCTGCTCAACAGCAACATC	769
Db	181	GCCGGCGGGCCACGAGGCCTGCCACGCCACGGAGAACTGGCTGCTCAACAGCAACATC	240
QY	770	CCCCTGGAGACCAGGAACCTAGGCAAGCAGCCATTCTTAGGACATTGCAGGACAACCTC	829
Db	241	CCCCTGGAGACCAGGAACCTAGGCAAGCAGCCATTCTTAGGACATTGCAGGACAACCTC	300
QY	830	ATTGAGATGGACATTCTCGGCGCCTCCCGCCATGATGGGCTTACAGTGACGGGCATTC	889
Db	301	ATTGAGATGGACATTCTCGGCGCCTCCCGCCATGATGGGCTTACAGTGACGGGCATTC	360
QY	890	CTCTTCAAGCCTGGAGGACCTCCCCGCTCTTCTGCACCACATCACCAGGGTACCCACTG	949
Db	361	CTCTTCAAGCCTGGAGGACCTCCCCGCTCTTCTGCACCACATCACCAGGGTACCCACTG	420
QY	950	ACGTCCAGCAGTGTACTCTCTCCGCCCCGACCCCTGCCCGCCGAGCACCTTCGCCCGG	1009
Db	421	ACGTCCAGCAGTGTACTCTCTCCGCCCCGACCCCTGCCCGCCGAGCACCTTCGCCCGG	480
QY	1010	CCGGCCTTTAACCTCAAGAAGCCCTCCAAGTACTGTAACTGGAAGTGCAGGCCCTGAGC	1069

Db 481 CCGGCTTTAACTCAAGAAGCCCTCCAAGTACTGTAAGTGGAAGTGGCAGCCCTGAGC 540  
QY 1070 GCCATCGTCATCTCAGCCACTCTGGTCATCCTGCTGGCATACTTTGTGGCCATGCACCTG 1129  
Db 541 GCCATCGTCATCTCAGCCACTCTGGTCATCCTGCTGGCATACTTTGTGGCCATGCACCTG 600  
QY 1130 TTTGGCCTAAACTGGCACCTGCAGCCGATGGAGGGGCAGATGTATGAGATCACGGAGGAC 1189  
Db 601 TTTGGCCTAAACTGGCACCTGCAGCCGATGGAGGGGCAGATGTATGAGATCACGGAGGAC 660  
QY 1190 ACAGCCAGCAGTTGGCCTGTGCCAACCGACGTCTCCCTATACCCCTCAGGGGGCACTGGC 1249  
Db 661 ACAGCCAGCAGTTGGCCTGTGCCAACCGACGTCTCCCTATACCCCTCAGGGGGCACTGGC 720  
QY 1250 TTAGAGACCCCTGCACAGGAAAGGCAAGAAACCAACAGAAAGGAAAGCCCAAGTTCCTTT 1309  
Db 721 TTAGAGACCCCTGCACAGGAAAGGCAAGAAACCAACAGAAAGGAAAGCCCAAGTTCCTTT 780  
QY 1310 CCAGAGGACAGTTTCATAGATTCTGGAGAAATTGATGTGGGAAGGGCGAGCTCCCGAGAAG 1369  
Db 781 CCAGAGGACAGTTTCATAGATTCTGGAGAAATTGATGTGGGAAGGGCGAGCTCCCGAGAAG 840  
QY 1370 ATTCTCTCTGGCATTCTCTGGAGATCTCAAGTTCATAGACCATCTCTGTGCATCTGAAA 1429  
Db 841 ATTCTCTCTGGCATTCTCTGGAGATCTCAAGTTCATAGACCATCTCTGTGCATCTGAAA 900  
QY 1430 TTCAATGTGTCTCTGGGAAAGGCAGCCCTGGTTGGCATTTATGGCAGAAAGGCCCTCCCT 1489  
Db 901 TTCAATGTGTCTCTGGGAAAGGCAGCCCTGGTTGGCATTTATGGCAGAAAGGCCCTCCCT 960  
QY 1490 CCTTCACATACACAGTTTGACTTTGTGGAGCTGTGGATGGCAGGAGCTCCTAAACCCAG 1549  
Db 961 CCTTCACATACACAGTTTGACTTTGTGGAGCTGTGGATGGCAGGAGCTCCTAAACCCAG 1020  
QY 1550 GAGGCGGGAGCCTAGAGGGGACCCCGCCAGTCTCGGGGAACCTGTGCCCCCTCCAGC 1609  
Db 1021 GAGGCGGGAGCCTAGAGGGGACCCCGCCAGTCTCGGGGAACCTGTGCCCCCTCCAGC 1080  
QY 1610 CATGAGACAGGCTTCATCCAGTATTTGGATTTCAGGAATCTGGCAGCTTGGCTTTTACAAT 1669  
Db 1081 CATGAGACAGGCTTCATCCAGTATTTGGATTTCAGGAATCTGGCAGCTTGGCTTTTACAAT 1140  
QY 1670 GACGGAAGGAGTCAAGATGGTTTCTTTCTCACACTGCCATTGAGTCGGTGGATAAC 1729  
Db 1141 GACGGAAGGAGTCAAGATGGTTTCTTTCTCACACTGCCATTGATTCAGTGGGTACA 1200  
QY 1730 TGCCCCAG 1737  
Db 1201 GGACAGAG 1208

RESULT 8  
US-09-514-573-11  
; Sequence 11, Application US/09514573  
; Patent No. 6500941  
; GENERAL INFORMATION:  
; APPLICANT: Schaefer, Gabriele M.  
; APPLICANT: Sliwowski, Mark  
; TITLE OF INVENTION: Gamma-Herregulin  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 460 Point San Bruno Blvd  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPatin (Genentech)

; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/514,573  
; FILING DATE: 28 FEB 2000  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/891845  
; FILING DATE: 10 JULY 1997  
; APPLICATION NUMBER: 60/021640  
; FILING DATE: 07/12/96  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Lee, Wendy M.  
; REGISTRATION NUMBER: 40,378  
; REFERENCE/DOCKET NUMBER: P1043  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415/225-1994  
; TELEFAX: 415/952-9881  
; TELEX: 910/371-7168  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2387 base pairs  
; TYPE: Nucleic Acid  
; STRANDEDNESS: Single  
; TOPOLOGY: Linear  
; US-09-514-573-11

Query Match 14.2%; Score 1185.6; DB 3; Length 2387;  
Best Local Similarity 98.8%; Pred. No. 2.le-279;  
Matches 1194; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 530 CATCCGGGGCGGCTGCAGAAACACGGCGGGCTCCGGACGCCGCCGCCGGCTCTCGCAC 589  
Db 1 CATCCGGGGCGGCTGCAGAAACACGGCGGGCTCCGGACGCCGCCGCCGGCTCTCGCAC 60  
QY 590 GCCCACACCCCAACACGACACCGGGCTCCATTAACTCCCTGAACCGGGGCAACTTC 649  
Db 61 GCCCACACCCCAACACGACACCGGGCTCCATTAACTCCCTGAACCGGGGCAACTTC 120  
QY 650 ACGCCGAGGAGCAACCCAGCCCGGCCACCGGAGAACTGGTGTCTCAACAGCAACATC 769  
Db 181 GCGGGCGGCCAGGAGCTGCCACCGCCAGGAGAACTGGTGTCTCAACAGCAACATC 240  
QY 770 CCCCTGGAGACCAGGAACCTAGGCAAGCAGCCATTCTAGGGACATTGCAGGACAACTC 829  
Db 241 CCCCTGGAGACCAGGAACCTAGGCAAGCAGCCATTCTAGGGACATTGCAGGACAACTC 300  
QY 830 ATTGAGATGGACATTCTCGGCGCTCCCGCATGATGGGGTTTACGTACGGGCACTTC 889  
Db 301 ATTGAGATGGACATTCTCGGCGCTCCCGCATGATGGGGTTTACGTACGGGCACTTC 360  
QY 890 CTCTTCAAGCCTGGAGGCACCTCCCGCTCTTCTGCACCACATCACCGGTACCCACTG 949  
Db 361 CTCTTCAAGCCTGGAGGCACCTCCCGCTCTTCTGCACCACATCACCGGTACCCACTG 420  
QY 950 ACGTCCAGCACAGTGTACTCTCTCCGCCCGACCCCTGCCCGCAGCACCTTCGCCCGG 1009  
Db 421 ACGTCCAGCACAGTGTACTCTCTCCGCCCGACCCCTGCCCGCAGCACCTTCGCCCGG 480  
QY 1010 CCGGCCTTTAACTCAAGAACCCCTCCAAGTACTGTAACTGGAAGTCCGAGCCCTGAGC 1069  
Db 481 CCGGCCTTTAACTCAAGAACCCCTCCAAGTACTGTAACTGGAAGTCCGAGCCCTGAGC 540  
QY 1070 GCCATCGTCATCTCAGCCACTCTGGTCTATCTGTGGCATACTTTGTGGCCATGCACCTG 1129  
Db 541 GCCATCGTCATCTCAGCCACTCTGGTCTATCTGTGCATCTCTGTGGCATACTTTGTGGCCATGCACCTG 600  
QY 1130 TTTGGCCTAAACTGGCACCTGCAGCCGATGGAGGGGCAGATGTATGAGATCACGGAGGAC 1189  
Db 601 TTTGGCCTAAACTGGCACCTGCAGCCGATGGAGGGGCAGATGTATGAGATCACGGAGGAC 660





Db 781 CCAGAGGACAGTTTTCATAGATTCTGGAGAAATTGATGTGGGAAGGCGAGCTTCCAGAAG 840

Qy 1370 ATTCTCTCGCACCTTCTTGAGATCTCAAGTGTTCATAGACCAATCCTGTGCATCTGAAA 1429

Db 841 ATTCTCTCGCACCTTCTTGAGATCTCAAGTGTTCATAGACCAATCCTGTGCATCTGAAA 900

Qy 1430 TTCAATGTGTCTCTGGGAAAGGCAGCCCTGGTTGGCATTTATGGCAGAAAAGGCCTCCCT 1489

Db 901 TTCAATGTGTCTCTGGGAAAGGCAGCCCTGGTTGGCATTTATGGCAGAAAAGGCCTCCCT 960

Qy 1490 CCTTCACATACACAGTTTGACTTTGTGGAGCTGCTGGATGGCAGGAGGCTCCTAACCCAG 1549

Db 961 CCTTCACATACACAGTTTGACTTTGTGGAGCTGCTGGATGGCAGGAGGCTCCTAACCCAG 1020

Qy 1550 GAGGCGGGAGCTTAGAGGGGACCCCGCCAGTCTCGGGGAACTGTGCCCCCTCCAGC 1609

Db 1021 GAGGCGGGAGCTTAGAGGGGACCCCGCCAGTCTCGGGGAACTGTGCCCCCTCCAGC 1080

Qy 1610 CATGAGACAGGCTTCATCCAGTATTGTGATTGAGGAACTTGGCACTTGGCTTTTACAAT 1669

Db 1081 CATGAGACAGGCTTCATCCAGTATTGTGATTGAGGAACTTGGCACTTGGCTTTTACAAT 1140

Qy 1670 GACGGAAGGAGTCAGAAAGTGTTTCTCTTCTCACCACCTGCCATTGATCGGTGGATAAC 1729

Db 1141 GACGGAAGGAGTCAGAAAGTGTTTCTCTTCTCACCACCTGCCATTGATCCAGTGGTACA 1200

Qy 1730 TGCCCCAG 1737

Db 1201 GGACAGAG 1208

RESULT 10

US-09-976-594-407/c

; Sequence 407, Application US/09976594

; Patent No. 6673549

; GENERAL INFORMATION:

; APPLICANT: Furness, Michael

; APPLICANT: Buchbinder, Jenny

; TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS

; FILE REFERENCE: PA-0041 US

; CURRENT APPLICATION NUMBER: US/09/976,594

; CURRENT FILING DATE: 2001-10-12

; PRIOR APPLICATION NUMBER: 60/240,409

; PRIOR FILING DATE: 2000-10-12

; NUMBER OF SEQ ID NOS: 1143

; SOFTWARE: PERL Program

; SEQ ID NO 407

; LENGTH: 2007

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc feature

; OTHER INFORMATION: Incyte ID No. 6673549 474200.1

US-09-976-594-407

Query Match 2.5%; Score 208.6; DB 3; Length 2007;

Best Local Similarity 72.7%; Pred. No. 1.7e-40;

Matches 296; Conservative 0; Mismatches 109; Indels 2; Gaps 2;

Qy 7941 GGGGGCGGGAACCCCTGGAGAAATGGGGTCAACGTCACTGTGTCCCAGATCAACACAGTAC 8000

Db 2007 GCGGCCGCAAGCGCTGGAGAACGGCATCAACGTGACGGTGTGCGAGTCCACCAAGGTGG 1948

Qy 8001 TTAATGGCAGGACTAGACGTACACAGACATCCAGTCCAGTACGGGGCACT-GTGCTTG 8059

Db 1947 TGATCGGCAGGACGCGCAGGTTGCGGGACGTGGAGATGCAGTTCGGCGCGCTGGCGCTGC 1888

Qy 8060 AACACACGCTACGGGACACGTTGGATG-AGGAGAAGGCACGGGTCTCTGGAGCTGGCCCCG 8118

Db 1887 CACGTGCGCTACGGCATGACCTTGGACGAAGGAGAAGCGCGCATCTCTGGAGCAGGCGCG 1828

Qy 8119 GCAGAGAGCCGTGCGCCAAAGCGTGGGCCCCGCGAGCAGAGACTGCGGGGAAGGGGAGGA 8178

Db 1827 GCAGCGCGGCTCGCCCCGGCCCTGGCGCGCGAGCAGCAGCGCGTGC CGCAGCGGAGGA 1768

Qy 8179 AGGCCTCGCGGCTTGACAGAGGGGAGAAAGCAGCAGAGTGTGAGCACAGGGCGGGTGCA 8238

Db 1767 GGGCGCGGCTCTGGACGGAGGGCGAGAAAGCGCAGCTGTGAGCGCGGCAAGGTGCA 1708

Qy 8239 AGGTACGACGGCTTTTTCGTGATCTCTGTGAGCAGTACCCAGAACTGTGAGACAGCGC 8298

Db 1707 GGGCTACGACGGGTACTACGTACTCTCGGTGGAGCAGTACCCCGAGCTGGCCGACAGCGC 1648

Qy 8299 CAACAACATCCACTTCATGAGACAGAGCGAGATGGGCCGAGGTGAC 8345

Db 1647 CAACAACATCCAGTTCTCTGCGGCAGAGCGAGATCGGCAGGAGGTAAC 1601

RESULT 11

US-09-949-016-3399

; Sequence 3399, Application US/09949016

; Patent No. 6812339

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; FILE REFERENCE: CL001307

; CURRENT APPLICATION NUMBER: US/09/949,016

; CURRENT FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60/241,755

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/237,768

; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: 60/231,498

; PRIOR FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 3399

; LENGTH: 6763

; TYPE: DNA

; ORGANISM: Human

US-09-949-016-3399

Query Match 1.3%; Score 109; DB 3; Length 6763;

Best Local Similarity 52.3%; Pred. No. 7.1e-16;

Matches 350; Conservative 0; Mismatches 295; Indels 24; Gaps 4;

Qy 1729 CTGCCCCAGCAACTGCTATGGCAATGGTGACTGTCATCTCTGGACCTTGCACACTGCTTCCT 1788

Db 411 CTGCCCAGATGACTGCAATGATCAGGGTCCGTGTGTCGGTGGTTCGTGCTTCCCTTCC 470

Qy 1789 GGGTTTCCTGGGCCCCGACTGTGGCAGAGCCTCCTGCCCCGTCCTCTGTAGCGGAAATGG 1848

Db 471 CGGCTACACTGGCCCCAGCTGTGGCTGGCCATCCTGTCCCGGGGACTGCCAAGCCGTGG 530

Qy 1849 CCAATACATGAAAGGCAGATGCTTGTGCCACAGTGGCTGGAAGGCGCTGAGTGCATGT 1908

Db 531 GCGCTGCGTGCAAGGCGGTGTGTGTGTGTCGGGCAGGCTTCTCAGGCCCGGACTGCAGCCA 590

Qy 1909 GCCCACCAACCAGTGTATCGATGTGGCCTGCGAGCAACCATATGGCACCTGCATCAGGGCAC 1968

Db 591 GCGCTCCTGCC-----CTCGAGGTTGCAGCCAGAGGGGACGCTGTGAGGGTGGGCG 641

Qy 1969 CTGCATCTGCAACCTGGCTACAAGGCGGAGAGCTGTGAGGAAAGTGGACTGCATGGACCC 2028

Db 642 CTGCGTGTGTGACCCAGGCTACACTGGTGACGACTGTGGCATGAGGAGCTGC-----CCT 696

Qy 2029 CACATGTTACGGCCGGGTGTCTCGGTGAGAGCGGAATGCCATTGCTTTGTGGGATGGGG 2088

Db 697 CGCGGTTGCAGTCAGAGGGGGCGCTGTGAGAATGGGC-----GCTGCGTGTGTAACCC 749

Qy 2089 AGGCACCAACTGCGAGACCCCCAGGGCCCATGCTTAGACCAGTGTTCAGGCCACGGAAC 2148

Db 750 CGGCTACACTGGCAGGAGCTGTGGGGTGAAGAGCTGCCCCCTCGGGGCTGCAGCCAGCGGG 809

Qy 2149 CTTCTCTCCCGACACCCGGGCTTTGACGCTGTGACCCCAAGCTGGACTGGACACGACTGTTC 2208

Db 810 ACGCTGCAAGGA---CGGGCGCTGCGTGTGTGACCCCGGCTACACTGGCGAGGACTGTGG 866  
QY 2209 TATCGAGATCTGTGCTGCCGACTGTGGTGGCCATGGCGTGTGCGTAGGGGGACACCTGCCG 2268  
Db 867 TACGGGAGTGCCTTGGGACTGTGGCGAGGGCGGCGTGTGCGTGGACGGCCGCTGCGT 926  
QY 2269 CTGCGAGGATGGCTGGATGGGGCAGCCTGCGACCAAGTGGAGTGCAGCCCTGGCTGCCACCCGCGCTGTGC 2328  
Db 927 GTGCTGCCCGGGTACACAGGCGAGGACTGCAGCACGCGGACATGTCCGAGGGACTGCCG 986  
QY 2329 CGAGCATGGGACCTGCCCGCAGCGCAAGTGCAGTGCAGCCCTGGCTGGAATGGCGAACA 2388  
Db 987 GGGCCGCGGCGCTGCGAGGACGGCGAATGCATTTCGACACGGGCTACAGCGGGGACGA 1046  
QY 2389 CTGCACCAT 2397  
Db 1047 CTGCGGCGT 1055

RESULT 12

US-09-620-312D-75  
; Sequence 75, Application US/09620312D  
; Patent No. 6569662  
; GENERAL INFORMATION:  
; APPLICANT: Tang, Y. Tom  
; APPLICANT: Liu, Chenghua  
; APPLICANT: Asundi, Vinod  
; APPLICANT: Zhang, Jie  
; APPLICANT: Ren, Feiyan  
; APPLICANT: Chen, Rui-hong  
; APPLICANT: Zhao, Qing A.  
; APPLICANT: Wehrman, Tom  
; APPLICANT: Xue, Aidong J.  
; APPLICANT: Yang, Yonghong  
; APPLICANT: Wang, Jian-Rui  
; APPLICANT: Zhou, Ping  
; APPLICANT: Ma, Yunqing  
; APPLICANT: Wang, Dunrui  
; APPLICANT: Wang, Zhiwei  
; APPLICANT: John Tillinghast  
; APPLICANT: Drmanac, Radoje T.  
; TITLE OF INVENTION: No. 6569662el Nucleic Acids and  
; FILE REFERENCE: 784CIP2B  
; CURRENT APPLICATION NUMBER: US/09/620,312D  
; CURRENT FILING DATE: 2000-07-19  
; PRIOR APPLICATION NUMBER: 09/552,317  
; PRIOR FILING DATE: 2000-04-25  
; PRIOR APPLICATION NUMBER: 09/488,725  
; PRIOR FILING DATE: 2000-01-21  
; NUMBER OF SEQ ID NOS: 1105  
; SOFTWARE: pt\_FL\_genes Version 1.0  
; SEQ ID NO 75  
; LENGTH: 13857  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(13857)

US-09-620-312D-75  
Query Match 1.3%; Score 109; DB 3; Length 13857;  
Best Local Similarity 52.3%; Pred. No. 1e-15;  
Matches 350; Conservative 0; Mismatches 295; Indels 24; Gaps 4;  
QY 1729 CTGCCCCAGCAACTGCTATGGCAATGGTGACTGCATCTCTGGGACCTGCCACTGCTTCCT 1788  
Db 555 CTGCCAGATGACTGCAATGATCAGGGTCGCTGTGTCGGTGGTCGTTGGCTGTGCTTCC 614  
QY 1789 GGGTTTCCTGGGCCCCGACTGTGGCAGAGCCTCCTGCCCCGTGCTCTGTAGCGGAATGG 1848  
Db 615 CGGCTACACTGGCCCCCAGCTGTGGCTGGCCATCCTGTCCGGGACTGCCAAGCCGTGG 674

QY 1849 CCAATACATGAAGGCAGATGCTTTGTGCCACAGTGGCTGGAAAGGCGCTGAGTGCATGT 1908  
Db 675 GCGTGCCTGACGGGCGTGTGTGTGTCGGGCAGGCTTCTCAGGCCCCGACTGCAGCCA 734  
QY 1909 GCCCACCAACCAAGTGTATCGATGTGGCTGTGCAGCAACCATGGCACCTGCATCACGGGCAC 1968  
Db 735 GCGCTCCTGCC-----CTCGAGGTTGCAGCCAGAGGGACGCTGTGAGGGTGGCG 785  
QY 1969 CTGCATCTGCAACCCCTGGCTACAAGGGCGAGAGCTGTGAGGAAGTGGACTGCATGGACCC 2028  
Db 786 CTGCGTGTGTGACCCAGGCTACACTGGTGACGACTGTGGCATGAGGAGCTGC-----CCT 840  
QY 2029 CACATGTTCAGGCGGGGTGTCTGCGTGAGAGGCGAATGCCATTGCTTTGTGGATGGG 2088  
Db 841 CGCGGTTGCAGTCAGAGGGGCGCTGTGAGAATGGGC-----GCTCGTGTGTAACCC 893  
QY 2089 AGGCACCAACTGCGAGACCCCCAGGGCCACATGCTTAGACCAGTGTTCAGGGCCACGGAAC 2148  
Db 894 CGGCTACACTGGCGAGGACTGTGGGGTGAGGAGCTGCCCTCGGGGCTGCAGCCAGCGGG 953  
QY 2149 CTTCTCCCGGACACCGGGCTTTGACGCTGTGACCCAAAGCTGGAGTGGACACGACTGTT 2208  
Db 954 ACGTGCAAAGGA---CGGGCGCTGCGTGTGTGACCCCGGCTACACTGGCAGGACTGTGG 1010  
QY 2209 TATCGAGATCTGTGCTGCCGACTGTGGTGGCCCATGGCGTGTGCGTAGGGGGCACCTGCCG 2268  
Db 1011 TACGCGGAGCTGCCCTTGGGACTGTGGCAGGGCGGCGCTGCGTGGACGGCCGCTGCGT 1070  
QY 2269 CTGCGAGGATGGCTGGATGGGGCAGCCTCGCACCCAGCGGCGCTGCCACCCCGCGTGTGC 2328  
Db 1071 GTGCTGGCCCGGTACACAGGCGAGGACTGCAGCACGCGGACATGTCCGAGGACTGCCG 1130  
QY 2329 CGAGCATGGGACCTGCCCGCAGCGGCAAGTCCGAGTGCAGCCCTGGCTGGAATGGCGAACA 2388  
Db 1131 GGGCCGCGGCGCTGCGAGGACGGCGAATGCATTTCGACACCGGGCTACAGCGGGGACGA 1190  
QY 2389 CTGCACCAT 2397  
Db 1191 CTGCGGCGT 1199

RESULT 13

US-09-949-016-15141  
; Sequence 15141, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 15141  
; LENGTH: 34534  
; TYPE: DNA  
; ORGANISM: Human  
; US-09-949-016-15141

Query Match 1.3%; Score 109; DB 3; Length 34534;  
Best Local Similarity 52.3%; Pred. No. 1.6e-15;  
Matches 350; Conservative 0; Mismatches 295; Indels 24; Gaps 4;  
QY 1729 CTGCCCCAGCAACTGCTATGGCAATGGTGACTGCATCTCTGGGACCTGCCACTGCTTCCT 1788



Db 2901 CTGCCAGATGACTGCAATGATCAGGGTCGTGTGTCCGTGGTGGTGTGCTTTC 2960  
QY 1789 GGGTTTCTGGCCCGGACTGTGGCAGAGCCTCTGCCCGTGTCTCTGAGCGAAATGG 1848  
Db 2961 CGGCTACACTGGCCCGGACTGTGGTGGCCATCCTGTCCCGGACTGCCAAGGCCGTGG 3020  
QY 1849 CCAATACATGAAGGCAGATGCTTGTGCCACAGTGGCTGGAAGCGCTGAGTGCATGT 1908  
Db 3021 GCGTCGCTGCAGGCGTGTGTGTGCCGSCAGGCTTCTCAGGCCCGACTGCAGCCA 3080  
QY 1909 GCCCACCAACCACTGTATCGATGTGGCCTGCAGCAACCATGGCACCTGCATCACGGGCAC 1968  
Db 3081 GCGCTCCTGCC-----CTCAGAGTTGCAGCCAGAGGGACGCTGTGAGGGTGGCG 3131  
QY 1969 CTGCATCTGCAACCCTGGCTACAAGGGCGAGAGCTGTGAGGAAGTGAAGTGCATGCATGCC 2028  
Db 3132 CTGCGTGTGTACCCAGGCTACACTGGTGACACTGTGGCATGAGGAGTGC-----CCT 3186  
QY 2029 CACATGTTCAGGCCGGGTGTCTGCGTGAGAGGCGAATGCCATTTGCTTTGTGGGATGGG 2088  
Db 3187 CGCGTTGCAGTCAGAGGGGCGCTGTGAGAAATGGGC-----GCTGCGTGTAAACCC 3239  
QY 2089 AGGCACCAACTCGAGACCCCCAGGGCCACATGCTTAGACCAGTGTTCAGGCCACGGAAC 2148  
Db 3240 CGGCTACACTGGCGAGGACTGTGGGTGAGGAGTGCCTCGGGCTGCAGCCAGCGGG 3299  
QY 2149 CTTCTCCGGACACCGGGCTTTGCAGCTGTGACCCAAAGCTGGACTGGACACGACTGTT 2208  
Db 3300 ACGTGCAAGGA---CGGCGCTGCGTGTGTGACCCCGGTACACTGGCGAGGACTGTGG 3356  
QY 2209 TATCGAGATCTGTGTCGCCGACTGTGGTGGCCATGGCGTGTGCTAGGGGCACCTGCCG 2268  
Db 3357 TACGCGAGCTGCCCTGGGACTGTGGCGAGGGCGGCGCTGCGTGGACGCGCTGCGT 3416  
QY 2269 CTGCGAGGATGGTGGATGGGGCAGCCTGCGACAGCGGCGCTGCCACCGCGCTGTGC 2328  
Db 3417 GTGCTGGCCCGGTACACAGCGGAGGACTGCAGCACGCGGACATGTCCGAGGACTGCCG 3476  
QY 2329 CGAGCATGGGACCTGCCCGACGGCAAGTGCAGTGCAGCCCTGGCTGGAATGGCGAACA 2388  
Db 3477 GGGCCGCGGCGCTGCAGGACGGCGAATGCATTTGCGACACGGGCTACAGCGGGGACGA 3536  
QY 2389 CTGCACCAT 2397  
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RESULT 14  
US-09-861-893-29  
; Sequence 29, Application US/09861893  
; Patent No. 6960434  
; GENERAL INFORMATION:  
; APPLICANT: Feinberg, Andrew  
; APPLICANT: Strichman-Almashanu, Liora  
; APPLICANT: Jiang, Shan  
; TITLE OF INVENTION: METHODS FOR ASSAYING GENE IMPRINTING AND METHYLATED CpG ISLANDS  
; FILE REFERENCE: 01107.00128  
; CURRENT APPLICATION NUMBER: US/09/861,893  
; CURRENT FILING DATE: 2001-05-22  
; PRIOR APPLICATION NUMBER: 60/206,158  
; PRIOR FILING DATE: 2000-05-22  
; PRIOR APPLICATION NUMBER: 60/206,161  
; PRIOR FILING DATE: 2000-05-22  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 29  
; LENGTH: 399  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-861-893-29

Query Match 1.2%; Score 96.4; DB 3; Length 399;

Best Local Similarity 56.0%; Pred. No. 2e-13;  
Matches 204; Conservative 0; Mismatches 156; Indels 4; Gaps 1;  
QY 7584 AGTCTATCCTCGGGGTACAGTGTGAAGTACAGAAGCAGCTCAAGSCCTTTGTACACCTTAG 7643  
Db 40 AGCCCATCTTCGGAGTCCAGCAGCAAGTGGCGCGGCAAGGCCCTTCTGTGCTGCGTGG 99  
QY 7644 AACGTTTGACCAGCTCTATGGCTCCACAATCACCCAGCTGCCAGAGGCTCCAAAGACCA 7703  
Db 100 GGAAGATGGCCGAGGTGCAGGTGAGC-----CGGCGCCGGGCCGCGCAGTCTCTGG 155  
QY 7704 AGAAGTTTGCATCCAGCGGCTCAGTCTTTGGCAAGGGGGTCAAGTTTGCCTTTGAAGGATG 7763  
Db 156 CTGTGTTCCGCCACGGTCAAGTCGCTGATCGGCAAGGGCGTCAATGCTGGCCCTCAGCCAGG 215  
QY 7764 GCCGAGTGACACAGACATCATAGTGTGGCCCAATGAGGATGGCGAAGGGTTGCTGCCA 7823  
Db 216 GCCGCGTGCAGACCAACGTCGCTCAACATCGCCAACGAGGACTGCATCAAGGTGGCGCGG 275  
QY 7824 TCTTGAACCATGCCCACTACCTAGAGAACCTGCACTTTACCATTGATGGGTGGATACCC 7883  
Db 276 TGCTCAACAACGCCCTTCTACCTGGAGAACCTGCACCTTACCATCGAGGGCAAGGACACGC 335  
QY 7884 ATTACTTTGTGAAACAGGACCTTCAGAAGGTGACCTGGCCCATCTTGGGCTCAGTGGGG 7943  
Db 336 ACTACTTCATCAAGACCACCAACGCCCGGAGAGCGACCTGGGCACGCTGCGGTTGACCAGCG 395  
QY 7944 GGCG 7947  
Db 396 GCCG 399

RESULT 15  
US-09-949-016-121669/c  
; Sequence 121669, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 121669  
; LENGTH: 601  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-121669

Query Match 1.1%; Score 93.2; DB 3; Length 601;  
Best Local Similarity 51.9%; Pred. No. 1.5e-12;  
Matches 321; Conservative 0; Mismatches 273; Indels 24; Gaps 4;  
QY 1775 TGCCACTGCTTCTCTGGGTTTCTTGGGCCCCGACTGTGGCAGAGCCTCTGCCCCGTGCTC 1834  
Db 600 TGCATTTGCGACACGGGCTACAGCGGGGACGACTGCGGCGTGCAGCTGCCCTGGCGAC 541  
QY 1835 TGTAGCGGAAATGGCCAAATACATGAAAGGCAGATGCTTGTGCCACAGTGGCTGGAAGGC 1894  
Db 540 TGCAACCAAGGGGCGCTGCGAGGACGCGCGCTGCTGTGCTGGCCGGGTACACTGGA 481  
QY 1895 GCTGAGTGGGATGTGCCCAACCAACAGTGTATCGATGTGGCTGCAGCAACCATGGCACC 1954  
Db 480 ACCGATTGGGCTCGCGGCGCTGCCACGC-----GACTGTAGAGGTCCGCGGCGC 430

QY	1955	TGCATACGGGCACCTGCATCTGCAACCTTGGCTACAAGGGCGAGAGCTGTGAGGAAAGTG	2014
Db	429	TGCGAGAACGGCGTGTGTGTTTGCAATGCGGGCTACAGCGCGAGGACTGCGGTGTGCGC	370
QY	2015	GACTGCATGGACCCACATGTTCAGGCCGGGGTGTCTGCTGAGAGGGCGAATGCCATTGC	2074
Db	369	AGCTGTCTGGGGAC---TGTCGTGGCCGGGGCCGCTGTGAGAGTGGCCGCTGCATGTGT	313
QY	2075	TTTGTGGATGGGAGGCACCACTGCGAGACCCCGAGGCCACATGCTTAGACCAAGTGT	2134
Db	312	TGGCCGGGGTACACAGGCCGGGACTGCGGCACGCGCG-----CCTGTCTGGCGACTGT	259
QY	2135	TCAGGCCACGGAACCTTCCTCCCGGACACCGGGCTTTGCAGCTGTGACCCCAAGCTGGACT	2194
Db	258	CGCGGGCGGGCGCTGCGTGGATGGCCGCTGCGTGTGCA-----ACCCGGGCTTCACC	205
QY	2195	GGACACGACTGTTCTATCGAGATCTGTGCTGCCGACTGTGGTGGCCCATGGCGTGTGCGTA	2254
Db	204	GGTGAGGACTGTGGAGCCGTGCTGTCCCAGGACTGCCGTGGGCACGGCCTTTGCGAG	145
QY	2255	GGGGGCACCTGCCGCTGCGAGGATGGCTGGATGGGGGCAAGCCTGCCACCGGGGCTGC	2314
Db	144	GATGGCGTGTGCGTGTGTGACGAGGCTACTCAGGGGAAGACTGCAGCACCGCGCAGCTGC	85
QY	2315	CACCCGCGCTGTGCCGAGCATGGGACCTGCCGCGACGGCAAGTGCAGTGCAGCCCTGGC	2374
Db	84	CCCGGGGCTGCCGAGGGCCGCGCCAGTGCCTAGATGSSCGGTGTGTGCGGAGACGGC	25
QY	2375	TGGAATGGCGAACACTGC	2392
Db	24	TACTCTGGCGAGGATTGC	7

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: December 9, 2005, 18:38:31 ; Search time 4392 Seconds  
(without alignments)  
12676.877 Million cell updates/sec

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Perfect score: 8354  
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Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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1: geneseqn1980s:\*  
2: geneseqn1990s:\*  
3: geneseqn2000s:\*  
4: geneseqn2001as:\*  
5: geneseqn2001bs:\*  
6: geneseqn2002as:\*  
7: geneseqn2002bs:\*  
8: geneseqn2003as:\*  
9: geneseqn2003bs:\*  
10: geneseqn2003cs:\*  
11: geneseqn2003ds:\*  
12: geneseqn2004as:\*  
13: geneseqn2004bs:\*  
14: geneseqn2005s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	8354	100.0	8354	6	ABS52100	AbS52100 Human TEN
2	8354	100.0	8354	10	ADF74829	AdF74829 Murine NO
3	8225	98.5	8645	6	ABS78652	AbS78652 Human CDN
4	7991.2	95.7	8355	10	ADF74841	AdF74841 Murine NO
5	7779.2	93.1	8438	6	ABN85378	AbN85378 Human NOV
6	3680.8	44.1	8624	12	ADQ20349	AdQ20349 Human sof
7	3621.6	43.4	8774	12	ADQ24356	AdQ24356 Human sof
8	3544.6	42.4	8964	12	ADH01384	AdH01384 Teneurin
9	3504.6	42.0	8645	6	ABQ82344	AbQ82344 Human NOV
10	3500.6	41.9	8645	12	ADH41968	AdH41968 Novel hum
11	3473.8	41.6	8204	12	ADH41972	AdH41972 Novel hum
12	3473.8	41.6	8657	12	ADH41990	AdH41990 Novel hum
13	3473.8	41.6	8657	12	ADH41932	AdH41932 Novel hum
14	3472.6	41.6	8675	6	ABQ82343	AbQ82343 Human NOV
15	3472.2	41.6	8636	12	ADH41998	AdH41998 Novel hum
16	3472.2	41.6	8657	12	ADH41992	AdH41992 Novel hum
17	3472.2	41.6	8657	12	ADH41994	AdH41994 Novel hum
18	3472.2	41.6	8657	12	ADH41996	AdH41996 Novel hum
19	3424.4	41.0	8473	6	ABQ82345	AbQ82345 Human NOV

20	3422	41.0	8473	12	ADH41948	AdH41948 Novel hum
21	3418.4	40.9	9852	12	ADH71219	AdH71219 Human gen
22	3399.8	40.7	8487	6	ABQ82346	AbQ82346 Human NOV
23	3398.8	40.7	8487	12	ADH41976	AdH41976 Novel hum
24	3385	40.5	9668	12	ADH71239	AdH71239 Human gen
25	3385	40.5	9756	12	ADH71249	AdH71249 Human gen
26	3385	40.5	9823	12	ADH71257	AdH71257 Human gen
27	3385	40.5	9823	12	ADH71245	AdH71245 Human gen
28	3385	40.5	9826	5	AAS14085	AaS14085 Human FCT
29	3385	40.5	9826	12	ADH71253	AdH71253 Human gen
30	3384.8	40.5	8797	12	ADJ75919	AdJ75919 Marker ge
31	3362.6	40.3	9826	10	ADB32023	AdB32023 Human FCT
32	3351.4	40.1	9729	5	AAS14089	AaS14089 Human FCT
33	3351.4	40.1	9729	10	ADB32028	AdB32028 Human FCT
34	3351.4	40.1	9729	12	ADH71251	AdH71251 Human gen
35	3335.6	39.9	6999	12	ADH71273	AdH71273 Human gen
36	3274.2	39.2	13202	4	AAK51828	AaK51828 Human pol
37	3258	39.0	8297	12	ADQ21281	AdQ21281 Human sof
38	3258	39.0	12879	6	ABK92230	AbK92230 Prostate
39	3258	39.0	12880	11	ADN39609	AdN39609 Cancer/an
40	3256.4	39.0	8297	13	ADU06138	Adu06138 Novel bro
41	3165	37.9	9695	8	ACC72052	Acc72052 BCU0205B
42	3158.4	37.8	8575	6	ADI16607	AdI16607 Human NOV
43	3158.4	37.8	8575	12	ADH71271	AdH71271 Human gen
44	3137.4	37.6	7781	12	ADQ19483	AdQ19483 Human sof
45	3068.6	36.7	9058	8	ACC72051	Acc72051 BCU0205A

ALIGNMENTS

RESULT 1  
ABS52100  
ID ABS52100 standard; DNA; 8354 BP.

AC ABS52100;

XX 05-NOV-2002 (first entry)

XX Human TEN-M4-like gene.

Human; NOVX; NOVX-associated disorder; cardiomyopathy; atherosclerosis; cell signal processing; metabolic pathway modulation; metabolic disorder; obesity; diabetes; infectious disease; neurodegenerative disorder; acne; Alzheimer's disease; Parkinson's disease; immune disorder; cancer; haematopoietic disorder; cirrhosis; pancreatitis; learning defect; memory defect; infertility; congenital heart defect; hair growth; pigmentation disorder; endocrine disorder; respiratory disease; health; gastro-intestinal disease; reproductive; neurological disease; bone marrow transplantation; endocrine disease; allergy; inflammation; nephrological disorder; urinary system disorder; age-related disorder; neuropsychiatric disorder; EGF-related protein; SCUBE1; TEN-M4; adipocyte complement-related Clq tumour necrosis factor; out at first; beta adrenergic receptor kinase; EphA6/ehk-2; glucose transporter; type 1a membrane sushi-containing domain; butyrophilin; type 1a membrane-sushi domain containing; SNP; gene; ds; single nucleotide polymorphism.

OS Homo sapiens.

Key	Location/Qualifiers
variation	replace(117,G)
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	/standard name= "Single nucleotide polymorphism (SNP)"
variation	replace(225,C)
	/*tag= b
	/standard name= "Single nucleotide polymorphism (SNP)"
variation	replace(260,A)
	/*tag= c
	/standard_name= "Single nucleotide polymorphism (SNP)"

WO200257453-A2.



PD 25-JUL-2002.  
XX 19-DEC-2001; 2001WO-US050331.  
PF  
XX  
PR 19-DEC-2000; 2000US-0256704P.  
PR 20-DEC-2000; 2000US-0257314P.  
PR 02-MAY-2001; 2001US-0288153P.  
PR 29-MAY-2001; 2001US-0294075P.  
PR 24-JUL-2001; 2001US-0307506P.  
PR 10-AUG-2001; 2001US-0311590P.  
PR 10-AUG-2001; 2001US-0311613P.  
PR 29-AUG-2001; 2001US-0315617P.  
PR 14-SEP-2001; 2001US-0322358P.  
XX  
PA (CURA-) CURAGEN CORP.  
XX  
PI Gangolli EA, Patturajan M, Vernet CAM, Malyankar UM, Kekuda R;  
PI Stone DJ, Anderson D, Shimkets RA, Burgess CE, Zerhusen BD, Liu X;  
PI Spytek KA, Casman SJ, Boldog FL, Smithson G, Li L, Ji W;  
XX  
DR WPI; 2002-590744/63.  
DR P-PSDB; ABG70388.  
XX  
PT Novel isolated NOVX polypeptide useful for treating cardiomyopathy,  
PT atherosclerosis, metabolic disorders, diabetes, obesity, infectious  
PT disease, anorexia, neurodegenerative disorders, Alzheimer's disease or  
PT cancer.  
XX  
PS Claim 8; Page 50-52; 318pp; English.  
XX  
CC The present invention relates to new NOVX polypeptides. The invention is  
CC useful for treating or preventing a NOVX-associated disorder such as  
CC cardiomyopathy or atherosclerosis, where the disorder is related to cell  
CC signal processing and metabolic pathway modulation in a subject,  
CC preferably human. The invention is also useful for treating metabolic  
CC disorders (e.g. obesity), diabetes, infectious disease, neurodegenerative  
CC disorders (e.g. Alzheimer's disease, Parkinson's disease), immune  
CC disorders, haematopoietic disorders and various cancers. The molecules of  
CC the invention are also useful for treating or preventing cirrhosis,  
CC pancreatitis, learning and memory defects, infertility, congenital heart  
CC defects, acne, hair growth, pigmentation disorders, endocrine disorders,  
CC respiratory disease, gastro-intestinal diseases, reproductive, health,  
CC neurological diseases, bone marrow transplantation, endocrine diseases,  
CC allergy and inflammation, nephrological disorders, urinary system  
CC disorders, neuropsychiatric disorders and age-related disorders. The  
CC present nucleic acid sequence represents a NOVX gene. This sequence  
CC encodes a NOVX protein of the invention  
XX  
SQ Sequence 8354 BP; 1968 A; 2437 C; 2271 G; 1678 T; 0 U; 0 Other;  
Query Match 100.0%; Score 8354; DB 6; Length 8354;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 8354; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GTTTGTGGATGTGGAGAGCGCGGGCCGGAGGCCATGGACGTGAAGGAGAGAGCCCTTA 60  
Db |||||  
1 GTTTGTGGATGTGGAGAGCGCGGGCCGGAGGCCATGGACGTGAAGGAGAGAGCCCTTA 60  
Qy 61 CCGTCTCGTACCCGGCGCGGACGCCGAGCGCGCTACACAGCTCGTCCGGGACAG 120  
Db |||||  
61 CCGTCTCGTACCCGGCGCGGACGCCGAGCGCGCTACACAGCTCGTCCGGGACAG 120  
Qy 121 CGAGGAGGGCAAGCCCGCAGAAATCGTACAGCTCCAGCGAGACCCCTGAAGSCTTACGA 180  
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121 CGAGGAGGGCAAGCCCGCAGAAATCGTACAGCTCCAGCGAGACCCCTGAAGSCTTACGA 180  
Qy 181 CCAGGACGCCCGCTAGCCCTATGGCAGCCGCGTCAAGGACATTGTGCCGAGAGGCCCGA 240  
Db |||||  
181 CCAGGACGCCCGCTAGCCCTATGGCAGCCGCGTCAAGGACATTGTGCCGAGAGGCCCGA 240  
Qy 241 GGAATTCTGCCGCACAGGTGCCAACTTCACCCCTGCCGGAGCTGGGGCTGGAAGAAGTAAC 300  
Db |||||  
241 GGAATTCTGCCGCACAGGTGCCAACTTCACCCCTGCCGGAGCTGGGGCTGGAAGAAGTAAC 300

Qy 301 GCCCCCTCACGGGACCCCTGTATCCGGACAGACATTGGCCCTGCCCCCAATGCGGCTACTCCAT 360  
Db |||||  
301 GCCCCCTCACGGGACCCCTGTATCCGGACAGACATTGGCCCTGCCCCCAATGCGGCTACTCCAT 360  
Qy 361 GGGGGCTGGCTCTGATGCCGACATGGAGGTGACACGGTGTGTCCCTGAGCACCCCGT 420  
Db |||||  
361 GGGGGCTGGCTCTGATGCCGACATGGAGGTGACACGGTGTGTCCCTGAGCACCCCGT 420  
Qy 421 GCGTCTGTGGGCGGAGCACACCGTCAAGGCGCAGCTCTGCTGTCAGCGGGCCAA 480  
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421 GCGTCTGTGGGCGGAGCACACCGTCAAGGCGCAGCTCTGCTGTCAGCGGGCCAA 480  
Qy 481 TTCCAATCTCACTCACCGACACCCGAGCATGAAAACACTGAGACTGATCATCCGGGCGG 540  
Db |||||  
481 TTCCAATCTCACTCACCGACACCCGAGCATGAAAACACTGAGACTGATCATCCGGGCGG 540  
Qy 541 CCTGCAGAACCAACGCGGGCTCCGGACGCCGCGCGCGCTCTCGGAGAGCCCCCTGCGGCGGC 600  
Db |||||  
541 CCTGCAGAACCAACGCGGGCTCCGGACGCCGCGCGCGCTCTCGGAGAGCCCCCTGCGGCGGC 600  
Qy 601 CAACCCAGCACCGCGGCTCCATTAACTCCCTGAAACCGGGGCAACTTACGCGCGAGGAG 660  
Db |||||  
601 CAACCCAGCACCGCGGCTCCATTAACTCCCTGAAACCGGGGCAACTTACGCGCGAGGAG 660  
Qy 661 CAACCCAGCCCCCGCCCCACGGACCACTCGCTCTCCGGAGAGCCCCCTGCGGCGGC 720  
Db |||||  
661 CAACCCAGCCCCCGCCCCACGGACCACTCGCTCTCCGGAGAGCCCCCTGCGGCGGC 720  
Qy 721 CCAGGAGCCTGCCACACGCCCGAGGAACTGGCTGCTCAACAGCAACATCCCCCTGGAGAC 780  
Db |||||  
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Db |||||  
781 CAGGAACCTAGSCAAGCAGCCATTCTCTAGSGACATTGCAGGACAACCTCATTTGAGATGGA 840  
Qy 841 CATTCTCGGCGCTCCCGCCATGTATGGGCTTACAGTGACGGGCATTTCTCTTCAAGCC 900  
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901 TGGAGGCACCTCCCGCTCTTCTGCACCAATCACCAGGTACCACTGACGTCCAGCAC 960  
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Qy 1141 CTGGCACCTGCAGCCGATGGAGGGGAGATGTATGAGATCACGGAGGACACAGCCAGCAG 1200  
Db |||||  
1141 CTGGCACCTGCAGCCGATGGAGGGGAGATGTATGAGATCACGGAGGACACAGCCAGCAG 1200  
Qy 1201 TTGGCCTGTGCCAACCGACGTCTCCCTATACCCCTCAGGGGGCATGGCTTAGAGACCCC 1260  
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1201 TTGGCCTGTGCCAACCGACGTCTCCCTATACCCCTCAGGGGGCATGGCTTAGAGACCCC 1260  
Qy 1261 TGACAGGAAAGGCAAGGAACCCACAGAAGAAAGCCAGTAGTTTCTTCCAGAGGACAG 1320  
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1261 TGACAGGAAAGGCAAGGAACCCACAGAAGAAAGCCAGTAGTTTCTTCCAGAGGACAG 1320  
Qy 1321 TTTCATAGATTCTGGAGAAATTGATGTGGGAAGGCGAGCCTCCCAGAAAGATTCTCTCTGG 1380  
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1321 TTTCATAGATTCTGGAGAAATTGATGTGGGAAGGCGAGCCTCCCAGAAAGATTCTCTCTGG 1380

QY 1381 CACTTCTGGAGATCTCAAGTGTTTCATAGACCATCCTGTGCATCTGAAATTCAAATGTGTC 1440  
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1381 CACTTCTGGAGATCTCAAGTGTTTCATAGACCATCCTGTGCATCTGAAATTCAAATGTGTC 1440  
QY 1441 TCTGGAAAGGCAGCCCTGGTTGGCATTTATGSCAGAAAAAGGCCCTCCCTCTTCACATAC 1500  
Db |||||  
1441 TCTGGAAAGGCAGCCCTGGTTGGCATTTATGSCAGAAAAAGGCCCTCCCTCTTCACATAC 1500  
QY 1501 ACAGTTTGACTTTGTGGAGCTGCTGGATGSCAGGAGGCTCCTAAACCCAGGAGGCGGGAG 1560  
Db |||||  
1501 ACAGTTTGACTTTGTGGAGCTGCTGGATGGCAGGAGGCTCCTAAACCCAGGAGGCGGGAG 1560  
QY 1561 CCTAGAGGGGACCCCGCGCCAGTCTCGGGGAACTGTGCCCCCTCCAGGCCATGAGACAGG 1620  
Db |||||  
1561 CCTAGAGGGGACCCCGCGCCAGTCTCGGGGAACTGTGCCCCCTCCAGGCCATGAGACAGG 1620  
QY 1621 CTTCATCCAGTATTTGGATTGAGGAATCTGGCACTTGGCTTTTACAAATGACGGAAAGGA 1680  
Db |||||  
1621 CTTCATCCAGTATTTGGATTGAGGAATCTGGCACTTGGCTTTTACAAATGACGGAAAGGA 1680  
QY 1681 GTCAGAAGTGTTTCTCTTCTCACCACTGCCATFGAGTCGGTGGATAACTGCCCCAGCAA 1740  
Db |||||  
1681 GTCAGAAGTGTTTCTCTTCTCACCACTGCCATFGAGTCGGTGGATAACTGCCCCAGCAA 1740  
QY 1741 CTGCTATGGCAATGGTGACTGCATCTCTGGGACCTGCCACTGCTTCTTGGGTTTCTCTGGG 1800  
Db |||||  
1741 CTGCTATGGCAATGGTGACTGCATCTCTGGGACCTGCCACTGCTTCTTGGGTTTCTCTGGG 1800  
QY 1801 CCCCAGACTGTGGCAGAGCCCTCCTGCCCCGCTGCTGTAGCGGAAATGGSCAAATACATGAA 1860  
Db |||||  
1801 CCCCAGACTGTGGCAGAGCCCTCCTGCCCCGCTGCTGTAGCGGAAATGGSCAAATACATGAA 1860  
QY 1861 AGGCAGATGCTTGTGCCACAGTGGCTGGAAAGCGCTGAGTCGATGTGCCACCAACCA 1920  
Db |||||  
1861 AGGCAGATGCTTGTGCCACAGTGGCTGGAAAGCGCTGAGTCGATGTGCCACCAACCA 1920  
QY 1921 GTGTATCGATGTGGCCTGCAGCAACCATGGCACCTGCATCACGGGCACCTGCATCTGCAA 1980  
Db |||||  
1921 GTGTATCGATGTGGCCTGCAGCAACCATGGCACCTGCATCACGGGCACCTGCATCTGCAA 1980  
QY 1981 CCCTGGCTACAAGSGCGAGAGCTGTGAGGAAGTGGACTGCATGGACCCCAACATGTTTCAGG 2040  
Db |||||  
1981 CCCTGGCTACAAGSGCGAGAGCTGTGAGGAAGTGGACTGCATGGACCCCAACATGTTTCAGG 2040  
QY 2041 CCGGGGTGCTCGCTGAGAGCGGAATGCCATTGCTTTGTGGATGGGGAGSCACCAACTG 2100  
Db |||||  
2041 CCGGGGTGCTCGCTGAGAGCGGAATGCCATTGCTTTGTGGATGGGGAGSCACCAACTG 2100  
QY 2101 CGAGACCCCGAGGGCCACATGCTTAGACCAAGTGTTCAGGCCACGGAACTTCTCCCGGA 2160  
Db |||||  
2101 CGAGACCCCGAGGGCCACATGCTTAGACCAAGTGTTCAGGCCACGGAACTTCTCCCGGA 2160  
QY 2161 CACCGGGCTTTGCAGCTGTGACCCCAAGCTGGACTGGACACGACTGTTCTATCGAGATCTG 2220  
Db |||||  
2161 CACCGGGCTTTGCAGCTGTGACCCCAAGCTGGACTGGACACGACTGTTCTATCGAGATCTG 2220  
QY 2221 TGCTGCCGACTGTGGTGGCCATGGCGTGTGCGTAGSGGGCACCTGCCGCTGCAGGATGG 2280  
Db |||||  
2221 TGCTGCCGACTGTGGTGGCCATGGCGTGTGCGTAGSGGGCACCTGCCGCTGCAGGATGG 2280  
QY 2281 CTGGATGGGGGACGCTCGACACGCGGGCCTGCCACCCGCGCTGTGCCGAGCATGGGAC 2340  
Db |||||  
2281 CTGGATGGGGGACGCTCGACACGCGGGCCTGCCACCCGCGCTGTGCCGAGCATGGGAC 2340  
QY 2341 CTGCCCGCAGCGGCAAGTGCAGTGCAGCCCTGGCTGGAAATGGCGAAACACTGCACCATCGC 2400  
Db |||||  
2341 CTGCCCGCAGCGGCAAGTGCAGTGCAGCCCTGGCTTGGAAATGGCGAAACACTGCACCATCGC 2400  
QY 2401 TCACTATCTGGATAGGGTAGTTAAAGAGGGTTGCCCTGGGTTGTGCAATGGCAACGGCAG 2460  
Db |||||  
2401 TCACTATCTGGATAGGGTAGTTAAAGAGGGTTGCCCTGGGTTGTGCAATGGCAACGGCAG 2460  
QY 2461 ATGTACCTTAGACCTGAATGGTTGGCACTGCGTCTGCCAGCTGGGCTGGAGAGGAGCTGG 2520

Db 2461 ATGTACCTTAGACCTGAATGGTTGGCACTGCGTCTGCCAGCTGGCTGGAGAGGAGCTGG 2520  
QY 2521 CTGTGACACTTCCATGGAGACTGCCCTGGGTTGACAGCAAAAGACAAATGATGGAGATGGCCT 2580  
Db |||||  
2521 CTGTGACACTTCCATGGAGACTGCCCTGGGTTGACAGCAAAAGACAAATGATGGAGATGGCCT 2580  
QY 2581 GGTGGACTGCATGGACCCCTGACTGCTGCCTCCAGCCCCCTGTGCCATATCAACCCGCTGTG 2640  
Db |||||  
2581 GGTGGACTGCATGGACCCCTGACTGCTGCCTCCAGCCCCCTGTGCCATATCAACCCGCTGTG 2640  
QY 2641 CCTTGGCTCCCCTAACCCCTCTGGACATCATCCAGGAGACACAGGTCCTGTGTACAGCA 2700  
Db |||||  
2641 CCTTGGCTCCCCTAACCCCTCTGGACATCATCCAGGAGACACAGGTCCTGTGTACAGCA 2700  
QY 2701 GAACCTACACTCCTTCTATGACCGCATCAAGTTCTCTGTGGCAGGACACGCACAT 2760  
Db |||||  
2701 GAACCTACACTCCTTCTATGACCGCATCAAGTTCTCTGTGGCAGGACACGCACAT 2760  
QY 2761 AATCCCCGGGAGAAACCCCTTTGATGGAGGGCATGCTTGTGTTATTCTGTGCCAAAGTGAT 2820  
Db |||||  
2761 AATCCCCGGGAGAAACCCCTTTGATGGAGGGCATGCTTGTGTTATTCTGTGCCAAAGTGAT 2820  
QY 2821 GACATCAGATGGAAACCCCTGGTTGGTGTGAACATCAGTTTTGTCAATAAACCCCTCTCTT 2880  
Db |||||  
2821 GACATCAGATGGAAACCCCTGGTTGGTGTGAACATCAGTTTTGTCAATAAACCCCTCTCTT 2880  
QY 2881 TGGATATACAAATCAGCAGGCAAGATGGCAGCTTTGACTTGGTGACAAATGGCGGCATCTC 2940  
Db |||||  
2881 TGGATATACAAATCAGCAGGCAAGATGGCAGCTTTGACTTGGTGACAAATGGCGGCATCTC 2940  
QY 2941 CATCATCTGCGGTTTCGAGCGGGCACCTTTTCATCACACAGGAGCACACCTGTGGCTGCC 3000  
Db |||||  
2941 CATCATCTGCGGTTTCGAGCGGGCACCTTTTCATCACACAGGAGCACACCTGTGGCTGCC 3000  
QY 3001 ATGGGATCGCTTCTTGTTCATGGAAACCATCATCATGAGACATGAGGAGAAATGAGATTCC 3060  
Db |||||  
3001 ATGGGATCGCTTCTTGTTCATGGAAACCATCATCATGAGACATGAGGAGAAATGAGATTCC 3060  
QY 3061 CAGCTGTGACCTGAGCAATTTTGCCCGCCCCAACCCAGTCGTCCTCCATCCCCACTGAC 3120  
Db |||||  
3061 CAGCTGTGACCTGAGCAATTTTGCCCGCCCCAACCCAGTCGTCCTCCATCCCCACTGAC 3120  
QY 3121 GTCCTTCGCCAGCTCCTGTGCAGAGAAAGGCCCCCATTTGTGCCGGAATTCAGGCTTTGCA 3180  
Db |||||  
3121 GTCCTTCGCCAGCTCCTGTGCAGAGAAAGGCCCCCATTTGTGCCGGAATTCAGGCTTTGCA 3180  
QY 3181 GGAGGAAATCTCTATCTCTGGCTGCAAGATGAGGCTGAGCTACCTGAGCAGCCGGACCCC 3240  
Db |||||  
3181 GGAGGAAATCTCTATCTCTGGCTGCAAGATGAGGCTGAGCTACCTGAGCAGCCGGACCCC 3240  
QY 3241 TGGCTACAAATCTGTCTGAGGATCAGCCTCACCCACCCAGCCATCCCTTCAACCTCAT 3300  
Db |||||  
3241 TGGCTACAAATCTGTCTGAGGATCAGCCTCACCCACCCAGCCATCCCTTCAACCTCAT 3300  
QY 3301 GAAGGTGCACCTCATGGTAGCGGTGGAGGGCGCGCTCTTCAGGAAGTGGTTTCGCTGCAGC 3360  
Db |||||  
3301 GAAGGTGCACCTCATGGTAGCGGTGGAGGGCGCGCTCTTCAGGAAGTGGTTTCGCTGCAGC 3360  
QY 3361 CCCAGACCTGTCTTATTATTTTCATTTGGGACAAAGACAGACGCTCTACAAACCAAGAGGTGTT 3420  
Db |||||  
3361 CCCAGACCTGTCTTATTATTTTCATTTGGGACAAAGACAGACGCTCTACAAACCAAGAGGTGTT 3420  
QY 3421 TGGGCTTTCAGAAAGCCTTGTTCCTGGGTTATGAAATATGAATCTCTGCCCCAGATCTAAT 3480  
Db |||||  
3421 TGGGCTTTCAGAAAGCCTTGTTCCTGGGTTATGAAATATGAATCTCTGCCCCAGATCTAAT 3480  
QY 3481 CCTGTGGGAAAAAAGAACAAACAGTGTGCAGGCTATGAAATTGACGCGTCAAGCTTGG 3540  
Db |||||  
3481 CCTGTGGGAAAAAAGAACAAACAGTGTGCAGGCTATGAAATTGACGCGTCAAGCTTGG 3540  
QY 3541 AGGATGGAGCCCTAGACAAACATCATGCCCTCAACATTCAAAGTGGTATCCTGCACAAAGG 3600  
Db |||||



Db 3541 AGGATGGAGCCTAGACAAACATCATGCCCCTCAACATTCAAAGTGGTATCCTGCACAAAGG 3600

Qy 3601 GAATGGGGAGAACCAAGTTTGTGTCTCAGCAGCCTCCTGTCAATTGGGAGCATCATGGGCAA 3660

Db 3601 GAATGGGGAGAACCAAGTTTGTGTCTCAGCAGCCTCCTGTCAATTGGGAGCATCATGGGCAA 3660

Qy 3661 TGGGCGCGGAGAGCATCTCCTGCCCCAGCTGCAACGSCCTTGCTGACGGCAACAAGCT 3720

Db 3661 TGGGCGCGGAGAGCATCTCCTGCCCCAGCTGCAACGSCCTTGCTGACGGCAACAAGCT 3720

Qy 3721 CCTGSCCCCAAGTGGCCCTCACCTGTGGCTCTGACGGGAGCCTCTATGTGGGTGATTTCAA 3780

Db 3721 CCTGSCCCCAAGTGGCCCTCACCTGTGGCTCTGACGGGAGCCTCTATGTGGGTGATTTCAA 3780

Qy 3781 CTACATTAGAAGGATCTTCCCTCTGGAAATGTCAACCAACATCCTAGAGCTGAGGAATAA 3840

Db 3781 CTACATTAGAAGGATCTTCCCTCTGGAAATGTCAACCAACATCCTAGAGCTGAGGAATAA 3840

Qy 3841 AGATTTCAGACATAGTCACAGTCCAGCACACAAAATCTACCTGGCCACAGACCCCATGAG 3900

Db 3841 AGATTTCAGACATAGTCACAGTCCAGCACACAAAATCTACCTGGCCACAGACCCCATGAG 3900

Qy 3901 TGGGCGCGTCTTCCCTTCTGACAGCAACAGCCGCGGGTCTTTAAATCAAGTCCACTGT 3960

Db 3901 TGGGCGCGTCTTCCCTTCTGACAGCAACAGCCGCGGGTCTTTAAATCAAGTCCACTGT 3960

Qy 3961 GGTGTTGAAGGACCTTGTCAAGAACTCTGAGGTGGTTGCGGGACAGGTGACCACTGCCT 4020

Db 3961 GGTGTTGAAGGACCTTGTCAAGAACTCTGAGGTGGTTGCGGGACAGGTGACCACTGCCT 4020

Qy 4021 CCCCTTTGATGACACTCGCTGCGGGGATGGTGGGAAGGCCACAGAAGCCACACTCACCAA 4080

Db 4021 CCCCTTTGATGACACTCGCTGCGGGGATGGTGGGAAGGCCACAGAAGCCACACTCACCAA 4080

Qy 4081 TCCAGGGGTATTACAGTGGACAAAGTTTGGGCTGATCTACTTCTGATGGCACCATGAT 4140

Db 4081 TCCAGGGGTATTACAGTGGACAAAGTTTGGGCTGATCTACTTCTGATGGCACCATGAT 4140

Qy 4141 CAGACGCATCGATCAGAATGGGATCATCTCCACCCTGCTCGGCTCTAATGATCTCACATC 4200

Db 4141 CAGACGCATCGATCAGAATGGGATCATCTCCACCCTGCTCGGCTCTAATGATCTCACATC 4200

Qy 4201 AGCCCGGCCACTCAGCTGTGATTTCTGTCATGGATATTTCCAGGTAAGACTGGAGTGGCC 4260

Db 4201 AGCCCGGCCACTCAGCTGTGATTTCTGTCATGGATATTTCCAGGTAAGACTGGAGTGGCC 4260

Qy 4261 CACAGACTTAGCCATCAACCCCAATGGACAACTCACTTTATGTCTCTCGACAACAATGTGGT 4320

Db 4261 CACAGACTTAGCCATCAACCCCAATGGACAACTCACTTTATGTCTCTCGACAACAATGTGGT 4320

Qy 4321 CCTGCAAAATCTCTGAAAACCAACAGGTGCGCATTTGTGCGGGAGGCCCATGCACTGCCA 4380

Db 4321 CCTGCAAAATCTCTGAAAACCAACAGGTGCGCATTTGTGCGGGAGGCCCATGCACTGCCA 4380

Qy 4381 GGTCCCTGGCATTGACCACTTCCTGCTAAGCAAGTGGCCATCCACGCAACCCCTGGAGTC 4440

Db 4381 GGTCCCTGGCATTGACCACTTCCTGCTAAGCAAGTGGCCATCCACGCAACCCCTGGAGTC 4440

Qy 4441 AGCCACCGCTTTGGCTGTTTACACAAATGGGGTCCCTGATATTTGCTGAGACTGATGAGAA 4500

Db 4441 AGCCACCGCTTTGGCTGTTTACACAAATGGGGTCCCTGATATTTGCTGAGACTGATGAGAA 4500

Qy 4501 AAAGATCAACCGCATCAGGCAAGTCAACCACTAGTGGAGAGATCTCACTCGTTGCTGGGGC 4560

Db 4501 AAAGATCAACCGCATCAGGCAAGTCAACCACTAGTGGAGAGATCTCACTCGTTGCTGGGGC 4560

Qy 4561 CCCAGTGGCTGTGACTGTAAAATGATGCCAACTGTGATTTTTTCTGGAGACGATGG 4620

Db 4561 CCCAGTGGCTGTGACTGTAAAATGATGCCAACTGTGATTTTTTCTGGAGACGATGG 4620

Qy 4621 TTATGCCAAGGATGCAAAGTTAAATACCCCATCTTCTTGGCTGTGTGTGATGGGGA 4680

Db 4621 TTATGCCAAGGATGCAAAGTTAAATACCCCATCTTCTTGGCTGTGTGTGATGGGGA 4680

Qy 4681 GCTCTACGTGSCCGACCTTGGGAACATCCGAATTCGGTTTATCCGGAAGAACAGCCTTT 4740

Db 4681 GCTCTACGTGSCCGACCTTGGGAACATCCGAATTCGGTTTATCCGGAAGAACAGCCTTT 4740

Qy 4741 CCTCAACACCCAGAAACATGTATGAGCTGTCTTCCACCAATTGACCCAGGAGCTCTATCTGTT 4800

Db 4741 CCTCAACACCCAGAAACATGTATGAGCTGTCTTCCACCAATTGACCCAGGAGCTCTATCTGTT 4800

Qy 4801 TGATACCACCGGCAAGCACCTGTATACACCCAAAGCCTGCCACAGGAGACTACCTGTACAA 4860

Db 4801 TGATACCACCGGCAAGCACCTGTATACACCCAAAGCCTGCCACAGGAGACTACCTGTACAA 4860

Qy 4861 CTTACCTTACCTGSGGACGGGACATCACTCATCACAGACAAATGCGAACATGGT 4920

Db 4861 CTTACCTTACCTGSGGACGGGACATCACTCATCACAGACAAATGCGAACATGGT 4920

Qy 4921 AAATGTCCGCGAGACTCTACTGGGATGCCCTCTGGTGGTCCCAGATGGCCAGGT 4980

Db 4921 AAATGTCCGCGAGACTCTACTGGGATGCCCTCTGGTGGTCCCAGATGGCCAGGT 4980

Qy 4981 GTACTGGGTGACCATGGGCACCAACAGTGCACCTCAAGAGTGTGACCACACAAGGACACGA 5040

Db 4981 GTACTGGGTGACCATGGGCACCAACAGTGCACCTCAAGAGTGTGACCACACAAGGACACGA 5040

Qy 5041 GTTGGCCATGATGACATACCATGGCAATTCGGCCCTTCTGGCAACCAAAAGCAATGAAAA 5100

Db 5041 GTTGGCCATGATGACATACCATGGCAATTCGGCCCTTCTGGCAACCAAAAGCAATGAAAA 5100

Qy 5101 CGGATGGACAAATTTATGAGTACGACAGCTTTGGCCGCTTGACAAAATGTGACCTTCCC 5160

Db 5101 CGGATGGACAAATTTATGAGTACGACAGCTTTGGCCGCTTGACAAAATGTGACCTTCCC 5160

Qy 5161 TACTGGCCAGGTGAGCAGTTTCCGAAGTGATACAGACAGTTTCAAGTGATGTCAGGTTAGA 5220

Db 5161 TACTGGCCAGGTGAGCAGTTTCCGAAGTGATACAGACAGTTTCAAGTGATGTCAGGTTAGA 5220

Qy 5221 GACCTCCAGCAAGGATGATGTCAACCAACCAACCTGTCTGCCCTCAGGCGCTTCTA 5280

Db 5221 GACCTCCAGCAAGGATGATGTCAACCAACCAACCTGTCTGCCCTCAGGCGCTTCTA 5280

Qy 5281 CACACTGCTGCAAGACCAAGTCCGGAAACAGTACTACATCGGGGCCGATGGCTCCTTGCG 5340

Db 5281 CACACTGCTGCAAGACCAAGTCCGGAAACAGTACTACATCGGGGCCGATGGCTCCTTGCG 5340

Qy 5341 GCTGTGCTGCCAACGGCATGGAGTGGCGCTGCAGACTGAGCCCCACTTGCTGGCTGG 5400

Db 5341 GCTGTGCTGCCAACGGCATGGAGTGGCGCTGCAGACTGAGCCCCACTTGCTGGCTGG 5400

Qy 5401 CACCGTCAACCCACCGTGGGCAAGAGGAATGTACGTCGCCATCGAACACGGCCTCAA 5460

Db 5401 CACCGTCAACCCACCGTGGGCAAGAGGAATGTACGTCGCCATCGAACACGGCCTCAA 5460

Qy 5461 CCTGTTGGAGTGGCGCCAGCGCAAGAGCAGGCTCGGGGCCAGGTCACTGTCTTTGGGCG 5520

Db 5461 CCTGTTGGAGTGGCGCCAGCGCAAGAGCAGGCTCGGGGCCAGGTCACTGTCTTTGGGCG 5520

Qy 5521 CCGGCTGCGGGTGCAAAACCGAAATCTCCTATCTCTGGACTTTGATCGCGTAACACGCAC 5580

Db 5521 CCGGCTGCGGGTGCAAAACCGAAATCTCCTATCTCTGGACTTTGATCGCGTAACACGCAC 5580

Qy 5581 AGAGAAGATCTATGATGACCAACCGCAAGTTTACCCTTCGGATTCTGTACGACCGGGGG 5640

Db 5581 AGAGAAGATCTATGATGACCAACCGCAAGTTTACCCTTCGGATTCTGTACGACCGGGGG 5640

Qy 5641 GCGGCCAGCCTCTGGTCAACCCAGCAGCAGGCTGAATGGTGTCAACGTGACATCTCCCC 5700

Db 5641 GCGGCCAGCCTCTGGTCAACCCAGCAGCAGGCTGAATGGTGTCAACGTGACATCTCCCC 5700

Qy 5701 TGGGGGTTACATTTGCTGGCATCCAGAGGGGSCATCATGTCTGAAAAGAAATGGAATACGACCA 5760

Db 5701 TGGGGGTTACATTTGCTGGCATCCAGAGGGGSCATCATGTCTGAAAAGAAATGGAATACGACCA 5760



QY	5761	GGCGGCGCATCACATCCAGGATCTTCGCTGATGGGAAGACATGGAGCTACACATACTT	5820
Db	5761	GGCGGCGCGCATCACATCCAGGATCTTCGCTGATGGGAAGACATGGAGCTACACATACTT	5820
QY	5821	AGAGAAAGTCCATGGTGTCTACTACACAGCCAGAGGAGTATATCTTTGAGTTCGACAA	5880
Db	5821	AGAGAAAGTCCATGGTGTCTACTACACAGCCAGAGGAGTATATCTTTGAGTTCGACAA	5880
QY	5881	GAATGACCGCCTCTCTTCTGTGACGATGCCCAACGTCGCGCGGAGACACTAGACCCAT	5940
Db	5881	GAATGACCGCCTCTCTTCTGTGACGATGCCCAACGTCGCGCGGAGACACTAGACCCAT	5940
QY	5941	CCGCTCAGTGGGCTACTACAGAAACATCTATCAGCCCCCTGAGGGCAATGCCTCAGTCAT	6000
Db	5941	CCGCTCAGTGGGCTACTACAGAAACATCTATCAGCCCCCTGAGGGCAATGCCTCAGTCAT	6000
QY	6001	ACAGGACTTCACGTAGGATGGGCACCTCTTTCACACCTTCTACCTGGGCACTGGCGCGAG	6060
Db	6001	ACAGGACTTCACGTAGGATGGGCACCTCTTTCACACCTTCTACCTGGGCACTGGCGCGAG	6060
QY	6061	GGTGATATACAAAGTATGGCAAACTGTCAAAGCTGGCAGAGACGCTCTATGACACCACCAA	6120
Db	6061	GGTGATATACAAAGTATGGCAAACTGTCAAAGCTGGCAGAGACGCTCTATGACACCACCAA	6120
QY	6121	GGTCAGTTTCACCTATGACGAGACGGCAGGCATGCTGAAGACCATCAACCTACAGAATGA	6180
Db	6121	GGTCAGTTTCACCTATGACGAGACGGCAGGCATGCTGAAGACCATCAACCTACAGAATGA	6180
QY	6181	GGGCTTCACCTGCACCATCCGCTACCGTCAGATTGGGCCCCCTGATTGACCGACAGATCTT	6240
Db	6181	GGGCTTCACCTGCACCATCCGCTACCGTCAGATTGGGCCCCCTGATTGACCGACAGATCTT	6240
QY	6241	CCGCTTCACGTAGGAAAGGATGGTCAACGCCCGTTTGTGACTAACACTATGACAAACAGCTT	6300
Db	6241	CCGCTTCACGTAGGAAAGGATGGTCAACGCCCGTTTGTGACTAACACTATGACAAACAGCTT	6300
QY	6301	CCGGGTGACAGCATGCAGGCTGTGATCAACGAGACCCCACTGCCCATTTGATCTCTATCG	6360
Db	6301	CCGGGTGACAGCATGCAGGCTGTGATCAACGAGACCCCACTGCCCATTTGATCTCTATCG	6360
QY	6361	CTATGATGATGTGTGAGGCAAGACAGAGCAGATTGGGGAAGTTTGGTGCTATTACTATGA	6420
Db	6361	CTATGATGATGTGTGAGGCAAGACAGAGCAGATTGGGGAAGTTTGGTGCTATTACTATGA	6420
QY	6421	CATTAAACCAGATCATCAACAGCTGTCAATGACCCACACCAAGCATTTTGTGATGCATATGG	6480
Db	6421	CATTAAACCAGATCATCAACAGCTGTCAATGACCCACACCAAGCATTTTGTGATGCATATGG	6480
QY	6481	CAGGATGAAGGAAGTGCAGTATGAGATCTTCCGCTCGCTCATGTACTGGATGACCGTCCA	6540
Db	6481	CAGGATGAAGGAAGTGCAGTATGAGATCTTCCGCTCGCTCATGTACTGGATGACCGTCCA	6540
QY	6541	GTATGATAACATGGGGCGAGTAGTGAAGAAGGAGCTGAAGTGAAGACCTACGCCAATAC	6600
Db	6541	GTATGATAACATGGGGCGAGTAGTGAAGAAGGAGCTGAAGTGAAGACCTACGCCAATAC	6600
QY	6601	CACTCGCTACTCCTATGAGTATGATGTGCTGACGGCCAGCTGCAGACAGTCTCCATCAATGA	6660
Db	6601	CACTCGCTACTCCTATGAGTATGATGTGCTGACGGCCAGCTGCAGACAGTCTCCATCAATGA	6660
QY	6661	CAAGCCACTCTGGCGCTACAGCTACGACCTCAATGGGAACCTGCACCTTACTGAGCCCTGG	6720
Db	6661	CAAGCCACTCTGGCGCTACAGCTACGACCTCAATGGGAACCTGCACCTTACTGAGCCCTGG	6720
QY	6721	GAACAGTGCACGGCTCACACCACTACGGTATGACATCCGCGACCGCATCACTCGGCTGGG	6780
Db	6721	GAACAGTGCACGGCTCACACCACTACGGTATGACATCCGCGACCGCATCACTCGGCTGGG	6780
QY	6781	TGACGTGCAATACAAGATGGATGAGGATGGCTTCCCTGAGGCGAGGGCGGTGATATCTT	6840
Db	6781	TGACGTGCAATACAAGATGGATGAGGATGGCTTCCCTGAGGCGAGGGCGGTGATATCTT	6840
QY	6841	TGAGTACAACCTCAGCTGGCCTGCTCATCAAGGCCTACAACCGGGCTGGCAGCTGGAGTGT	6900

Db	6841	TGAGTACAACCTCAGCTGGCCTGCTCATCAAGGCTTACAACCGGCTGGCAGCTGGAGTGT	6900
QY	6901	CAGGTACCGCTACGATGGCCTGGGGCGGCGGTGTCCAGCAAGAGCAGCCACAGCCACCA	6960
Db	6901	CAGGTACCGCTACGATGGCCTGGGGCGGCGGTGTCCAGCAAGAGCAGCCACAGCCACCA	6960
QY	6961	CCTGCAGTTCTTCTATGCAGACCTTGACCAACCCCAAGGTCAACCCACCTGTACAACCA	7020
Db	6961	CCTGCAGTTCTTCTATGCAGACCTTGACCAACCCCAAGGTCAACCCACCTGTACAACCA	7020
QY	7021	CTCCAGCTCTGAGATCACCTCCCTCTACTACGACTTGCAAGGACACCTCTTTGCCATGGA	7080
Db	7021	CTCCAGCTCTGAGATCACCTCCCTCTACTACGACTTGCAAGGACACCTCTTTGCCATGGA	7080
QY	7081	GCTGAGCAGTGGTGATGAGTTTACATAGCTTGTGACAAACATCGGACCCCTCTTGTCTGT	7140
Db	7081	GCTGAGCAGTGGTGATGAGTTTACATAGCTTGTGACAAACATCGGACCCCTCTTGTCTGT	7140
QY	7141	CTTTAGTGGAAACAGTTTGATGATCAAGCAAAATCCTGTACACAGCCTATGGGGAGATCTA	7200
Db	7141	CTTTAGTGGAAACAGTTTGATGATCAAGCAAAATCCTGTACACAGCCTATGGGGAGATCTA	7200
QY	7201	CATGGATACCAACCCCAACTTTTCAGATCATATAGGCTACCATGGTGGCCTCTATGATCC	7260
Db	7201	CATGGATACCAACCCCAACTTTTCAGATCATATAGGCTACCATGGTGGCCTCTATGATCC	7260
QY	7261	ACTCACCAGCTTGTCCACATGGGCCGGGAGATTATGATGTGTGGCCGGACCGCTGGAC	7320
Db	7261	ACTCACCAGCTTGTCCACATGGGCCGGGAGATTATGATGTGTGGCCGGACCGCTGGAC	7320
QY	7321	TAGCCCAGACCACGAGCTGTGGAAGCACCTTATGAPAGCAGCAACGTCATGCCCTTTAATCT	7380
Db	7321	TAGCCCAGACCACGAGCTGTGGAAGCACCTTATGAPAGCAGCAACGTCATGCCCTTTAATCT	7380
QY	7381	CTATATGTTCAAAAAACAACCAACCCCATCAGCAACTCCAGGACATCAAGTGTTCATGAC	7440
Db	7381	CTATATGTTCAAAAAACAACCAACCCCATCAGCAACTCCAGGACATCAAGTGTTCATGAC	7440
QY	7441	AGATGTTAACAGCTGGCTGCTCACCTTTGGATTCCAGCTACACAACGTCATCCCTGGTTA	7500
Db	7441	AGATGTTAACAGCTGGCTGCTCACCTTTGGATTCCAGCTACACAACGTCATCCCTGGTTA	7500
QY	7501	TCCAAAACAGACATGGATGCCATGGAAACCTCTTACGAGCTCATCCACACACAGATGAA	7560
Db	7501	TCCAAAACAGACATGGATGCCATGGAAACCTCTTACGAGCTCATCCACACACAGATGAA	7560
QY	7561	AACGCAGGAGTGGGCAACAGCAAGTCTATCCTCGGGTACAGTGTGAAGTACAGAAGCA	7620
Db	7561	AACGCAGGAGTGGGCAACAGCAAGTCTATCCTCGGGTACAGTGTGAAGTACAGAAGCA	7620
QY	7621	GCTCAAGGCCCTTTGTCACTTAGAACGGTTTGACCAAGTCTATGGCTCCACAATCACAG	7680
Db	7621	GCTCAAGGCCCTTTGTCACTTAGAACGGTTTGACCAAGTCTATGGCTCCACAATCACAG	7680
QY	7681	CTGCCAGCAGGCTCCAAAGACCAAGAAGTTTGCATCCAGCGGCTCAGTCTTTGGCAAGGG	7740
Db	7681	CTGCCAGCAGGCTCCAAAGACCAAGAAGTTTGCATCCAGCGGCTCAGTCTTTGGCAAGGG	7740
QY	7741	GGTCAAGTTTGCCCTTGAAGGATGGCCGAGTGACCAAGACATCATCAGTGTGGCCCAATGA	7800
Db	7741	GGTCAAGTTTGCCCTTGAAGGATGGCCGAGTGACCAAGACATCATCAGTGTGGCCCAATGA	7800
QY	7801	GGATGGGCGAAGGGTTGCTGCCATCTTGAACCATGCCACTACCTAGAGAACCTGCACCT	7860
Db	7801	GGATGGGCGAAGGGTTGCTGCCATCTTGAACCATGCCACTACCTAGAGAACCTGCACCT	7860
QY	7861	CACCATTTGATGGGGTGGATACCCATTACTTTGTGAAACCAAGGACCTTCAGAAGGTGACCT	7920
Db	7861	CACCATTTGATGGGGTGGATACCCATTACTTTGTGAAACCAAGGACCTTCAGAAGGTGACCT	7920
QY	7921	GGCCATCCTGGGCCCTCAGTGGGGGGCGGGAACCTTGAGAAATGGGGTCAACGTCACCTGT	7980
Db	7921	GGCCATCCTGGGCCCTCAGTGGGGGGCGGGAACCTTGAGAAATGGGGTCAACGTCACCTGT	7980

Db 7921 GGCCATCCTGGGCCTCAGTGGGGGGCGGGAACCTTGGAGATGGGGTCAACGTCACGTGT 7980

Qy 7981 GTCCCGAGATCAACACAGACTACTTAATGGCAGGACTAGACGCTACACAGACATCCAGCTCCA 8040

Db 7981 GTCCCGAGATCAACACAGACTACTTAATGGCAGGACTAGACGCTACACAGACATCCAGCTCCA 8040

Qy 8041 GTACGGGGCAGCTGTGCTTGAACACACACGCTACGGGACAACGTTGGATGAGGAGAAGGCACG 8100

Db 8041 GTACGGGGCAGCTGTGCTTGAACACACACGCTACGGGACAACGTTGGATGAGGAGAAGGCACG 8100

Qy 8101 GGTCTGTGAGCTGGCCCGCAGAGAGCCGTGCGCCAAGCGTGGGCCCGCAGCAGAGAG 8160

Db 8101 GGTCTGTGAGCTGGCCCGCAGAGAGCCGTGCGCCAAGCGTGGGCCCGCAGCAGAGAG 8160

Qy 8161 ACTCGGGGAAGGGAGGAAGSCCTGCGGGCCTGGACAGAGGGGAGAGCAGCAGCTGCT 8220

Db 8161 ACTCGGGGAAGGGAGGAAGSCCTGCGGGCCTGGACAGAGGGGAGAGCAGCAGCTGCT 8220

Qy 8221 GAGCACAGGGCGGTGCAAGGCTACGACGGCTTTTTCGTGATCTCTGTCGAGCAGTACCC 8280

Db 8221 GAGCACAGGGCGGTGCAAGGCTACGACGGCTTTTTCGTGATCTCTGTCGAGCAGTACCC 8280

Qy 8281 AGAACTGTCAGACAGCGGCCAACACATCCACTTTCATGACAGAGCGAGATGGGCCGGAG 8340

Db 8281 AGAACTGTCAGACAGCGGCCAACACATCCACTTTCATGACAGAGCGAGATGGGCCGGAG 8340

Qy 8341 GTGACAGAGAGGAC 8354

Db 8341 GTGACAGAGAGGAC 8354

RESULT 2

ADF74829

ID ADF74829 standard; cDNA; 8354 BP.

XX ADF74829;

XX 26-FEB-2004 (first entry)

XX Murine NOVX cDNA to treat human pathological conditions (SeqID 43).

KW gene; ss; mouse; murine; NOVX; metabolic disorder; diabetes; anorexia; cancer; cardiovascular; infectious; neurodegenerative; immune; haematopoietic disease; dyslipidaemia; anorectic; virucide; nootropic; antiinflammatory; neuroprotective; antilipaemic; anabolic; cardiant; neurogenesis; wound healing; angiogenesis; chromosome mapping; tissue typing; preventive medicine; pharmacogenomic; single nucleotide polymorphism; SNP.

XX Mus musculus.

FH Key Location/Qualifiers

FT variation replace(536,a) /\*tag= a

FT variation replace(1550,c) /\*tag= b

FT variation replace(4693,t) /\*tag= c

FT variation replace(6739,g) /\*tag= d

FT variation replace(6847,t) /\*tag= e

FT variation replace(6909,c) /\*tag= f

FT variation replace(standard\_name= "Single nucleotide polymorphism" /\*standard\_name= "Single nucleotide polymorphism"

XX WO2003076578-A2.

PN

XX

PD

XX 18-SEP-2003.

PF 06-MAR-2003; 2003WO-US006794.

XX 06-MAR-2002; 2002US-0361974P.

PR 08-MAR-2002; 2002US-00093463.

PR 08-MAR-2002; 2002WO-US007288.

PR 15-MAR-2002; 2002US-0365034P.

PR 19-MAR-2002; 2002US-0365477P.

PR 20-MAR-2002; 2002US-0365884P.

PR 20-MAR-2002; 2002US-0365984P.

PR 20-MAR-2002; 2002US-0365985P.

PR 22-MAR-2002; 2002US-0366928P.

PR 12-APR-2002; 2002US-0372018P.

PR 12-APR-2002; 2002US-0372022P.

PR 23-APR-2002; 2002US-0374682P.

PR 12-JUN-2002; 2002US-0388096P.

PR 14-JUN-2002; 2002US-0389143P.

PR 26-JUN-2002; 2002US-0391779P.

PR 15-AUG-2002; 2002US-0403743P.

PR 13-SEP-2002; 2002US-0410755P.

PR 23-SEP-2002; 2002US-0412957P.

PR 22-OCT-2002; 2002US-0420382P.

PR 05-MAR-2003; 2003US-00420382.

XX (CURA-) CURAGEN CORP.

XX Alsobrook JP, Anderson DW, Boldog FL, Burgess CE, Chaudhuri A;

PI Colman SD, Edinger SR, Ettenberg S, Gangolli EA, Gerlach VL;

PI Gorman L, Guo X, Kekuda R, Li L, MacIachlan T, Malyankar UM;

PI Mezes PS, Miller CE, Millet I, Padigar M, Patturajan M, Peyman J;

PI Qian X, Rastelli L, Rieger DK, Smithson G, Spytek KA, Stone DJ;

PI Sukumaran S, Vernet CAM, Voss EZ, Zhong M;

XX WPI; 2003-697890/66.

DR P-PSDB; ADF74830.

XX

PT New isolated NOVX polypeptides and polynucleotides, useful for

PT preventing, diagnosing or treating NOVX-associated disorders, e.g.

PT osteoarthritis, obesity, atherosclerosis, cancer, Parkinson's disease,

PT asthma, or infections.

XX Claim 20; SEQ ID NO 43; 282pp; English.

PS

XX

CC This invention relates to a novel nucleic acids, and encoded polypeptides

CC thereof, which have properties related to the stimulation of biochemical

CC or physiological responses in a cell, tissue, organ or organism.

CC Specifically, it refers to the use of biologically active fragments for

CC diagnostic and prognostic assays and furthermore in the treatment of

CC diverse pathological conditions. The present invention describes novel

CC human and murine NOVX proteins, as well as methods to modulate their

CC expression using antisense oligos, ribozymes and peptide nucleic acids.

CC The polypeptides, nucleic acid molecules and antibodies are useful in the

CC manufacture of a medicament for treating metabolic disorders, diabetes,

CC anorexia, cancer, cardiovascular, infectious, neurodegenerative, immune

CC and haematopoietic diseases as well as various dyslipidaemias.

CC Accordingly, these molecules have many activities including anorectic,

CC virucide, nootropic, antiinflammatory, neuroprotective, antilipaemic,

CC anabolic and cardiant. Furthermore, they are useful in screening assays

CC to identify small molecules that modulate or inhibit, for example,

CC neurogenesis, wound healing and angiogenesis. The nucleic acids are also

CC used as in chromosome mapping, tissue typing, preventive medicine and

CC pharmacogenomics. This polynucleotide is a murine NOVX cDNA of the

CC invention.

XX

SQ Sequence 8354 BP; 1968 A; 2437 C; 2271 G; 1678 T; 0 U; 0 Other;

Query Match 100.0%; Score 8354; DB 10; Length 8354;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 8354; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy

1 GTTTGTGGATGTGGAGCGCGGGCCGGAGGCCATGACGTGAAGGAGAGGAGCCTTA 60

|||||



Db 1 GTTTGTGGATGTGGAGGAGCGCGGCGCGGATGGACGTGAAGGAGGAAGCCTTA 60  
QY 61 CCGCTCGCTGACCCGSGCGCGACGCGGAGGSGCGCTACACCAGCTCGTCCGGGACAG 120  
Db 61 CCGCTCGCTGACCCGSGCGCGACGCGGAGGSGCGCTACACCAGCTCGTCCGGGACAG 120  
QY 121 CGAGGAGGGCAAAGCCCGCAGAAATCGTACAGCTCCAGCGAGACCCTGAAGGCCCTACGA 180  
Db 121 CGAGGAGGGCAAAGCCCGCAGAAATCGTACAGCTCCAGCGAGACCCTGAAGGCCCTACGA 180  
QY 181 CCAGGACGCCCGCTAGCCCTATGGCAGCCCGCTCAAGGACATTTGTGCCGAGGAGGCCGA 240  
Db 181 CCAGGACGCCCGCTAGCCCTATGGCAGCCCGCTCAAGGACATTTGTGCCGAGGAGGCCGA 240  
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Db 301 GCCCCCTACGGGACCCCTGTACCGGACAGACATTTGGCCCTGCCCAAATGGCGCTACTCCAT 360  
QY 361 GGGGGCTGGCTCTGATCCGACATGGAGGCTGACACGGTGTCTCCCTGAGCACCCCGT 420  
Db 361 GGGGGCTGGCTCTGATCCGACATGGAGGCTGACACGGTGTCTCCCTGAGCACCCCGT 420  
QY 421 GCGTCTGTGGGCGCGGAGCACACGGTCAGGGCGCAGCTCCTGCCTGTCAGCCCGGGCCAA 480  
Db 421 GCGTCTGTGGGCGCGGAGCACACGGTCAGGGCGCAGCTCCTGCCTGTCCAGCCGGGCCAA 480  
QY 481 TTCCAAATCTCACTACCGGACACCGAGCATGAAGCACTGAGACTGATCATCCGGGCGG 540  
Db 481 TTCCAAATCTCACTACCGGACACCGAGCATGAAGCACTGAGACTGATCATCCGGGCGG 540  
QY 541 CCTGCAGAACACGGCGGCTCCGGACGCGCGCGCGCGCTCTCGCACGCCACACCCC 600  
Db 541 CCTGCAGAACACGGCGGCTCCGGACGCGCGCGCGCGCTCTCGCACGCCACACCCC 600  
QY 601 CAACACGACCAACGCGSCTCCATTAACTCCCTGAACCGGGCAACTTCAACGCGGAGG 660  
Db 601 CAACACGACCAACGCGSCTCCATTAACTCCCTGAACCGGGCAACTTCAACGCGGAGG 660  
QY 661 CAACCCCGAGCCCGCCCCACGGACCACTCGCTCTCCGGAGAGCCCCCTGCGCGCGCGC 720  
Db 661 CAACCCCGAGCCCGCCCCACGGACCACTCGCTCTCCGGAGAGCCCCCTGCGCGCGCGC 720  
QY 721 CCAGGAGCTGCCACGCCAGGAGAACTGGCTGTCAACAGCAACATCCCCCTGGAGAC 780  
Db 721 CCAGGAGCTGCCACGCCAGGAGAACTGGCTGTCAACAGCAACATCCCCCTGGAGAC 780  
QY 781 CAGGAACCTAGGCAAGCAGCCATTCTTAGGGACATTGCAGGACAACCTCAATTGAGATGGA 840  
Db 781 CAGGAACCTAGGCAAGCAGCCATTCTTAGGGACATTGCAGGACAACCTCAATTGAGATGGA 840  
QY 841 CATTTCTGGCGCCTCCCGCCATGATGGGGCTTACAGTGACGGGCACTTCCTCTTCAAGCC 900  
Db 841 CATTTCTGGCGCCTCCCGCCATGATGGGGCTTACAGTGACGGGCACTTCCTCTTCAAGCC 900  
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QY 1261 TGACAGAAAGGCAAAGGAACCAACAGAAAGAAAGCCAGTAGTTTCTTTCCAGAGGACAG 1320  
Db 1261 TGACAGAAAGGCAAAGGAACCAACAGAAAGAAAGCCAGTAGTTTCTTTCCAGAGGACAG 1320  
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QY 1501 ACAGTTTGACTTTGTGGAGCTGCTGGATGGCAGGAGGCTCCTAACCCAGGAGGCGGAG 1560  
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Db 1561 CCTAGAGGGACCCCGCGCCAGTCTCGGGAACTGTGCCCCCTCCAGCCATGAGACAGG 1620  
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Db 1801 CCCCAGCTTGGCAGAGCCTCCTGCCCGTGTGAGGAAAGCGCTGAGTGCATGTGCCCAATGCGAA 1860  
QY 1861 AGGCAGATGCTTGTGCCACAGTGGCTGGAAGGCGCTGAGTGCATGTGCCCAACCA 1920  
Db 1861 AGGCAGATGCTTGTGCCACAGTGGCTGGAAGGCGCTGAGTGCATGTGCCCAACCA 1920  
QY 1921 GTGTATCGATGTGGCCTGCAGCAACCATGGCACCTGCATCACGGGCACCTGTCATCTGCAA 1980  
Db 1921 GTGTATCGATGTGGCCTGCAGCAACCATGGCACCTGCATCACGGGCACCTGTCATCTGCAA 1980  
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Db 2101 CGAGACCCCGAGGCGCACATGCTTAGACAGTGTTCAGGCCACGGAACCTTCTCCCGGA 2160  
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DB 2581 GGTGACTGCATGGACCCCTGACTGCTGCCCTCCAGCCCTGTGCCATATCAACCCGCTGTG 2640  
QY 2641 CCTTGGCTCCCCATAACCCTCTGGACATCATCCAGGAGACACAGGTCCCTGTGTACAGCA 2700  
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QY 2701 GAACCTACACTCCTTCTATGACCGCATCAAGTTCCCTGTTGGCGAGGACAGCACAT 2760  
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QY 2761 AATCCCCGGGGAGAACCCCTTGTGATGGAGGCGATGCTTGTGTATTTCGTGGCCAAAGTGAT 2820  
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QY 2821 GACATCAGATGGAACCCCCCTTGGTGTGAACATCAGTTTGTCAATAACCCCTCTCTT 2880  
DB 2821 GACATCAGATGGAACCCCCCTTGGTGTGAACATCAGTTTGTCAATAACCCCTCTCTT 2880  
QY 2881 TGGATATACAATCAGCAGGCAAGATGGCAGCTTTGACTTGGTGACAAATGGCGGCATCTC 2940  
DB 2881 TGGATATACAATCAGCAGGCAAGATGGCAGCTTTGACTTGGTGACAAATGGCGGCATCTC 2940  
QY 2941 CATCATCCTGCGGTTTCGAGCGGGCACCTTTTCATCACACAGGAGCACACCCTGTGGCTGCC 3000  
DB 2941 CATCATCCTGCGGTTTCGAGCGGGCACCTTTTCATCACACAGGAGCACACCCTGTGGCTGCC 3000  
QY 3001 ATGGGATCGCTTCTTTGTATGGAACCATCATCATGAGACATGAGGAGAAATGAGATTCC 3060  
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QY 3421 TGGGCTTTCAGAAAGCCCTTTGTTTCCGTGGGTTATGAATATGAATCCTGCCAGATCTAAT 3480  
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DB 3481 CCTGTGGGAAAAAGAAACAACAGTGTGCAGGGCTATGAAATTGACGCGTCCAAGCTTGG 3540  
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DB 3541 AGGATGGAGCCTTAGACAAAACATCATGCCCTCAACATTTCAAAGTGGTATCTTCACAAAGG 3600  
QY 3601 GAATGGGAGAACCAAGTTTGTGTCTCAGCAGCCCTCCTGTCAATGGGAGCATCATGGGCAA 3660  
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QY 3961 GGTGTGAAGGACCTTGTCAAGAACTCTGAGTGGTTCGGGGACAGGTGACAGTGCCT 4020  
DB 3961 GGTGTGAAGGACCTTGTCAAGAACTCTGAGTGGTTCGGGGACAGGTGACAGTGCCT 4020  
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DB 4021 CCCCTTTGATGACACTCGCTGCGGGATGTTGGGAAAGCCACAGAAAGCCACTCACCAA 4080  
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QY 4141 CAGACGCATCGATCAGAATGGGATCATCTCCACCTGCTCGGCTCTAATGATCTCACATC 4200  
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QY 4201 AGCCCCGCCACTCAGCTGTGATTCTGTCTCATGGATATTTCCCAGGTAAGACTGGAGTGGCC 4260  
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QY 4261 CACAGACTTAGCCATCAACCCCAATGGACAACCTCACTTTATGTCTCGACAACAATGTGGT 4320  
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DB 4321 CCTGCAAAATCTCTGAAAAACCAACAGGTGCGCATTTGTCGCCGGAGGCCCATGCACTGCCA 4380  
QY 4381 GGTCCCTGGCATTGACCACTTCTCTGCTAAGCAAGGTGGCCCATCCACGCAACCTTGAGTTC 4440

Db 4381 GGTCCCTGGCATTGACCACTTCCTGCTAAGCAAGGTGGCCATCCACGCCAACCCCTGGAGTC 4440

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Db 4621 TTATGCCAAGGATGCAAGTTAAATACCCCATCTTCCTTGGCTGTGTGCTGCTGATGGGA 4680

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QY 5341 GCTGCTGCTGGCCAACCGGCATGGAGGTGGCGCTGCAGACTGAGCCCCACTTGTGGCTGG 5400

Db 5341 GCTGCTGCTGGCCAACCGGCATGGAGGTGGCGCTGCAGACTGAGCCCCACTTGTGGCTGG 5400

QY 5401 CACCGTCAACCCCACCGTGGCAAGAGGAATGTACGCTGCCCATCGACAACGGCCTCAA 5460

Db 5401 CACCGTCAACCCCACCGTGGCAAGAGGAATGTACGCTGCCCATCGACAACGGCCTCAA 5460

QY 5461 CCTGTGGAGTGGCGCAGCGCAAGAGCAGGCTCGGGGCCAGGTCACTGCTTTTGGGCG 5520

Db 5461 CCTGTGGAGTGGCGCAGCGCAAGAGCAGGCTCGGGGCCAGGTCACTGCTTTTGGGCG 5520

QY 5521 CCGGCTCGGGTGCAAAACCGAAATCTCCTATCTCTGGACTTTTGATCGCGTAACACGCAC 5580

Db 5521 CCGGCTCGGGTGCAAAACCGAAATCTCCTATCTCTGGACTTTTGATCGCGTAACACGCAC 5580

QY 5581 AGAGAAAGATCTATGATGACCAACCGCAAGTTCAACCCCTTCGGATTCTGTACGACCAGGCGG 5640

Db 5581 AGAGAAAGATCTATGATGACCAACCGCAAGTTCAACCCCTTCGGATTCTGTACGACCAGGCGG 5640

QY 5641 GCGGCCACGCTCTGGTCAACCCAGCAGCAGGCTGAATGGTGTCAACGCTGACATACTCCCC 5700

Db 5641 GCGGCCACGCTCTGGTCAACCCAGCAGCAGGCTGAATGGTGTCAACGCTGACATACTCCCC 5700

QY 5701 TGGGGTTACATTTGCTGGCATCCAGAGGGGCATCATGTCTGAAAGAAATGGAATACGACCA 5760

Db 5701 TGGGGTTACATTTGCTGGCATCCAGAGGGGCATCATGTCTGAAAGAAATGGAATACGACCA 5760

QY 5761 GCGGGCCGCATCACATCCAGGATCTTCGCTGATGGGAAGACATGGAGCTACACATACTT 5820

Db 5761 GCGGGCCGCATCACATCCAGGATCTTCGCTGATGGGAAGACATGGAGCTACACATACTT 5820

QY 5821 AGAGAAAGTCCATGGTCTACTACACAGCCAGGAGCAGTATATCTTTGAGTTTCGACAA 5880

Db 5821 AGAGAAAGTCCATGGTCTACTACACAGCCAGGAGCAGTATATCTTTGAGTTTCGACAA 5880

QY 5881 GAATGACCGCCTCTTCTGTGACGATGCCAAACGTTGGCGGCAGACACTAGAGACCAT 5940

Db 5881 GAATGACCGCCTCTTCTGTGACGATGCCAAACGTTGGCGGCAGACACTAGAGACCAT 5940

QY 5941 CCGCTCAGTGGGTACTACAGAAACATCTATCAGCCCCCTGAGGGCAATGCCTCAGTCAT 6000

Db 5941 CCGCTCAGTGGGTACTACAGAAACATCTATCAGCCCCCTGAGGGCAATGCCTCAGTCAT 6000

QY 6001 ACAGGACTTCACTGAGGATGGCACCTCTCTCACACCTTCTACCTTGGGCACTGGCGCGAG 6060

Db 6001 ACAGGACTTCACTGAGGATGGCACCTCTCTCACACCTTCTACCTTGGGCACTGGCGCGAG 6060

QY 6061 GGTGATATACAAGTATGGCAAACTGTCAAAGCTGGCAGAGACGCTCTATGACACCAACAA 6120

Db 6061 GGTGATATACAAGTATGGCAAACTGTCAAAGCTGGCAGAGACGCTCTATGACACCAACAA 6120

QY 6121 GGTCAAGTTTCAACCTATGACGAGACGGCAGGATGCTGAAGACCATCAACCTACAGAATGA 6180

Db 6121 GGTCAAGTTTCAACCTATGACGAGACGGCAGGATGCTGAAGACCATCAACCTACAGAATGA 6180

QY 6181 GGGCTTCACTGCAACCATCCGCTACCGTACCGTACAGATGGGCCCCCTGATTGACCGACAGATCTT 6240

Db 6181 GGGCTTCACTGCAACCATCCGCTACCGTACCGTACAGATGGGCCCCCTGATTGACCGACAGATCTT 6240

QY 6241 CCGCTTCACTGAGGAAGGCATGGTCAACGCCGTTTTGACTACAACTATGACAAACAGCTT 6300

Db 6241 CCGCTTCACTGAGGAAGGCATGGTCAACGCCGTTTTGACTACAACTATGACAAACAGCTT 6300

QY 6301 CCGGTTGACCAAGCATGAGGCTGTGATCAACGAGACCCCATGCCCCATTGATCTTATCG 6360

Db 6301 CCGGTTGACCAAGCATGAGGCTGTGATCAACGAGACCCCATGCCCCATTGATCTTATCG 6360

QY 6361 CTATGATGATGTGTAGGCAAGACAGAGCAGTTTGGGAAGTTTGGTGTCTATTACTATGA 6420

Db 6361 CTATGATGATGTGTAGGCAAGACAGAGCAGTTTGGGAAGTTTGGTGTCTATTACTATGA 6420

QY 6421 CATTAAACAGATCATCACACAGCTGTCTATGACCCACACCAAGCATTTTGTGATGATATGG 6480

Db 6421 CATTAAACAGATCATCACACAGCTGTCTATGACCCACACCAAGCATTTTGTGATGATATGG 6480

QY 6481 CAGGATGAAGGAAGTGCAGTATGAGATCTTCGCTCGCTCATGTACTGGATGACCGTCCA 6540

Db 6481 CAGGATGAAGGAAGTGCAGTATGAGATCTTCGCTCGCTCATGTACTGGATGACCGTCCA 6540

QY 6541 GTATGATAACATGGGGCAGTAGTGAAGAAAGGAGCTGAAGGTAGGACCCCTACGCCAATAC 6600

Db 6541 GTATGATAACATGGGGCAGTAGTGAAGAAAGGAGCTGAAGGTAGGACCCCTACGCCAATAC 6600



QY 6601 CACTCGCTACTCCTATGATGATGCTGACGGCCAGCTGCAGACAGTCTCCATCAATGA 6660  
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Db 6601 CACTCGCTACTCCTATGATGATGCTGACGGCCAGCTGCAGACAGTCTCCATCAATGA 6660  
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QY 6661 CAAGCCACTCTGGCGCTACAGCTACGACCTCAATGGGAACCTGCACTTACTGAGCCCTGG 6720  
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Db 6661 CAAGCCACTCTGGCGCTACAGCTACGACCTCAATGGGAACCTGCACTTACTGAGCCCTGG 6720  
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QY 6721 GAAAGTGCACGGCTCACACACTACGGTATGACATCCGCGACCGCATCACTCGGCTGGG 6780  
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Db 6721 GAAAGTGCACGGCTCACACACTACGGTATGACATCCGCGACCGCATCACTCGGCTGGG 6780  
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QY 6781 TGACGTGCAATACAAGATGGATGAGTGGCTTCCCTGAGGCAGCGGGCGGTGATATCTT 6840  
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Db 6781 TGACGTGCAATACAAGATGGATGAGTGGCTTCCCTGAGGCAGCGGGCGGTGATATCTT 6840  
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QY 6841 TGAGTACAACCTCAGCTGGCCTGCTCATCAAGGCCTACAACCGGCTGGCAGCTGGAGTGT 6900  
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Db 6841 TGAGTACAACCTCAGCTGGCCTGCTCATCAAGGCCTACAACCGGCTGGCAGCTGGAGTGT 6900  
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Db 6901 CAGGTACCGCTACGATGGCCTGGGCGGCGCTGTCCAGCAAGAGCAGCCACAGCCACCA 6960  
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QY 6961 CCTGCAGTTCTTCTATGCAGACCTGACCAACCCCAACCAAGGTCACTGTACAACTCA 7020  
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QY 7081 GCTGAGCAGTGGTATGATGATCAAGCAAAATCCTGTACACAGCCTATGGGGAGATCTA 7140  
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Db 7081 GCTGAGCAGTGGTATGATGATCAAGCAAAATCCTGTACACAGCCTATGGGGAGATCTA 7140  
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Db 7261 ACTCACAAGCTTGTCCACATGGGCGCGGAGATTATGATGTCTGGCCGGACGCTGGAC 7320  
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Db 7321 TAGCCCAGACCCAGAGCTGTGGAAGCACCTTAGTAGCAGCAACGTATGCCCTTTTAACTT 7380  
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Db 7381 CTATATGTTCAAAAAACAACCCCATCAGCAACTCCCAGGACATCAAGTGCTTCAATGAC 7440  
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Db 7441 AGATGTTAAAGCTGGCTGCTCACCTTTGGATTCCAGCTACACAACGTGATCCCTGGTTA 7500  
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QY 7501 TCCCAACACAGACATGGATGCCATGGAAACCTCTACGAGCTCATCCACACAGATGAA 7560  
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QY 7561 AACGCAGAGTGGGACAACAGCAAGTCTATCCTCGGGGTACAGTGTGAAGTACAGAAGCA 7620  
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Db 7561 AACGCAGAGTGGGACAACAGCAAGTCTATCCTCGGGGTACAGTGTGAAGTACAGAAGCA 7620  
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QY 7621 GCTCAAGGCTTTGTCACTTAGAACCGTTTGACCAGCTCTATGGCTCCACAATCACCAG 7680  
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QY 7681 CTGCCAGCAGGCTCCAAAGACCAAGAGTTTGCATCCAGCGGCTCAGTCTTTGGCAAGGG 7740

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QY 7741 GGTCAAGTTTGCCTTGAAGGATGGCCGAGTGACCACAGACATCATCAGTGTGGCCAAATGA 7800  
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Db 7741 GGTCAAGTTTGCCTTGAAGGATGGCCGAGTGACCACAGACATCATCAGTGTGGCCAAATGA 7800  
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QY 7801 GGATGGGCGAAGGTTGCTGCCATCTTGAACCATGCCCACTACCTAGAGAAACCTGCACCTT 7860  
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QY 7861 CACCATTGATGGGTTGGATACCCATTACTTTGTGTGAAACCAGGACCTTCAAGAGGTGACCT 7920  
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QY 7921 GGCCATCCTGGSCCTCAGTGGGGGCGGGAACCCCTGGAGAAATGGGTTCAACGTCACTGT 7980  
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Db 7921 GGCCATCCTGGSCCTCAGTGGGGGCGGGAACCCCTGGAGAAATGGGTTCAACGTCACTGT 7980  
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Db 7981 GTCCCAGATCAACACAGTACTTAATGGCAGGACTAGACGCTACACAGACATCCAGCTCCA 8040  
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QY 8041 GTACGGGGCACTGTGCTTGAACACACGCTACGGGACAACTTTGGATGAGGAGAAGGCACG 8100  
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Db 8041 GTACGGGGCACTGTGCTTGAACACACGCTACGGGACAACTTTGGATGAGGAGAAGGCACG 8100  
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QY 8101 GGTCTTGAGCTGGCCCCGGCAGAGAGCCGTGCGGCCAAAGCGTGGGCCCGCAGCAGAGAG 8160  
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Db 8101 GGTCTTGAGCTGGCCCCGGCAGAGAGCCGTGCGGCCAAAGCGTGGGCCCGCAGCAGAGAG 8160  
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QY 8161 ACTCGGGGAAGGGAGGAAGGCCCTGCGGGCCTGGACAGAGGGGGAGAAAGCAGAGGTGCT 8220  
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Db 8161 ACTCGGGGAAGGGAGGAAGGCCCTGCGGGCCTGGACAGAGGGGGAGAAAGCAGAGGTGCT 8220  
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QY 8221 GAGCACAGGGCGGTGCAAGGCTACGACGGCTTTTCTGTATCTCTGTGAGCAGTACCC 8280  
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Db 8221 GAGCACAGGGCGGTGCAAGGCTACGACGGCTTTTCTGTATCTCTGTGAGCAGTACCC 8280  
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QY 8281 AGAACTGTCAGACAGCGCCCAACAACATCCACTTCATGAGACAGAGCGAGATGGSCCGGAG 8340  
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Db 8281 AGAACTGTCAGACAGCGCCCAACAACATCCACTTCATGAGACAGAGCGAGATGGSCCGGAG 8340  
|||||  
QY 8341 GTGACAGAGAGGAC 8354  
|||||  
Db 8341 GTGACAGAGAGGAC 8354  
|||||  
RESULT 3  
ABS78652  
ID ABS78652 standard; cDNA; 8645 BP.  
XX  
AC ABS78652;  
XX  
DT 16-DEC-2002 (first entry)  
XX  
DE Human cDNA encoding CGDD10, INCYTE 7488573CB1.  
XX  
KW Human; ss; gene; cell growth; differentiation; death; CGDD; cancer;  
cell proliferative disorder; arteriosclerosis; atherosclerosis;  
cirrhosis; hepatitis; paroxysmal nocturnal haemoglobinuria; psoriasis;  
polycythaemia vera; primary thrombocytopaenia; developmental disorder;  
renal tubular acidosis; anaemia; mental retardation; epilepsy; AIDS;  
neurological disorder; Alzheimer disease; Parkinson's disease; asthma;  
reproductive disorder; infertility; autoimmune disorder; gout; allergy;  
inflammatory disorder; acquired immunodeficiency syndrome; uveitis;  
autoimmune thyroiditis; contact dermatitis; Crohn's disease; infection;  
diabetes mellitus; glomerulonephritis; irritable bowel syndrome;  
multiple sclerosis; osteoarthritis; osteoporosis; pancreatitis;  
rheumatoid arthritis.  
XX  
OS Homo sapiens.  
XX



PN WO200272830-A2.  
XX  
PD 19-SEP-2002.  
XX  
XX  
PF 08-FEB-2002; 2002WO-US003715.  
XX  
XX  
PR 09-FEB-2001; 2001US-0268111P.  
PR 23-FEB-2001; 2001US-0271175P.  
PR 08-MAR-2001; 2001US-0274503P.  
PR 09-MAR-2001; 2001US-0274552P.  
XX  
XX  
PA (INCY-) INCYTE GENOMICS INC.  
XX  
PI Yue H, Yao MG, Ison CH, Lu Y, Warren BA, Elliott VS, Baughn MR;  
PI Ding L, Xu Y, Gietzen KJ, Tang TY, Lal PG, Duggan BM, Burford N;  
PI Lu DAM, Richardson TW, Tran UK, Khare R, Walia NK;  
XX  
XX  
DR WPI; 2002-723356/78.  
DR P-PSDB; ABG97359.  
XX  
PT New human proteins associated with cell growth, differentiation and  
PT death, useful for diagnosing, treating or preventing autoimmune or  
PT inflammatory disorders (e.g. AIDS, allergy or anemia), cancer,  
PT atherosclerosis or hepatitis.  
XX  
PS Claim 5; Page 175-178; 181pp; English.  
XX  
CC The invention relates to an isolated polypeptide comprising CGDD1-12  
CC (cell growth, differentiation and death), a naturally occurring amino  
CC acid sequence at least 90% identical to CGDD, a biologically active  
CC fragment or an immunogenic fragment. Also included are the  
CC polynucleotides encoding CGDD1-12, a recombinant polynucleotide  
CC comprising a promoter sequence operably linked to the CGDD  
CC polynucleotides, a cell transformed with the recombinant polynucleotide,  
CC a transgenic organism comprising the recombinant polynucleotide, an anti-  
CC CGDD antibody, screening for compounds which bind to/modulate or are  
CC ant/agonists of CGDD or alter the expression of CGDD polynucleotide and a  
CC CGDD polynucleotide microarray. The polypeptides, polynucleotides,  
CC agonists and antagonists are useful for diagnosing, treating or  
CC preventing disorders associated with aberrant expression of CGDD,  
CC particularly cell proliferative (e.g. arteriosclerosis, atherosclerosis,  
CC cirrhosis, hepatitis, paroxysmal nocturnal haemoglobinuria, polycythaemia  
CC vera, psoriasis, primary thrombocytopaenia or cancer), developmental  
CC disorders (e.g. renal tubular acidosis, anaemia or mental retardation),  
CC neurological disorders (e.g. Alzheimer disease, Parkinson's disease or  
CC epilepsy), reproductive disorders (e.g. infertility or a disruption in  
CC the menstrual cycle), or autoimmune/inflammatory disorders (e.g. AIDS,  
CC (acquired immunodeficiency syndrome) allergies, asthma, autoimmune  
CC thyroiditis, contact dermatitis, Crohn's disease, diabetes mellitus,  
CC glomerulonephritis, gout, irritable bowel syndrome, multiple sclerosis,  
CC osteoarthritis, osteoporosis, pancreatitis, rheumatoid arthritis,  
CC uveitis, or viral, bacterial, fungal, parasitic, protozoal or helminthic  
CC infections. They are also useful in the assessment of the effects of  
CC exogenous compounds on the expression of nucleic acid and amino acid  
CC sequences of proteins associated with CGDD. The present sequence encodes  
XX a CGDD protein  
SQ Sequence 8645 BP; 2060 A; 2494 C; 2319 G; 1771 T; 0 U; 1 Other;  
Query Match 98.5%; Score 8225; DB 6; Length 8645;  
Best Local Similarity 99.4%; Pred. No. 0;  
Matches 8300; Conservative 0; Mismatches 21; Indels 33; Gaps 3;  
Qy 1 GTTTGTGGATGTGGAGGAGCGCGGCGCGGAGGCCATGGACGTGAAGGAGAGGAGCCTTA 60  
Db |||||  
Db 83 GTTTGTGGATNTGGAGGAGCGCGGCGCGGAGGCCATGGACGTGAAGGAGAGGAGCCTTA 142  
Qy 61 CCGCTCGCTGACCCGCGCGCGACGCCGAGCGCGCGCTACACCAGCTCGTCCGCGGACAG 120  
Db |||||  
Db 143 CCGCTCGCTGACCCGCGCGCGCGACGCCGAGCGCGCGCTACACCAGCTCGTCCGCGGACAG 202  
Qy 121 CGAGGAGGGCAAAGCCCCCGCAGAAATCGTACAGCTCCAGCGAGACCCTGAAGGCCTACGA 180  
|||

Db 203 CGAGAGGGCAAAGCCCCCGCAGAAATCGTACAGCTCCAGCGGAGACCCCTGAAGGCCTACGA 262  
Qy 181 CCAGGACGCGCGCCTAGCCTATGGCAGCCGCGTCAAGGACATTGTGCCGAGGAGGCCGA 240  
Db |||||  
Db 263 CCAGGACGCGCGCCTAGCCTATGGCAGCCGCGTCAAGGACATTGTGCCGAGGAGGCCGA 322  
Qy 241 GGAATTCTGCGGCACACAGGTGCCAACTTCAACCCTGCGGGAGCTGGGGCTGGAAGAATAAC 300  
Db 323 GGAATTCTGCGGCACACAGGTGCCAACTTCAACCCTGCGGGAGCTGGGGCTGGAAGAATAAC 382  
Qy 301 GCCCCTCACGGGACCCCTGTACCGGACAGACATTGGCCTGCCCAATGCGGCTACTCCAT 360  
Db 383 GCCCCTCACGGGACCCCTGTACCGGACAGACATTGGCCTCCCCCACTGCGGCTACTCCAT 442  
Qy 361 GGGGCTGGCTCTGATGCCGACATGGAGGCTGACACGGTGTCTGCCCTGAGCACCCCGT 420  
Db 443 GGGGCTGGCTCTGATGCCGACATGGAGGCTGACACGGTGTCTGCCCTGAGCACCCCGT 502  
Qy 421 GCGTCTGTGGGGCGGAGCACACGGTCAGGGCGCAGCTCCTGCCTGTCCAGCCGGGCCAA 480  
Db 503 GCGTCTGTGGGGCGGAGCACACGGTCAGGGCGCAGCTCCTGCCTGTCCAGCCGGGCCAA 562  
Qy 481 TTCCAATCTCACACTCACCGACACCGAGCATGAAAACACTGAGACTGATCCTCGGGCGG 540  
Db 563 TTCCAATCTCACACTCACCGACACCGAGCATGAAAACACTGAGAC-----TCCGGGCGG 616  
Qy 541 CCTGCAGAAACACGCGGCTCCGGACGCCGCCGCCGCTCTCGCACGCCCACACCCC 600  
Db 617 CCTGCAGAAACACGCGGCTCCGGACGCCGCCGCCGCTCTCGCACGCCCACACCCC 676  
Qy 601 CAACCAGCACCGCGGCTCCATTAACTCCCTGAACCGGGGCAACTTCACGCCGAGGAG 660  
Db 677 CAACCAGCACCGCGGCTCCATTAACTCCCTGAACCGGGGCAACTTCACGCCGAGGAG 736  
Qy 661 CAACCCAGCGCGCGCGCGCGCGCTCTCCGGAGAGCCCTTCCCGCGCGCGCGC 720  
Db 737 CAACCCAGCGCGCGCGCGCGCGCTCTCCGGAGAGCCCTTCCCGCGCGCGCGC 796  
Qy 721 CCAGGAGCTGCCCCACGCCCAGGAGAACTGGTGCTCAACAGCAACATCCCCCTGGAGAC 780  
Db 797 CCAGGAGCTGCCCCACGCCCAGGAGAACTGGTGCTCAACAGCAACATCCCCCTGGAGAC 856  
Qy 781 CAGGAACCTAGGCAAGCAGCCATTCTTAGGGACATTGCAGGACAACCTCATTTGAGATGGA 840  
Db 857 CAGAAACCTAGGCAAGCAGCCATTCTTAGGGACATTGCAGGACAACCTCATTTGAGATGGA 916  
Qy 841 CATTCCTGGCGCCTCCCGCCATGATGGGCTTACAGTGACGGGCACTTCTCTTCAAGCC 900  
Db 917 CATTCCTGGCGCCTCCCGCCATGATGGGCTTACAGTGACGGGCACTTCTCTTCAAGCC 976  
Qy 901 TGGAGGCACCTCCCGCTCTTCTGCACCCACATCACAGGGTACCCACTGACGTCCAGCAC 960  
Db 977 TGGAGGCACCTCCCGCTCTTCTGCACCCACATCACAGGGTACCCACTGACGTCCAGCAC 1036  
Qy 961 AGTGACTCTCTCCCGCGCGCGACCCCTGCGCGCGCAGCACCTTCCGCGCGCGCGCTTAA 1020  
Db 1037 AGTGACTCTCTCCCGCGCGCGACCCCTGCGCGCGCAGCACCTTCCGCGCGCGCGCTTAA 1096  
Qy 1021 CCTCAAGAAAGCCCTCCAAGTACTGTAACCTGGAAGTGCAGCCCTGAGCGCATCGTCAT 1080  
Db 1097 CCTCAAGAAAGCCCTCCAAGTACTGTAACCTGGAAGTGCAGCCCTGAGCGCATCGTCAT 1156  
Qy 1081 CTCAGCCACTCTGGTTCATCTGCTGGCATACTTTGTGGCCATGCACCTGTTGGCCCTAAA 1140  
Db 1157 CTCAGCCACTCTGGTTCATCTGCTGGCATACTTTGTGGTAAGCACCT-----CTTCAA 1210  
Qy 1141 CTGGCACCTGCAGCCGATGGAGGGGCGAGATGTATGAGATCACGGAGGACACAGCCAGCAG 1200  
Db 1211 CTGGCACCTGCAGCCGATGGAGGGGCGAGATGTATGAGATCACGGAGGACACAGCCAGCAG 1270  
Qy 1201 TTGGCCTGTGCCAAACCGACGTCTCCCTATACCCCTCAGGGGGCACTGGCTTAGAGACCCC 1260  
Db 1271 TTGGCCTGTGCCAAACCGACGTCTCCCTATATACCCCTCAGGGGGCACTGGCTTAGAGACCCC 1330

QY	1261	TGACAGGAAAGGCAAGGAACCAAGAAAGGAAAGCCAGTAGTTTCTTTCCAGAGGACAG	1320
Db	1331	TGACAGGAAAGGCAAGGAACCAAGAAAGGAAAGCCAGTAGTTTCTTTCCAGAGGACAG	1390
QY	1321	TTTCATAGATTCGGAGAAATTGATGTGGAAAGGCGAGCCTCCAGAAAGATTCTCTCTGG	1380
Db	1391	TTTCATAGATTCGGAGAAATTGATGTGGAAAGGCGAGCCTCCAGAAAGATTCTCTCTGG	1450
QY	1381	CACTTTCTGGAGATCTCAAGTGTTCATAGACCATCTGTGCATCTGAAAATTCAAATGTGT	1440
Db	1451	CACTTTCTGGAGATCTCAAGTGTTCATAGACCATCTGTGCATCTGAAAATTCAAATGTGT	1510
QY	1441	TCTGGGAAAGGCAGCCCTGGTTGGCATTATGSCAGAAAAAGGCCTCCCTCTTCACATAC	1500
Db	1511	TCTGGGAAAGGCAGCCCTGGTTGGCATTATGSCAGAAAAAGGCCTCCCTCTTCACATAC	1570
QY	1501	ACAGTTTGACTTTTGTGAGCTGCTGGATGGCAGGAGGCTCCTAACCCAGGAGGCGCGGAG	1560
Db	1571	ACAGTTTGACTTTTGTGAGCTGCTGGATGGCAGGAGGCTCCTAACCCAGGAGGCGCGGAG	1630
QY	1561	CCTAGAGGGGACCCCGGCCAGTCTCGGGGAACGTGTGCCCCCCTCCAGCCATGAGACAGG	1620
Db	1631	CCTAGAGGGGACCCCGGCCAGTCTCGGGGAACGTGTGCCCCCCTCCAGCCATGAGACAGG	1690
QY	1621	CTTCATCCAGTATTGGATTGAGGAATCTGGACCTGGCTTTTACAATGACGGAAGGA	1680
Db	1691	CTTCATCCAGTATTGGATTGAGGAATCTGGACCTGGCTTTTACAATGACGGAAGGA	1750
QY	1681	GTGAGAAAGTGTTTCCTTTCTCACCACTGCCATTGAGTCGGTGGATAACTGCCCCAGCAA	1740
Db	1751	GTGAGAAAGTGTTTCCTTTCTCACCACTGCCATTGAGTCGGTGGATAACTGCCCCAGCAA	1810
QY	1741	CTGCTATGGCAATGGTGACTGCATCTCTGGGACCTGCCACTGCTTCTCTGGTTCTCTGGG	1800
Db	1811	CTGCTATGGCAATGGTGACTGCATCTCTGGGACCTGCCACTGCTTCTCTGGTTCTCTGGG	1870
QY	1801	CCCCGACTGTGGCAGAGCCTCCTGCCCGTGTCTGTAGCGGAAATGGCCAAATACATGAA	1860
Db	1871	CCCCGACTGTGGCAGAGCCTCCTGCCCGTGTCTGTAGCGGAAATGGCCAAATACATGAA	1930
QY	1861	AGGCAGATGCTGTGCCACAGTGGCTGGAAAGGCGCTGAGTGGATGTGCCCAACCA	1920
Db	1931	AGGCAGATGCTGTGCCACAGTGGCTGGAAAGGCGCTGAGTGGATGTGCCCAACCA	1990
QY	1921	GTGTATCGATGTGGCCTGCAGCAACCATGGCACCTGCATCACGGGCACCTGTGCATCTGCAA	1980
Db	1991	GTGTATCGATGTGGCCTGCAGCAACCATGGCACCTGCATCATGGGCACCTGTGCATCTGCAA	2050
QY	1981	CCCTGGCTAACGGGCGAGAGCTGTGAGGAAGTGGACTGCATGGACCCACATGTTTCAGG	2040
Db	2051	CCCTGGCTAACGGGCGAGAGCTGTGAGGAAGTGGACTGCATGGACCCACATGTTTCAGG	2110
QY	2041	CCGGGGTGTCTGCGTGAGAGGCGAATGCCATTGCTTTGTGGGATGGGAGGACCAACTG	2100
Db	2111	CCGGGGTGTCTGCGTGAGAGGCGAATGCCATTGCTTTGTGGGATGGGAGGACCAACTG	2170
QY	2101	CGAGACCCCGAGGCGCCACATGCTTAGACCAGTGTTCAGGCCACGGAACCTTCTCCCGGA	2160
Db	2171	CGAGACCCCGAGGCGCCACATGCTTAGACCAGTGTTCAGGCCACGGAACCTTCTCCCGGA	2230
QY	2161	CACCGGGCTTTGCAGCTGTGACCCCAAGCTGGACTGGAACGACTGTTCTATCGAGATCTG	2220
Db	2231	CACCGGGCTTTGCAGCTGTGACCCCAAGCTGGACTGGAACGACTGTTCTATCGAGATCTG	2290
QY	2221	TGCTGCCGACTGTGGTGGCCATGGCGTGTCCGTAGGGGGCACCTGCCGTGCGAGGATGG	2280
Db	2291	TGCTGCCGACTGTGGTGGCCATGGCGTGTCCGTAGGGGGCACCTGCCGTGCGAGGATGG	2350
QY	2281	CTGGATGGGGCAGCCTGCGAACAGCGGGCCTGCCACCCCGCTGTGCCGAGCATGGGAC	2340
Db	2351	CTGGATGGGGCAGCCTGCGAACAGCGGGCCTGCCACCCCGCTGTGCCGAGCATGGGAC	2410

QY	2341	CTGCCGCGACGCAAGTCGAGTGCAGCCCTGGCTGGAATGGCGAACACTGCACCATCGC	2400
Db	2411	CTGCCGCGACGCAAGTCGAGTGCAGCCCTGGCTGGAATGGCGAACACTGCACCATCGC	2470
QY	2401	TCACTATCTGGATAGGGTAGTTAAAGAGGGTTGCCCTGGGTTGTGCAATGGCAACGGCAG	2460
Db	2471	TCACTATCTGGATAGGGTAGTTAAAGAGGGTTGCCCTGGGTTGTGCAATGGCAACGGCAG	2530
QY	2461	ATGTACCTTAGACCTGAATGGTTGGCACTGCGTCTGCCAGCTGGGCTGGAGAGGAGCTGG	2520
Db	2531	ATGTACCTTAGACCTGAATGGTTGGCACTGCGTCTGCCAGCTGGGCTGGAGAGGAGCTGG	2590
QY	2521	CTGTGACACTTCCATGGAGACTGCTTGCGGTGACAGCAAAGACAATGATGGAGATGGCCT	2580
Db	2591	CTGTGACACTTCCATGGAGACTGCTTGCGGTGACAGCAAAGACAATGATGGAGATGGCCT	2650
QY	2581	GGTGGACTGCATGGACCCCTGACTGCTGCTCCAGCCCCCTGTGCCATATCAACCCGCTGTG	2640
Db	2651	GGTGGACTGCATGGACCCCTGACTGCTGCTCCAGCCCCCTGTGCCATATCAACCCGCTGTG	2710
QY	2641	CCTTGGCTCCCTAAACCCCTCTGGACATCATCCAGGAGACACAGTCCCTGTGTACAGCA	2700
Db	2711	CCTTGGCTCCCTAAACCCCTCTGGACATCATCCAGGAGACACAGTCCCTGTGTACAGCA	2770
QY	2701	GAACCTACACTCCTTCTATGACCCGCATCAAGTTCCTCGTGGSCAGGGACAGCACGCACAT	2760
Db	2771	GAACCTACACTCCTTCTATGACCCGCATCAAGTTCCTCGTGGSCAGGGACAGCACGCACAT	2830
QY	2761	AATCCCCGGGAGAACCCCTTTGATGGAGGGCATGCTTGTGTATTTCGTGGCCAAAGTGAT	2820
Db	2831	AATCCCCGGGAGAACCCCTTTGATGGAGGGCATGCTTGTGTATTTCGTGGCCAAAGTGAT	2890
QY	2821	GACATCAGATGGAAACCCCTGGTTGGTGTGAACATCAGTTTGTCAATAACCCCTCTCTT	2880
Db	2891	GACATCAGATGGAAACCCCTGGTTGGTGTGAACATCAGTTTGTCAATAACCCCTCTCTT	2950
QY	2881	TGGATATACAATCAGCAGGCAAGATGGCAGCTTTGACTTGGTGACAAATGGCGGCATCTC	2940
Db	2951	TGGATATACAATCAGCAGGCAAGATGGCAGCTTTGACTTGGTGACAAATGGCGGCATCTC	3010
QY	2941	CATCATCCTGCGGTTGAGCGGGCACCTTTTCATCACACAGGAGCACACCTGTGGCTGCC	3000
Db	3011	CATCATCCTGCGGTTGAGCGGGCACCTTTTCATCACACAGGAGCACACCTGTGGCTGCC	3070
QY	3001	ATGGGATCGCTTCTTTGTCTATGGAAACCATCATCATGAGACATGAGGAGAAATGAGATTCC	3060
Db	3071	ATGGGATCGCTTCTTTGTCTATGGAAACCATCATCATGAGACATGAGGAGAAATGAGATTCC	3130
QY	3061	CAGCTGTGACCTGAGCAATTTTGCCCGCCCCAACCCAGTCGTCTCTCCATCCCCACTGAC	3120
Db	3131	CAGCTGTGACCTGAGCAATTTTGCCCGCCCCAACCCAGTCGTCTCTCCATCCCCACTGAC	3190
QY	3121	GTCCCTTGCAGCTCCTGTGCAGAGAAAGGCCCCCATTTGTGCGGAAATTCAGGCTTTGCA	3180
Db	3191	GTCCCTTGCAGCTCCTGTGCAGAGAAAGGCCCCCATTTGTGCGGAAATTCAGGCTTTGCA	3250
QY	3181	GGAGGAAATCTCTATCTCTGGCTGCAAGATGAGGCTGAGCTACCTGAGCAGCCGACCCC	3240
Db	3251	GGAGGAAATCTCTATCTCTGGCTGCAAGATGAGGCTGAGCTACCTGAGCAGCCGACCCC	3310
QY	3241	TGGCTACAAATCTGTCTCTGAGGATCAGCCTCACCCACCCGACCATCCCCCTTCAACCTCAT	3300
Db	3311	TGGCTACAAATCTGTCTCTGAGGATCAGCCTCACCCACCCGACCATCCCCCTTCAACCTCAT	3370
QY	3301	GAAGGTGCACCTCATTGTAGCGGTGGAGGGCCGCTCTTCAGGAAAGTGGTTCGCTGCAGC	3360
Db	3371	GAAGGTGCACCTCATTGTAGCGGTGGAGGGCCGCTCTTCAGGAAAGTGGTTCGCTGCAGC	3430
QY	3361	CCCAGACTGTCTCTATTATTTCATTTGGGACAAGACAGACGTCTACAACAGAAAGTGTT	3420
Db	3431	CCCAGACTGTCTCTATTATTTCATTTGGGACAAGACAGACGTCTACAACAGAAAGTGTT	3490
QY	3421	TGGGCTTTCAGAAGCCCTTTGTTTCGTGGGTTATGAATATGAATCTCTGCCAGATCTAAT	3480



Db 3491 TGGGCTTTCAGAAAGCCTTGTTCGTTGGTTATGAATATGAATCCTGCCAGATCTAAT 3550  
QY 3481 CCTGTGGGAAAAAAGAAACAACAGTCTGCAGGGCTATGAAATTGACGGTCCAAGCTTGG 3540  
Db 3551 CCTGTGGGAAAAAAGAAACAACAGTCTGCAGGGCTATGAAATTGATGGCTCCAAGCTTGG 3610  
QY 3541 AGGATGGAGCCTTAGACAAACATCATGCCCTCAACATTCAAAGTGGTATCCTGCACAAAGG 3600  
Db 3611 AGGATGGAGCCTTAGACAAACATCATGCCCTCAACATTCAAAGTGGCATCCTGCACAAAGG 3670  
QY 3601 GAATGGGGAGAACCAAGTTTGTCTCAGCAGCCTCCTGTCAATTGGGAGCATCATGGGCAA 3660  
Db 3671 GAATGGGGAGAACCAAGTTTGTCTCAGCAGCCTCCTGTCAATTGGGAGCATCATGGGCAA 3730  
QY 3661 TGGGGCCGGAGAAAGCATCTCCTGCCCCAGCTGCAACGGCCTTGTGACGGCAACAAGCT 3720  
Db 3731 TGGGGCCGGAGAAAGCATCTCCTGCCCCAGCTGCAACGGCCTTGTGACGGCAACAAGCT 3790  
QY 3721 CCTGGCCCCAGTGGCCCTCACCTGTGGCTCTGACGGGAGCCTCTATGTGGTGATTTCAA 3780  
Db 3791 CCTGGCCCCAGTGGCCCTCACCTGTGGCTCTGACGGGAGCCTCTATGTGGTGATTTCAA 3850  
QY 3781 CTACATTAGAAGGATCTTCCCCTCTCGAAATGTCAACCAACATCCTAGAGCTGAGGAATAA 3840  
Db 3851 CTACATTAGAAGGATCTTCCCCTCTCGAAATGTCAACCAACATCCTAGAGCTG----- 3902  
QY 3841 AGATTTCAGACATAGTCACAGTCCAGCACACAAATACTACCTGGCCACAGACCCCATGAG 3900  
Db 3903 -----AGTCACAGTCCAGCACACAAATACTACCTGGCCACAGACCCCATGAG 3949  
QY 3901 TGGGGCCGCTTTCCTTTCTGACAGCAACAGCCGGGGTCTTTAAATCAAGTCCACTGT 3960  
Db 3950 TGGGGCCGCTTTCCTTTCTGACAGCAACAGCCGGGGTCTTTAAATCAAGTCCACTGT 4009  
QY 3961 GGTGTTGAAGGACCTTGTCAAGAACTCTGAGGTGGTTGCGGGGACAGGTGACCAGTGCCT 4020  
Db 4010 GGTGTTGAAGGACCTTGTCAAGAACTCTGAGGTGGTTGCGGGGACAGGTGACCAGTGCCT 4069  
QY 4021 CCCCTTTGATGACACTCGCTGCGGGGATGGTGGGAAGGCCACAGAAGCCACACTCACCAA 4080  
Db 4070 CCCCTTTGATGACACTCGCTGCGGGGATGGTGGGAAGGCCACAGAAGCCACACTCACCAA 4129  
QY 4081 TCCCAGGGGTATTACAGTGGACAAGTTTGGGTGATCTACTTCGTGGATGGCACCATGAT 4140  
Db 4130 TCCCAGGGGCATTACAGTGGACAAGTTTGGGTGATCTACTTCGTGGATGGCACCATGAT 4189  
QY 4141 CAGACGCATCGATCAGAAATGGGATCATCTCCACCCCTGCTCGGCTCTAATGATCTCACATC 4200  
Db 4190 CAGACGCATCGATCAGAAATGGGATCATCTCCACCCCTGCTCGGCTCTAATGATCTCACATC 4249  
QY 4201 AGCCCCGGCCACTCAGCTGTGATTCTGTCAATGGATATTTCCCAGGTAAGACTGGAGTGGCC 4260  
Db 4250 AGCCCCGGCCACTCAGCTGTGATTCTGTCAATGGATATTTCCCAGGTTCACTGGAGTGGCC 4309  
QY 4261 CACAGACTTAGCCATCAACCCAATGGACAACTCACTTTATGTCTCGACAACAATGTGGT 4320  
Db 4310 CACAGACTTAGCCATCAACCCAATGGACAACTCACTTTATGTCTCGACAACAATGTGGT 4369  
QY 4321 CCTGCAAAATCTGTGAAAAACACACAGGTGCGCATTTGTCGGGGAGGCCCATGCACTGCCA 4380  
Db 4370 CCTGCAAAATCTGTGAAAAACACACAGGTGCGCATTTGTGCGGGAGGCCCATGCACTGCCA 4429  
QY 4381 GGTCCCTGGCATTTGACCACTTCTGTCTAAGCAAGGTGGCCATCCACGCAACCTGGAGTGC 4440  
Db 4430 GGTCCCTGGCATTTGACCACTTCTGTCTAAGCAAGGTGGCCATCCACGCAACCTGGAGTGC 4489  
QY 4441 AGCCACCGCTTTGGCTGTTTCACACAAATGGGGTCCGTATATTGCTGAGACTGATGAGAA 4500  
Db 4490 AGCCACCGCTTTGGCTGTTTCACACAAATGGGGTCCGTATATTGCTGAGACTGATGAGAA 4549  
QY 4501 AAGATCAACCGCATCAGGCAGGTCAACCCTAGTGGAGAGATCTCACTCGTTGCTGGGGC 4560

Db 4550 AAGATCAACCGCATCAGGCAGGTCAACCCTAGTGGAGAGATCTCACTCGTTGCTGGGC 4609  
QY 4561 CCCAGTGGCTGTGACTGTAAAAATGATGCCAACTGTGATTGTTTTTCTGGAGACGATGG 4620  
Db 4610 CCCAGTGGCTGTGACTGTAAAAATGATGCCAACTGTGATTGTTTTTCTGGAGACGATGG 4669  
QY 4621 TTATGCCAAGGATGCAAAAGTTAAATACCCCATCTTCCTTGGCTGTGTGCTGATGGGA 4680  
Db 4670 TTATGCCAAGGATGCAAAAGTTAAATACCCCATCTTCCTTGGCTGTGTGTTGATGGGA 4729  
QY 4681 GCTCTACGTGGCCGACCTTGGGAACATCCGAATTCGGTTTATCCGGGAAGAACAAAGCCTTT 4740  
Db 4730 GCTCTACGTGGCCGACCTTGGGAACATCCGAATTCGGTTTATCCGGGAAGAACAAAGCCTTT 4789  
QY 4741 CCTCAACACCCAGAACATGTATGAGCTGTCTTTCACCAATTGACAGGAGCTCTATCTGTT 4800  
Db 4790 CCTCAACACCCAGAACATGTATGAGCTGTCTTTCACCAATTGACAGGAGCTCTATCTGTT 4849  
QY 4801 TGATACCAACCGGCAAGCACCTGTACACCCCAAGCCTGCCACAGGAGACTACCTGTACAA 4860  
Db 4850 TGATACCAACCGGCAAGCACCTGTACACCCCAAGCCTGCCACAGGAGACTACCTGTACAA 4909  
QY 4861 CTTCACTTACACTCTGGGACGGGACATCACTCATCACAGACAACAATGGCAACATGGT 4920  
Db 4910 CTTCACTTACACTCTGGGACGGGACATCACTCATCACAGACAACAATGGCAACATGGT 4969  
QY 4921 AAATGTCGCGCCGAGACTCTACTGGGATGCCCTCTGGCTGGTGGTCCCAGATGGCCAGGT 4980  
Db 4970 AAATGTCGCGCCGAGACTCTACTGGGATGCCCTCTGGCTGGTGGTCCCAGATGGCCAGGT 5029  
QY 4981 GTACTGGGTGACCATGGGCACCACAGTGCACCTCAAGAGTGTGACCAACAAGGACACGA 5040  
Db 5030 GTACTGGGTGACCATGGGCACCACAGTGCACCTCAAGAGTGTGACCAACAAGGACACGA 5089  
QY 5041 GTTGGCCATGATGACATACCATGGCAATTCCGGCCTTCTGGCAACCAAAAGCAATGAAA 5100  
Db 5090 GTTGGCCATGATGACATACCATGGCAATTCCGGCCTTCTGGCAACCAAAAGCAATGAAA 5149  
QY 5101 CGGATGGACAACATTTTATGAGTACGACAGCTTTGGCCGCTTGACAAATGTGACCTTCCC 5160  
Db 5150 CGGATGGACAACATTTTATGAGTACGACAGCTTTGGCCGCTTGACAAATGTGACCTTCCC 5209  
QY 5161 TACTGGCCAGGTGAGCAGTTTCCGAAGTGATACAGACAGTTCAGTGCATGTCCAGGTAGA 5220  
Db 5210 TACTGGCCAGGTGAGCAGTTTCCGAAGTGATACAGACAGTTCAGTGCATGTCCAGGTAGA 5269  
QY 5221 GACCTCCAGCAAGGATGATGTCAACATAACCAACCTGTCTGCCTCAGGCGCCTTCTA 5280  
Db 5270 GACCTCCAGCAAGGATGATGTCAACATAACCAACCACTGTCTGCCTCAGGCGCCTTCTA 5329  
QY 5281 CACACTGCTGCAAGACCAAGTCCGGAACAGCTACTACATCGGGGCCGATGGCTCTTGCG 5340  
Db 5330 CACACTGCTGCAAGACCAAGTCCGGAACAGCTACTACATCGGGGCCGATGGCTCTTGCG 5389  
QY 5341 GCTGCTGTGGCCAAACGGCATGGAGTGGCGCTGCAGACTGAGCCCCACTTGCTGGCTGG 5400  
Db 5390 GCTGCTGTGGCCAAACGGCATGGAGTGGCGCTGCAGACTGAGCCCCACTTGCTGGCTGG 5449  
QY 5401 CACCGTCAACCCCAACCGTGGGCAAGAGGAATGTCAAGTGCCTGAGCCCCACTTGCTGGCTGG 5460  
Db 5450 CACCGTCAACCCCAACCGTGGGCAAGAGGAATGTCAAGTGCCTGAGCCCCACTTGCAACCGCCTCAA 5509  
QY 5461 CCTGGTGGAGTGGCCGACGCAAGAGCAGGCTCGGGCCAGGTCACTGTCTTGGGCG 5520  
Db 5510 CCTGGTGGAGTGGCCGACGCAAGAGCAGGCTCGGGCCAGGTCACTGTCTTGGGCG 5569  
QY 5521 CCGGCTGCGGTGCACAAACCGAAATCTCCTATCTCTGGACTTTTGATCGCGTAACACGCAC 5580  
Db 5570 CCGGCTGCGGTGCACAAACCGAAATCTCCTATCTCTGGACTTTTGATCGCGTAACACGCAC 5629  
QY 5581 AGAGAAGATCTATGATGACCAACCGCAAGTTCACCTTCGGATTCGTACGACCAAGGCGGG 5640  
Db 5630 AGAGAAGATCTATGATGACCAACCGCAAGTTCACCTTCGGATTCGTACGACCAAGGCGGG 5689



QY	5641	GCGGCCAGCCTCTGGTCACCCAGCAGCAGGCTGAATGGTGTCAACGTGACATACTCCCC	5700
Db	5690	GCGGCCAGCCTCTGGTCACCCAGCAGCAGGCTGAATGGTGTCAACGTGACATACTCCCC	5749
QY	5701	TGGGGTTACATTGCTGGCATCCAGAGGGGCATCATGTCTGAAAGAAATGGAATACGACCA	5760
Db	5750	TGGGGTTACATTGCTGGCATCCAGAGGGGCATCATGTCTGAAAGAAATGGAATACGACCA	5809
QY	5761	GCGGGCCGCATCACATCCAGGATCTTCGCTGATGGGAAGACATGGAGCTACACATACTT	5820
Db	5810	GCGGGCCGCATCACATCCAGGATCTTCGCTGATGGGAAGACATGGAGCTACACATACTT	5869
QY	5821	AGAGAAGTCCATGGTGTCTGTACTACACAGCCAGAGGCGAGTATATCTTTTGAGTTCGACAA	5880
Db	5870	AGAGAAGTCCATGGTGTCTGTACTACACAGCCAGAGGCGAGTATATCTTTTGAGTTCGACAA	5929
QY	5881	GAATGACCGCCTCTCTTCTGTGTGACGATGCCCAAACGTGGCGCGGCAGACACTAGAGACCAT	5940
Db	5930	GAATGACCGCCTCTCTTCTGTGTGACGATGCCCAAACGTGGCGCGGCAGACACTAGAGACCAT	5989
QY	5941	CCGCTCAGTGGGCTACTACAGAAACATCTATCAGCCCCCTGAGGGCAATGCCTCAGTCAT	6000
Db	5990	CCGCTCAGTGGGCTACTACAGAAACATCTATCAGCCCCCTGAGGGCAATGCCTCAGTCAT	6049
QY	6001	ACAGGACTTCACGTAGGATGGGCACCTCCTTCACACCTTCTACCTTGGGCACGTGGCGCAG	6060
Db	6050	ACAGGACTTCACGTAGGATGGGCACCTCCTTCACACCTTCTACCTTGGGCACGTGGCGCAG	6109
QY	6061	GGTGATATACAAGTATGGCAAACCTGTCAAAGCTGGCAGAGACGCTCTATGACACCAACCAA	6120
Db	6110	GGTGATATACAAGTATGGCAAACCTGTCAAAGCTGGCAGAGACGCTCTATGACACCAACCAA	6169
QY	6121	GGTCAGTTTCACCTATGACGAGACGGCAGGCATGCTGGAAGACCATCAACCTACAGAAATGA	6180
Db	6170	GGTCAGTTTCACCTATGACGAGACGGCAGGCATGCTGGAAGACCATCAACCTACAGAAATGA	6229
QY	6181	GGGCTTCACCTGCACCATCCGCTACCGTCAGATTGGGCCCTGATTGACCGACAGATCTT	6240
Db	6230	GGGCTTCACCTGCACCATCCGCTACCGTCAGATTGGGCCCTGATTGACCGACAGATCTT	6289
QY	6241	CCGCTTCACCTGAGGAAGGCATGGTCAACGCCCGTTTTTGACTACAACTATGACAAACGCTT	6300
Db	6290	CCGCTTCACCTGAGGAAGGCATGGTCAACGCCCGTTTTTGACTACAACTATGACAAACGCTT	6349
QY	6301	CCGGGTGACCAGCATGCAGGCTGTGATCAACGAGACCCCACTGCCATTGATCTCTATCG	6360
Db	6350	CCGGGTGACCAGCATGCAGGCTGTGATCAACGAGACCCCACTGCCATTGATCTCTATCG	6409
QY	6361	CTATGATGATGTGTCAAGCAAGACAGAGCAGTTTGGGAAGTTTGGTGTCAATTTACTATGA	6420
Db	6410	CTATGATGATGTGTCAAGCAAGACAGAGCAGTTTGGGAAGTTTGGTGTCAATTTACTATGA	6469
QY	6421	CATTAAACCAGATCATCACCACAGCTGTATGACCCACACCAAGCATTTTGTATGCAATATGG	6480
Db	6470	CATTAAACCAGATCATCACCACAGCTGTATGACCCACACCAAGCATTTTGTATGCAATATGG	6529
QY	6481	CAGGTGAAGGAAGTGCAGTATGAGATCTTCCGCTCGCTCATGTACTGGATGACCGTCCA	6540
Db	6530	CAGGTGAAGGAAGTGCAGTATGAGATCTTCCGCTCGCTCATGTACTGGATGACCGTCCA	6589
QY	6541	GTATGATAACATGGGGCGAGTAGTGAAGGAAGGAGCTGAAGGTAGGACCCCTACGCCAATAC	6600
Db	6590	GTATGATAACATGGGGCGAGTAGTGAAGGAAGGAGCTGAAGGTAGGACCCCTACGCCAATAC	6649
QY	6601	CACCTCGTACTCCTATGAGTATGATGTGACGGCCAGCTGCAGACAGTCTCCATCAATGA	6660
Db	6650	CACCTCGTACTCCTATGAGTATGATGTGACGGCCAGCTGCAGACAGTCTCCATCAATGA	6709
QY	6661	CAAGCCACTCTGGCGCTACAGCTACGACCTCAATGGGAACCTGCACCTTACTGAGCCCTGG	6720
Db	6710	CAAGCCACTCTGGCGCTACAGCTACGACCTCAATGGGAACCTGCACCTTACTGAGCCCTGG	6769

QY	6721	GAACAGTGCACGGCTCACACCACCTACGGTATGACATCCGCGACCCGATCACTCGGCTGGG	6780
Db	6770	GAACAGTGCACGGCTCACACCACCTACGGTATGACATCCGCGACCCGATCACTCGGCTGGG	6829
QY	6781	TGACGTGCAATACAAGATGGATGAGGATGGCTTCTTGAGGCAGCGGGCGGTGATATCTT	6840
Db	6830	TGACGTGCAATACAAGATGGATGAGGATGGCTTCTTGAGGCAGCGGGCGGTGATATCTT	6889
QY	6841	TGAGTACAACTCAGCTGGCCTGCTCATCAAGGCCTACAACCGGGCTGGCAGCTGGAGTGT	6900
Db	6890	TGAGTACAACTCAGCTGGCCTGCTCATCAAGGCCTACAACCGGGCTGGCAGCTGGAGTGT	6949
QY	6901	CAGGTACCGCTACGATGGCCTGGGGCGGCGGTGTCCAGCAAGAGCAGCCACAGCCACCA	6960
Db	6950	CAGGTACCGCTACGATGGCCTGGGGCGGCGGTGTCCAGCAAGAGCAGCCACAGCCACCA	7009
QY	6961	CCTGCAGTTCCTTCTATGCAGACCTGACCAACCCACCAAGGTCAACCCTGTACAACCA	7020
Db	7010	CCTGCAGTTCCTTCTATGCAGACCTGACCAACCCACCAAGGTCAACCCTGTACAACCA	7069
QY	7021	CTCCAGCTCTGAGATCACCTCCCTCTACTAGACCTTGCAAGGACACCTCTTTGCCATGGA	7080
Db	7070	CTCCAGCTCTGAGATCACCTCCCTCTACTACGACTTGCAAGGACACCTCTTTGCCATGGA	7129
QY	7081	GCTGAGCAGTGSTGATGAGTTTACATAGCTTTGTGACAAACATCGGGACCCCTCTTGCTGT	7140
Db	7130	GCTGAGCAGTGSTGATGAGTTTACATAGCTTTGTGACAAACATCGGGACCCCTCTTGCTGT	7189
QY	7141	CTTTAGTGGAAACAGGTTTGATGATCAAGCAAATCCTGTACACAGCCCTATGGGAGATCTA	7200
Db	7190	CTTTAGTGGAAACAGGTTTGATGATCAAGCAAATCCTGTACACAGCCCTATGGGAGATCTA	7249
QY	7201	CATGGATACCAACCCCAAACCTTTCAGATCATCATAGGCTACCATGGTGGCCTCTATGATCC	7260
Db	7250	CATGGATACCAACCCCAAACCTTTCAGATCATCATAGGCTACCATGGTGGCCTCTATGATCC	7309
QY	7261	ACTCACCAAGCTTGTCCACATGGGCCGGCGAGATTATGATGTGTGGCCGACGCTGGAC	7320
Db	7310	ACTCACCAAGCTTGTCCACATGGGCCGGCGAGATTATGATGTGTGGCCGACGCTGGAC	7369
QY	7321	TAGCCCAGACCCAGAGCTGTGGAAGCACCTTAGTAGCAGCAACGTCATGCTTTTAATCT	7380
Db	7370	TAGCCCAGACCCAGAGCTGTGGAAGCACCTTAGTAGCAGCAACGTCATGCTTTTAATCT	7429
QY	7381	CTATATGTTCAAAAAACAACACCCCATCAGCAACTCCAGGACATCAAGTCTTCATGAC	7440
Db	7430	CTATATGTTCAAAAAACAACACCCCATCAGCAACTCCAGGACATCAAGTCTTCATGAC	7489
QY	7441	AGATGTTAACAGCTGGTGCTCACCTTTGGATTCCAGCTACACAACGTCATCCCTGGTTA	7500
Db	7490	AGATGTTAACAGCTGGTGCTCACCTTTGGATTCCAGCTACACAACGTCATCCCTGGTTA	7549
QY	7501	TCCCAAAACAGACATGGATGCCATGGAAACCTTCCTACGAGCTCATCCACACAGATGAA	7560
Db	7550	TCCCAAAACAGACATGGATGCCATGGAAACCTTCCTACGAGCTCATCCACACAGATGAA	7609
QY	7561	AACGCAGGAGTGGACAAACAGCAAGTCTATTCCTCGGGGTACAGTGTGAAGTACAGAAATGA	7620
Db	7610	AACGCAGGAGTGGACAAACAGCAAGTCTATTCCTCGGGGTACAGTGTGAAGTACAGAAATGA	7669
QY	7621	GCTCAAGGCCCTTTGTACCTTAGAAACGGTTTGTGACCAAGCTCTATGGCTCCCAATCACCAG	7680
Db	7670	GCTCAAGGCCCTTTGTACCTTAGAAACGGTTTGTGACCAAGCTCTATGGCTCCCAATCACCAG	7729
QY	7681	CTGCCAGCAGGCTCCAAAGACCAAGAAAGTTTGCATCCAGCGGCTCAGTCTTTGGCAAGGG	7740
Db	7730	CTGCCAGCAGGCTCCAAAGACCAAGAAAGTTTGCATCCAGCGGCTCAGTCTTTGGCAAGGG	7789
QY	7741	GGTCAAGTTTGCCTTGAAGGATGGCCGAGTGACCAAGACATCATCAGTGTGGCCCAATGA	7800
Db	7790	GGTCAAGTTTGCCTTGAAGGATGGCCGAGTGACCAAGACATCATCAGTGTGGCCCAATGA	7849
QY	7801	GGATGGGCGAAGGGTTGTGCCATCTTTGAACCATGCCCACTACCTAGAGAACCTGCACCTT	7860

Db 7850 GGATGGGCGAAGGGTTGCTGCCATCTTGAACCATGCCCACTACCTAGAGAACCTGCACCTT 7909

QY 7861 CACCAATTGATGGGTGGATACCCATTACTTTGTGAACACGAGGACCTTTCAGAAGGTGACCT 7920

Db 7910 CACCAATTGATGGGTGGATACCCATTACTTTGTGAACACGAGGACCTTTCAGAAGGTGACCT 7969

QY 7921 GGCCATCCTGGGCCTCAGTGGGGCGGCGCAACCTGGAGAAATGGGTCAACGTCACTGT 7980

Db 7970 GGCCATCCTGGGCCTCAGTGGGGCGGCGCAACCTGGAGAAATGGGTCAACGTCACTGT 8029

QY 7981 GTCCCAGATCAACACAGTACTTAATGGCAGGACTAGACGCTACACAGACATCCAGCTCCA 8040

Db 8030 GTCCCAGATCAACACAGTACTTAATGGCAGGACTAGACGCTACACAGACATCCAGCTCCA 8089

QY 8041 GTACGGGGCACTGTGCTTGAACACACGCTACGGGACAACGTTGGATGAGGAGAAGGCACG 8100

Db 8090 GTACGGGGCACTGTGCTTGAACACACACGCTACGGGACAACGTTGGATGAGGAGAAGGCACG 8149

QY 8101 GGTCTGGAGCTGGCCCGGCAGAGAGCCGTGGCCCAAGCGTGGGCCCGGCAGCAGAG 8160

Db 8150 GGTCTGGAGCTGGCCCGGCAGAGAGCCGTGGCCCAAGCGTGGGCCCGGCAGCAGAG 8209

QY 8161 ACTCGGGGAAGGGAGGAAGGCCTCGGGCCTGGACAGAGGGGGAGAGCAGGTGCT 8220

Db 8210 ACTCGGGGAAGGGAGGAAGGCCTCGGGCCTGGACAGAGGGGGAGAGCAGGTGCT 8269

QY 8221 GAGCACAGGGCGGTGCAAGGCTACGACGGCTTTTCGTGATCTCTGTCCAGCAGTACCC 8280

Db 8270 GAGCACAGGGCGGTGCAAGGCTACGACGGCTTTTCGTGATCTCTGTCCAGCAGTACCC 8329

QY 8281 AGAACTGTCAGACAGCGCCCAACAACATCCACTTCATGAGACAGAGCGAGATGGGCCGGAG 8340

Db 8330 AGAACTGTCAGACAGCGCCCAACAACATCCACTTCATGAGACAGAGCGAGATGGGCCGGAG 8389

QY 8341 GTGACAGAGAGGAC 8354

Db 8390 GTGACAGAGAGGAC 8403

RESULT 4

ADF74841

ID ADF74841 standard; cDNA; 8355 BP.

XX

AC ADF74841;

XX

DT 26-FEB-2004 (first entry)

XX

DE Murine NOVX cDNA to treat human pathological conditions (SeqID 55).

XX

KW gene; ss; mouse; murine; NOVX; metabolic disorder; diabetes; anorexia;

KW cancer; cardiovascular; infectious; neurodegenerative; immune;

KW haematopoietic disease; dyslipidaemia; anorectic; virucide; nootropic;

KW antiinflammatory; neuroprotective; antilipaeamic; anabolic; cardiant;

KW neurogenesis; wound healing; angiogenesis; chromosome mapping;

XX tissue typing; preventive medicine; pharmacogenomic.

OS Mus musculus.

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PN WO2003076578-A2.

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PD 18-SEP-2003.

XX

PF 06-MAR-2003; 2003WO-US006794.

XX

PR 06-MAR-2002; 2002US-0361974P.

PR 08-MAR-2002; 2002US-00093463.

PR 08-MAR-2002; 2002WO-US007288.

PR 15-MAR-2002; 2002US-0365034P.

PR 19-MAR-2002; 2002US-0365477P.

PR 20-MAR-2002; 2002US-0365884P.

PR 20-MAR-2002; 2002US-0365984P.

PR 20-MAR-2002; 2002US-0365985P.

PR 22-MAR-2002; 2002US-0366928P.

PR 12-APR-2002; 2002US-0372018P.

PR 12-APR-2002; 2002US-0372022P.

PR 23-APR-2002; 2002US-0374682P.

PR 12-JUN-2002; 2002US-0388096P.

PR 14-JUN-2002; 2002US-0389143P.

PR 26-JUN-2002; 2002US-0391779P.

PR 15-AUG-2002; 2002US-0403743P.

PR 13-SEP-2002; 2002US-0410755P.

PR 23-SEP-2002; 2002US-0412957P.

PR 22-OCT-2002; 2002US-0420382P.

PR 05-MAR-2003; 2003US-00420382.

XX

PA (CURA-) CURAGEN CORP.

XX

PI Alsobrook JP, Anderson DW, Boldog FL, Burgess CE, Chaudhuri A;

PI Colman SD, Edinger SR, Ettenberg S, Gangolli EA, Gerlach VL;

PI Gorman L, Guo X, Kekuda R, Li L, MacLachlan T, Malyankar UM;

PI Mezes PS, Miller CE, Millet I, Padigar M, Patturajan M, Peyman J;

PI Qian X, Rastelli L, Rieger DK, Smithson G, Spytek KA, Stone DJ;

PI Sukumaran S, Vernet CAM, Voss EZ, Zhong M;

XX

DR WPI; 2003-697890/66.

DR P-PSDB; ADF74842.

XX

PT New isolated NOVX polypeptides and polynucleotides, useful for

PT preventing, diagnosing or treating NOVX-associated disorders, e.g.

PT osteoarthritis, obesity, atherosclerosis, cancer, Parkinson's disease,

PT asthma, or infections.

XX

PS Claim 20; SEQ ID NO 55; 282pp; English.

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CC This invention relates to a novel nucleic acids, and encoded polypeptides

CC thereof, which have properties related to the stimulation of biochemical

CC or physiological responses in a cell, tissue, organ or organism.

CC Specifically, it refers to the use of biologically active fragments for

CC diagnostic and prognostic assays and furthermore in the treatment of

CC diverse pathological conditions. The present invention describes novel

CC human and murine NOVX proteins, as well as methods to modulate their

CC expression using antisense oligos, ribozymes and peptide nucleic acids.

CC The polypeptides, nucleic acid molecules and antibodies are useful in the

CC manufacture of a medicament for treating metabolic disorders, diabetes,

CC anorexia, cancer, cardiovascular, infectious, neurodegenerative, immune

CC and haematopoietic diseases as well as various dyslipidaemias.

CC Accordingly, these molecules have many activities including anorectic,

CC virucide, nootropic, antiinflammatory, neuroprotective, antilipaeamic,

CC anabolic and cardiant. Furthermore, they are useful in screening assays

CC to identify small molecules that modulate or inhibit, for example,

CC neurogenesis, wound healing and angiogenesis. The nucleic acids are also

CC used as in chromosome mapping, tissue typing, preventive medicine and

CC pharmacogenomics. This polynucleotide is a murine NOVX cDNA of the

CC invention.

XX

SQ Sequence 8355 BP; 1967 A; 2450 C; 2260 G; 1678 T; 0 U; 0 Other;

Query Match 95.7%; Score 7991.2; DB 10; Length 8355;

Best Local Similarity 98.3%; Pred.No. 0;

Matches 8248; Conservative 0; Mismatches 18; Indels 126; Gaps 12;

QY 35 ATGGACGTGAAGGAGAGGAAGCCTTACCGTCGCTGACCCGGCGCGGACCGCGCGC 94

Db 1 ATGGACGTGAAGGAGAGGAAGCCTTACCGTCGCTGACCCGGCGCGCGGACCGCGC 60

QY 95 CGCTACACCAAGCTCGTCCGCGGACAGCGAGAGGGCAAAGCCCCGAGAAATCGTACAGC 154

Db 61 CGCTACACCAAGCTCGTCCGCGGACAGCGAGAGGGCAAAGCCCCGAGAAATCGTACAGC 120

QY 155 TCCAGCGGAGACCTGAAGGCTACGACCAAGGACCGCCCGCTAGCCTATGCGAGCCGCGTC 214

Db 121 TCCAGCGGAGACCTGAAGGCTACGACCAAGGACCGCCCGCTAGCCTATGCGAGCCGCGTC 180

QY 215 AAGGACATTGTGCCGAGGAGCGGAGGAATTCTGCCGACAGGTGCCAACTTCACCCCTG 274



Db 181 AAGGACATTGTGCCGAGAGGCCGAGGAATTCTGCGGCACAGGTGCCAACTTCACCCCTG 240

QY 275 CGGGAGCTGGGGCTGGAAGAGTAACGCCCCCTCACGGGACCCCTGTACCGGACAGACATT 334

Db 241 CGGGAGCTGGGGCTGGAAGAGTAACGCCCCCTCACGGGACCCCTGTACCGGACAGACATT 300

QY 335 GGCCTGCCCAATGCGGCTACTCCATGGGGGCTGGCTCTGATGCCGACATGGAGGCTGAC 394

Db 301 GGCCTCCCCACTGCGGCTACTCCATGGGGGCTGGCTCTGATGCCGACATGGAGGCTGAC 360

QY 395 ACGGTGCTGTCCCTTGAGCA CCCCGTGCGTCTGTGGGGCCGGAGCACACGGTCAGGGCGC 454

Db 361 ACGGTGCTGTCCCTTGAGCACCCCGTGCGTCTGTGGGGCCGGAGCACACGGTCAGGGCGC 420

QY 455 AGTCTGTGCTGTCCAGCCGGGCCAATTCCAATCTCACACTCACCGACCCGAGCATGAA 514

Db 421 AGTCTGTGCTGTCCAGCCGGGCCAATTCCAATCTCACACTCACCGACCCGAGCATGAA 480

QY 515 AACACTGAGACTGATCATCCGGGGGCTGCAGAACCCAGCGCGCTCCGGACCGCCCG 574

Db 481 AACACTGAGACTGATCATCCGGGGGCTGCAGAACCCAGCGCGCTCCGGACCGCCCG 540

QY 575 CCGCGCTCTGCA CGCCCAACCCCAACAGCACCCAGCGGCTCCATTAACTCCCTG 634

Db 541 CCGCGCTCTGCA CGCCCAACCCCAACAGCACCCAGCGGCTCCATTAACTCCCTG 600

QY 635 AACCGGGCAACTTCACGCGGAGGAGCAACCCAGCCCCGGCCCCCA CGGACCACTGCTC 694

Db 601 AACCGGGCAACTTCACGCGGAGGAGCAACCCAGCCCCGGCCCCCA CGGACCACTGCTC 660

QY 695 TCCGAGAGCCCCCTG CCGGGCGGCCAGGAGCCTGCCACGCCCAAGGAACTGGCTG 754

Db 661 TCCGAGAGCCCCCTG CCGGGCGGCCAGGAGCCTGCCACGCCCAAGGAACTGGCTG 720

QY 755 CTCACAGCAACATCCCCCTGGAGACCAGGAACCTAGGCAAGCAGCCATTCTTAGGGACA 814

Db 721 CTCACAGCAACATCCCCCTGGAGACCAGGAACCTAGGCAAGCAGCCATTCTTAGGGACA 780

QY 815 TTGCAGGCAACCTCATTTAGATGGACATTCTCGGCGCTCCCGCCATGATGGGCTTAC 874

Db 781 TTGCAGGCAACCTCATTTAGATGGACATTCTCGGCGCTCCCGCCATGATGGGCTTAC 840

QY 875 AGTGACGGGCACTTCCTCTTCAAGCCTGGAGGCACCTCCCGCTCTTCTGCACCAATCA 934

Db 841 AGTGACGGGCACTTCCTCTTCAAGCCTGGAGGCACCTCCCGCTCTTCTGCACCAATCA 900

QY 935 CCAGGCTACCCACTGACGCTCCAGCACAGTGTA CTCTCTCCGCCCCGACCCCTGCCCCGC 994

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QY 1055 TCGGAGCCCTGAGCGCCATCGTCACTCTCAGCCACTCTGGTCACTCTGTGGCATACTTT 1114

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Db 1735 TGCCACTGCTTCTGGGTTTCTTGGGCCCGACTGTGGCAGAGCCTCCTGCCCCCGTGCTC 1794

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QY 1895 GCTGAGTGCCATGTGCCCA CCAACAGTGTATCGATGTGGCCTGCAGCAACCATGGCAC 1954

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QY 1955 TGCATCACGGGCACCTGCATCTGCAACCTTGGCTACAAGGGCGAGACTGTGAGGAAAGT 2014

Db 1915 TGCATCACGGGCACCTGCATCTGCAACCTTGGCTACAAGGGCGAGACTGTGAGGAA- - - 1971

QY 2015 GACTGCATGGACCCCA CATGTTTCAAGCGGGGTGTCTGCTGAGAGCGAATGCCATTGC 2074

Db 1972 GACTGCATGGACCCCA CATGTTTCAAGCGGGGTGTCTGCTGAGAGCGAATGCCACTGC 2031

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QY 2135 TCAGGCCACGGAACCTTCTCTCCCGGACACCGGGCTTTGCAGCTGTGACCCCAAGCTGGACT 2194

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RESULT 5  
ABN85378

ID ABN85378 standard; DNA; 8438 BP.

XX AC ABN85378;

XX DT 21-OCT-2002 (first entry)

XX Human NOV1, TEN-M4 like protein, coding sequence.

DE Human; NOV1; cytostatic; Cardiant; Antiinflammatory; Immunosuppressive;  
XX Antiallergic; Haemostatic; Anti-HIV; Antidiabetic; Anorectic;  
KW Antiasthmatic; Nephrotropic; Hepatotropic; Neuroprotective; Nootropic;  
KW Antibacterial; Virucide; Antiparasitic; Relaxant; Anticonvulsant;  
KW Gene Therapy; NOV; cancer; heart disease; inflammation;  
KW autoimmune disorder; allergy; blood disorder; AIDS; diabetes; obesity;  
KW asthma; IgA nephropathy; cirrhosis; arthritis; Alzheimer's disease;  
KW infection; stroke; muscular dystrophy; epilepsy; wasting disorder;  
KW TEN-M4 like protein; chromosome 11; gene; ds.

XX Homo sapiens.

XX Key Location/Qualifiers  
CDS 4..8395

FT /\*tag= a  
FT /trans except= (pos: 1138..1147,aa:Met)  
FT /product= "NOV1 protein"

XX WO200255704-A2.

PD 18-JUL-2002.

XX 09-JAN-2002; 2002WO-US000554.

XX 09-JAN-2001; 2001US-0260417P.

PR 10-JAN-2001; 2001US-0260831P.

PR 28-FEB-2001; 2001US-0272338P.





QY 1645 AATCTGGCACTTGGCTTTTACAATGACGGAAAGGAGTCAAGAGTGGTTTCCTTTCTCAC 1704  
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Db 1621 AATCTGGCACTTGGCTTTTACAATGACGGAAAGGAGTCAAGAGTGGTTTCCTTTCTCAC 1680  
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QY 1945 CCATGGCACCTGCATCAGCGGCACCTGCATCTGCAACCCTGGCTACAAAGSGGAGAGCTG 2004  
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QY 3253 TGTCTGAGGATCAGCCTCACCCACCCAGCATCCCCTTCAACCTCATGAAGGTGACACT 3312  
|||||  
Db 3232 TGTCTGAGGATCAGCCTCACCCACCCAGCATCCCCTTCAACCTCATGAAGGTGACACT 3291  
|||||  
QY 3313 CATGGTAGCGGTGGAGGGCGCCTCTTTCAGGAAGTGGTTCGCTGCAGCCCCCAGACCTGTC 3372  
|||||  
Db 3292 CATGGTAGCGGTGGAGGGCGCCTCTTTCAGGAAGTGGTTCGCTGCAGCCCCCAGACCTGTC 3351  
|||||  
QY 3373 CTATTATTTCAATTGGGACAAGACAGACGCTCTAACACCAGAGGTGTTTGGGCTTTTCTCAGA 3432  
|||||  
Db 3352 CTATTATTTCAATTGGGACAAGACAGACGCTCTAACACCAGAGGTGTTTGGGCTTTTCTCAGA 3411  
|||||  
QY 3433 AGCCTTTGTTCCGTGGGTTATGAATATGAATCTCTGCCAGATCTAATCTCTGTGGGAAAA 3492  
|||||  
Db 3412 AGCCTTTGTTCCGTGGGTTATGAATATGAATCTCTGCCAGATCTAATCTCTGTGGGAAAA 3471  
|||||  
QY 3493 AAGAACAAACAGTGTGCAGGGCTATGAAATFGACGCTCCTCAAGCTTGGAGATGGAGCCT 3552  
|||||  
Db 3472 AAGAACAAACAGTGTGCAGGGCTATGAAATFGACGCTCCTCAAGCTTGGAGATGGAGCCT 3531  
|||||  
QY 3553 AGACAAAACATCATGCCCTCAACATTTCAAAGTGGTGGCATCTCTGCACAAAGGGAATGGGGA 3609  
|||||  
Db 3532 AGACAAAACATCATGCCCTCAACATTTCAAAGTGGTGGCATCTCTGCACAAAGGGAATGGGGA 3591  
|||||  
QY 3610 GAACCAAGTTTGTCTCAGCAGCCTCCTGTTCATTTGGGAGCATCATGGGCAATGGGCGCCG 3669  
|||||  
Db 3592 GAACCAAGTTTGTCTCAGCAGCCTCCTGTTCATTTGGGAGCATCATGGGCAATGGGCGCCG 3651  
|||||  
QY 3670 GAGAAAGCATCTCTTGCCCCCAGCTGCAACCGGCTTCTGTACGGCAACAGCTCTGGCCCCC 3729  
|||||  
Db 3652 GAGAAAGCATCTCTTGCCCCCAGCTGCAACCGGCTTCTGTACGGCAACAGCTCTGGCCCCC 3711  
|||||  
QY 3730 AGTGGCCCTCACCTGTGGCTCTGACGGGAGCCTCTATGTGGGTGATTTCAACTACATTAG 3789  
|||||  
Db 3712 AGTGGCCCTCACCTGTGGCTCTGACGGGAGCCTCTATGTGGGTGATTTCAACTACATTAG 3771  
|||||  
QY 3790 AAGGATCTTCCCCCTCTTGGAAATGTCAACCAACATCTTAGAGCTGAGG-----AATAAAGA 3843  
|||||



Db 3772 AAGGATCTTCCCTCTGGAAATGTCACCAACATCCTAGAGCTGAGGCTCAGAAATAAAGA 3831

Qy 3844 TTTTCAGACATAGTCACAGTCCAGCACACAATACTACCTGGCCACAGACCCCATGAGTGG 3903

Db 3832 TTTTCAGACATAGTCACAGTCCAGCACACAATACTACCTGGCCACAGACCCCATGAGTGG 3891

Qy 3904 GGCCGCTCTTCCTTTCTGACAGCAACAGCCGGCGGGTCTTTTAAATCAAGTCCACTGTGGT 3963

Db 3892 GGCCGCTCTTCCTTTCTGACAGCAACAGCCGGCGGGTCTTTTAAATCAAGTCCACTGTGGT 3951

Qy 3964 GGTGAAGGACCTTGTCAAGAACTCTGAGGTGGTTGCGGGACAGGTGACCAAGTGCCTCCC 4023

Db 3952 GGTGAAGGACCTTGTCAAGAACTCTGAGGTGGTTGCGGGACAGGTGACCAAGTGCCTCCC 4011

Qy 4024 CTTTGTATGACACTCGCTGCGGGATGTTGGGAAGGCCACAGAAAGCCACACTCACCAATCC 4083

Db 4012 CTTTGTATGACACTCGCTGCGGGATGTTGGGAAGGCCACAGAAAGCCACACTCACCAATCC 4071

Qy 4084 CAGGGGT-----ATTACAGTGGACAAAGTTTGGGCTGATCTACTTTCGTGGATGGCAC 4134

Db 4072 CAGGGGTCCCCAGGCATTACAGTGGACAAAGTTTGGGCTGATCTACTTTCGTGGATGGCAC 4131

Qy 4135 CATGATCAGACGCATCGATCAGAAATGGGATCATCTCCACCCTGCTCGGCTCTAATGATCT 4194

Db 4132 CATGATCAGACGCATCGATCAGAAATGGGATCATCTCCACCCTGCTCGGCTCTAATGATCT 4191

Qy 4195 CACATCAGCCCGGCCACTCAGCTGTGATTTCTGTCAATGGATATTTCCCAGGTAAGA----- 4249

Db 4192 CACATCAGCCCGGCCACTCAGCTGTGATTTCTGTCAATGGATATTTCCCAGGTAAGACAGGT 4251

Qy 4250 ----CTGGAGTGGCCCCACAGACTTAGCCATCAACCCCAATGGACAACTCACTTTATGTCTT 4305

Db 4252 TCACCTGGAGTGGCCCCACAGACTTAGCCATCAACCCCAATGGACAACTCACTTTATGTCTT 4311

Qy 4306 CGACAACAATGTGGTCTTGAAATCTCTGAAATCCACAGGTGCGCATTTGTCGCCGGAG 4365

Db 4312 CGACAACAATGTGGTCTTGAAATCTCTGAAATCCACAGGTGCGCATTTGTCGCCGGAG 4371

Qy 4366 GCCCATGCACTGCCAGGTCCCTGGCAFTGACCACTTCCCTGCTAAGCAAGGTGGCCATCCA 4425

Db 4372 GCCCATGCACTGCCAGGTCCCTGGCAFTGACCACTTCCCTGCTAAGCAAGGTGGCCATCCA 4431

Qy 4426 CGCAACCCCTGGAGTCAGCCACCGCTTTGGCTGTTTCACACAAATGGGTCCTGTATATTGC 4485

Db 4432 CGCAACCCCTGGAGTCAGCCACCGCTTTGGCTGTTTCACACAAATGGGTCCTGTATATTGC 4491

Qy 4486 TGAGACTGATGAGAAAAAGATCAACCGCATCAGGCAGGTCAACCACCTAGTGGAGAGATCTC 4545

Db 4492 TGAGACTGATGAGAAAAAGATCAACCGCATCAGGCAGGTCAACCACCTAGTGGAGAGATCTC 4551

Qy 4546 ACTCGTTGCTGGGGCCCCCAGTGGCTGTGACTGTAAAAATGATGCCAACTGTGATTGTTT 4605

Db 4552 ACTCGTTGCTGGGGCCCCCAGTGGCTGTGACTGTAAAAATGATGCCAACTGTGATTGTTT 4611

Qy 4606 TTCTGGAGACGATGGTTATGCCAAGGATGCAAAAGTTAAATACCCCATCTTCCCTGGCTGT 4665

Db 4612 TTCTGGAGACGATGGTTATGCCAAGGATGCAAAAGTTAAATACCCCATCTTCCCTGGCTGT 4671

Qy 4666 GTGTGCTGATGGGGAGCTCTACGTGGCCGACCTTGGGAACATCCGAATTCGGTATTATCCG 4725

Db 4672 GTGTGCTGATGGGGAGCTCTACGTGGCCGACCTTGGGAACATCCGAATTCGGTATTATCCG 4731

Qy 4726 GAAGAAACAAGCCTTTCCCTCAACACCCAGAAACATGTATGAGCTGTCTTCACCAATTGACCA 4785

Db 4732 GAAGAAACAAGCCTTTCCCTCAACACCCAGAAACATGTATGAGCTGTCTTCACCAATTGACCA 4791

Qy 4786 GGAGCTCTATCTGTTTGATACACCGGCAAGCACCTGTACACCCAAAGCCTGCCACAGG 4845

Db 4792 GGAGCTCTATCTGTTTGATACACCGGCAAGCACCTGTACACCCAAAGCCTGCCACAGG 4851

Qy 4846 AGACTACCTGTACAACTTCACCTACACTGGGGACGGGACATCACACTCATACAGACAA 4905

Db 4852 AGACTACCTGTACAACTTCACCTACACTGGGGACGGGACATCACACTCATACAGACAA 4911

Qy 4906 CAATGGCAACATGTFAAATGTCCGCCGAGACTCTACTTGGGATGCCCCCTCTGGCTGGTGGT 4965

Db 4912 CAATGGCAACATGTFAAATGTCCGCCGAGACTCTACTTGGGATGCCCCCTCTGGCTGGTGGT 4971

Qy 4966 CCCAGATGGCCAGGTGTACTTGGGTGACCATGGGCACCAACAGTGCACCTCAAGAGTGTGAC 5025

Db 4972 CCCAGATGGCCAGGTGTACTTGGGTGACCATGGGCACCAACAGTGCACCTCAAGAGTGTGAC 5031

Qy 5026 CACACAAGGACACGAGTTGGCCATGATGACATACCATGGCAATTCCCGGCCTTCTGGCAAC 5085

Db 5032 CACACAAGGACACGAGTTGGCCATGATGACATACCATGGCAATTCCCGGCCTTCTGGCAAC 5091

Qy 5086 CAAAAGCAATGAAAAACGGATGGACAACTTTTATGAGTACGACAGCTTTGGCCGCCTGAC 5145

Db 5092 CAAAAGCAATGAAAAACGGATGGACAACTTTTATGAGTACGACAGCTTTGGCCGCCTGAC 5151

Qy 5146 AAATGTGACCTTCCCTACTGGCCAGGTGAGCAGTTTCCGAAGTGATACAGACAGTTTCAGT 5205

Db 5152 AAATGTGACCTTCCCTACTGGCCAGGTGAGCAGTTTCCGAAGTGATACAGACAGTTTCAGT 5211

Qy 5206 GCATGTCCAGGTAGAGACCTCCAGCAAGGATGTCAACCATAAACCAACACCTGTCTGC 5265

Db 5212 GCATGTCCAGGTAGAGACCTCCAGCAAGGATGTCAACCATAAACCAACACCTGTCTGC 5271

Qy 5266 CTCAGGCGCCTTCTACACACTGCTGCAAGACCAAGTCCGGAACAGCTACTACTACATCGGGC 5325

Db 5272 CTCAGGCGCCTTCTACACACTGCTGCAAGACCAAGTCCGGAACAGCTACTACTACATCGGGC 5331

Qy 5326 CGATGGCTCCTTTGCGGCTGCTGCTGGCCAAACGGCATGGAGGTGGCGCTGCAGACTGAGCC 5385

Db 5332 CGATGGCTCCTTTGCGGCTGCTGCTGGCCAAACGGCATGGAGGTGGCGCTGCAGACTGAGCC 5391

Qy 5386 CCACCTTGCTGGCTGGCACCCGTCAACCCACCCCGTGGGCAAGAGGAATGTACCGTGCCCAT 5445

Db 5392 CCACCTTGCTGGCTGGCACCGTCAACCCACCCCGTGGGCAAGAGGAATGTACCGTGCCCAT 5451

Qy 5446 CGACAAACGGCCTCAACCTGGTGGAGTGGCGCCAGCGCAAGAGAGGCTCGGGGCCAGGT 5505

Db 5452 CGACAAACGGCCTCAACCTGGTGGAGTGGCGCCAGCGCAAGAGAGGCTCGGGGCCAGGT 5511

Qy 5506 CACTGTCTTTGGGCGCCGGCTGCGGGTG-----CACAAACGAAATCTCCTATCTCT 5556

Db 5512 CACTGTCTTTGGGCGCCGGCTGCGGGTGCTCCAGGTTCAAAACGAAATCTCCTATCTCT 5571

Qy 5557 GGACTTTGATCGCGTAAACACGCACAGAGAAAGATCTATGATGACACCGCAAGTTCAACCT 5616

Db 5572 GGACTTTGATCGCGTAAACACGCACAGAGAAAGATCTATGATGACACCGCAAGTTCAACCT 5631

Qy 5617 TCGGATTCTGTACGACAGGCGGGCGGCCAGCCTCTGGTCAACAGCAGCAGGCTGAA 5676

Db 5632 TCGGATTCTGTACGACAGGCGGGCGGCCAGCCTCTGGTCAACAGCAGCAGGCTGAA 5691

Qy 5677 TGGTGTCAACGTGACATACTCCCTTGGGGGTTACATTGCTGGCATCCAGAGGGGCATCAT 5736

Db 5692 TGGTGTCAACGTGACATACTCCCTTGGGGGTTACATTGCTGGCATCCAGAGGGGCATCAT 5751

Qy 5737 GTCTGAAAGAAATGGAATACGACAGCGGGCGCCGATCAATCCAGGATCTTCGCTGATGG 5796

Db 5752 GTCTGAAAGAAATGGAATACGACAGCGGGCGCCGATCAATCCAGGATCTTCGCTGATGG 5811

Qy 5797 GAAGACATGGAGCTACACATACTTAGAGA-----AGTCCATGGTGTCTACT 5844

Db 5812 GAAGACATGGAGCTACACATACTTAGAGAAGGCAGGTGTCCAGTCCATGGTGTCTACT 5871

Qy 5845 ACACAGCCAGAGGCAGTATATCTTTGAGTTTCGACAAAGAAATGACCGCCTCTCTTCTGTGAC 5904

Db 5872 ACACAGCCAGAGGCAGTATATCTTTGAGTTTCGACAAAGAAATGACCGCCTCTCTTCTGTGAC 5931

Qy 5905 GATGCCCAACGTGGCGGCGCAGACACTAGAGACCATCCGCTCAGTGGGCTACTACAGAAA 5964

Db 5932 GATGCCCAACGTGGCGGCGCAGACACTAGAGACCATCCGCTCAGTGGGCTACTACAGAAA 5991





Db 8152 GGTCTGGAGCTGGCCGCGAGAGCCGTGCGCCAAGCGTGGGCCCGCGAGCAGAG 8211

QY 8161 ACTGCGGAAGGGAGGAGGCCCTGCGGGCCTGGACAGAGGGGAGAAAGCAGCAGGTGCT 8220

Db 8212 ACTGCGGAAGGGAGGAGGCCCTGCGGGCCTGGACAGAGGGGAGAAAGCAGCAGGTGCT 8271

QY 8221 GAGCACAGGCGGGTGCAGGCTACGACGGCTTTTTCGTGATCTCTGTGAGCAGTACCC 8280

Db 8272 GAGCACAGGCGGGTGCAGGCTACGACGGCTTTTTCGTGATCTCTGTGAGCAGTACCC 8331

QY 8281 AGAACTGTCAGACAGCGGCCAACAAATCCACTTCATGAGACAGAGCGGATGGCCGGAG 8340

Db 8332 AGAACTGTCAGACAGCGGCCAACAAATCCACTTCATGAGACAGAGCGGATGGCCGGAG 8391

QY 8341 GTGACAGAGAGGAC 8354

Db 8392 GTGACAGAGAGGAC 8405

RESULT 6

ID ADQ20349

XX ADQ20349 standard; DNA; 8624 BP.

AC ADQ20349;

XX

DT 26-AUG-2004 (first entry)

XX

DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 3169.

XX

KW soft tissue sarcoma; cytostatic; gene therapy; vaccine; screening; human;

KW ds.

XX

OS Homo sapiens.

XX

PN WO2004048938-A2.

XX

PD 10-JUN-2004.

XX

PF 26-NOV-2003; 2003WO-US038193.

XX

PR 26-NOV-2002; 2002US-0429739P.

XX

PA (PROT-) PROTEIN DESIGN LABS INC.

XX

PI Aziz N, Ginsburg WM, Zlotnik A;

XX

DR WPI; 2004-441208/41.

XX

PT Early detection of soft tissue sarcoma comprises determining expression

PT of a gene in a first soft tissue sample and a normal soft tissue sample

PT and comparing the gene expression, also useful in treating soft tissue

PT sarcoma.

XX

PS Example 2; SEQ ID NO 3169; 210pp; English.

XX

CC The invention relates to a novel method for detecting soft tissue sarcoma

CC which comprises obtaining a first soft tissue sample from an individual

CC and a normal soft tissue sample from the same or different individual,

CC determining the expression of a gene in both samples and comparing the

CC expression of the gene in both soft tissue samples, where a higher level

CC of protein expression in the first soft tissue sample indicates the

CC presence of soft tissue sarcoma. The method of the invention has

CC cytotstatic applications and may be useful for detecting soft tissue

CC sarcoma, possibly via gene therapy or vaccine production. The nucleic

CC acid sequences may be useful in diagnostic and screening applications.

CC The current sequence is that of a human soft tissue sarcoma-upregulated

CC DNA of the invention. The current sequence is not shown within the

CC specification per se but was submitted in CD format by the inventor.

XX

SQ Sequence 8624 BP; 2166 A; 2260 C; 2175 G; 2023 T; 0 U; 0 Other;

Query Match 44.1%; Score 3680.8; DB 12; Length 8624;

Best Local Similarity 97.8%; Pred. No. 0;

Matches 3775; Conservative 0; Mismatches 2; Indels 83; Gaps 1;

QY 4578 GTAAAAATGATGCCAAACTGTGATTGTTTTTCTGGAGACGATGGTTATGCCAAGGATGCAA 4637

Db 1 GTAAAAATGATGCCAAACTGTGATTGTTTTTCTGGAGACGATGGTTATGCCAAGGATGCAA 60

QY 4638 AGTTAAATACCCCATCTTCTTGGCTGTGTGCTGATGGGAGCTCTACGTGGCCGACC 4697

Db 61 AGTTAAATACCCCATCTTCTTGGCTGTGTGCTGATGGGAGCTCTACGTGGCCGACC 120

QY 4698 TTGGGAACATCCGAATTCGGTTTATCCGGAAGAAACAAGCCTTTCCTCAACACCCAGAACA 4757

Db 121 TTGGGAACATCCGAATTCGGTTTATCCGGAAGAAACAAGCCTTTCCTCAACACCCAGAACA 180

QY 4758 TGTATGAGCTGTCTTCACCAATTGACCAGGAGCTCTATCTGTTTGTATACCACCGCAAGC 4817

Db 181 TGTATGAGCTGTCTTCACCAATTGACCAGGAGCTCTATCTGTTTGTATACCACCGCAAGC 240

QY 4818 ACCTGTACACCCAAAGCCTGCCCCACAGGAGACTACCTGTACAACTTTCACCTACACTGGGG 4877

Db 241 ACCTGTACACCCAAAGCCTGCCCCACAGGAGACTACCTGTACAACTTTCACCTACACTGGGG 300

QY 4878 ACGGCGACATCACACTCATCACAGACAACAATGGCAACATGGTAAATGTCGCGCGAGACT 4937

Db 301 ACGGCGACATCACACTCATCACAGACAACAATGGCAACATGGTAAATGTCGCGCGAGACT 360

QY 4938 CTACTGGGATGCCCCCTCTGGCTGGTCCAGATGGCCAGGTGTACTGGGTGACCATGG 4997

Db 361 CTACTGGGATGCCCCCTCTGGCTGGTCCAGATGGCCAGGTGTACTGGGTGACCATGG 420

QY 4998 GCACCAACAGTGCACCTCAAGAGTGTGACCACACAAGGACACGAGTTGGCCATGATGACAT 5057

Db 421 GCACCAACAGTGCACCTCAAGAGTGTGACCACACAAGGACACGAGTTGGCCATGATGACAT 480

QY 5058 ACCATGGCAATTCGCGCCTTCTGGCAACCAAAAGCAATGAAAAACGGATGGACAACATTTT 5117

Db 481 ACCATGGCAATTCGCGCCTTCTGGCAACCAAAAGCAATGAAAAACGGATGGACAACATTTT 540

QY 5118 ATGA----- 5121

Db 541 ATGACAACCTCAGATGGCAGGAATTATCATCCACATTTTTTACATATGAAGTACAGAGAG 600

QY 5122 -----GTACGACAGCTTTTGGCCGCTTGACAAATGTGAC 5154

Db 601 ATTAGATAACAAGCCTGAAACCAACACGCTACGACAGCTTTGGCCGCTGACAAATGTGAC 660

QY 5155 CTTCCCTACTGSCCAGGTGAGCAGTTTCCGAAGTGATACAGACAGTTTCAGTGCATGTCCA 5214

Db 661 CTTCCCTACTGSCCAGGTGAGCAGTTTCCGAAGTGATACAGACAGTTTCAGTGCATGTCCA 720

QY 5215 GGTAGAGACCTCCAGCAAGGATGATGTCACCATAACCACCAACCTGTCTGCCTCAGGCGC 5274

Db 721 GGTAGAGACCTCCAGCAAGGATGATGTCACCATAACCACCAACCTGTCTGCCTCAGGCGC 780

QY 5275 CTTCTACACACTGCTGCAAGACCAAGTCCGGAACAGCTACTACATCGGGGCCGATGGCTC 5334

Db 781 CTTCTACACACTGCTGCAAGACCAAGTCCGGAACAGCTACTACATCGGGGCCGATGGCTC 840

QY 5335 CTTGCGGCTGCTGCTGGCCCAACGGCATGGAGTGGCGCTGCAGACTGAGCCCACTTGCT 5394

Db 841 CTTGCGGCTGCTGCTGGCCCAACGGCATGGAGTGGCGCTGCAGACTGAGCCCACTTGCT 900

QY 5395 GGCTGGCACCGTCAACCCACCGTGGGCAAGAGGAATGTACCGTGCCTCCCATCGACAACGG 5454

Db 901 GGCTGGCACCGTCAACCCACCGTGGGCAAGAGGAATGTACCGTGCCTCCCATCGACAACGG 960

QY 5455 CCTCAACCTGGTGGAGTGGCGCCAGCGCAAAAGACAGGCTCGGGGCCAGGTCACTGTCTT 5514

Db 961 CCTCAACCTGGTGGAGTGGCGCCAGCGCAAAAGACAGGCTCGGGGCCAGGTCACTGTCTT 1020

QY 5515 TGGGCGCCGGTGGCGGTGCACAACCGAAATCTCTTGACTTCTTGACTTTTGATCGCGTAAC 5574

Db 1021 TGGGCGCCGGTGGCGGTTCACAACCGAAATCTCTTGACTTCTTGACTTTTGATCGCGTAAC 1080



QY	5575	ACGCACAGAGAAGATCTATGATGACCAACCGCAAGTTTCAACCTTCCGATTCTGTACGACCA	5634
Db	1081	ACGCACAGAGAAGATCTATGATGACCAACCGCAAGTTTCAACCTTCCGATTCTGTACGACCA	1140
QY	5635	GGCGGGGGCCCGACGCTCTGGTCAACCCAGCAGCAGGCTGAATGGTGTCAACGCTGACATA	5694
Db	1141	GGCGGGGGCCCGACGCTCTGGTCAACCCAGCAGCAGGCTGAATGGTGTCAACGCTGACATA	1200
QY	5695	CTCCCCCTGGGGTTACATTGCTGGCATCCAGAGGGGCATCATGTCTGAAAGAAATGGAATA	5754
Db	1201	CTCCCCCTGGGGTTACATTGCTGGCATCCAGAGGGGCATCATGTCTGAAAGAAATGGAATA	1260
QY	5755	CGACCAGGCGGGCCGCATCACATCCAGGATCTTCGCTGATGGGAAGACATGGAGCTACAC	5814
Db	1261	CGACCAGGCGGGCCGCATCACATCCAGGATCTTCGCTGATGGGAAGACATGGAGCTACAC	1320
QY	5815	ATACTTAGAGAAAGTCCATGGTGTCTACTACACAGCCAGAGGCAGTATATCTTTGAGTT	5874
Db	1321	ATACTTAGAGAAAGTCCATGGTGTCTACTACACAGCCAGAGGCAGTATATCTTTGAGTT	1380
QY	5875	CGACAAGAATGACCGCCTCTCTTCTGTGACGATGCCCAACGTTGGCGCGGCGAGACACTAGA	5934
Db	1381	CGACAAGAATGACCGCCTCTCTTCTGTGACGATGCCCAACGTTGGCGCGGCGAGACACTAGA	1440
QY	5935	GACCATCCGCTCAGTGGGCTACTACAGAAACATCTATCAGCCCCCTGAGGCAATGCCTC	5994
Db	1441	GACCATCCGCTCAGTGGGCTACTACAGAAACATCTATCAGCCCCCTGAGGCAATGCCTC	1500
QY	5995	AGTCATACAGGACTTCACCTGAGGATGGGCACCTCCTTACACCTTCTACCTGGGCACCTGG	6054
Db	1501	AGTCATACAGGACTTCACCTGAGGATGGGCACCTCCTTACACCTTCTACCTGGGCACCTGG	1560
QY	6055	CCGCAGGGTGATATACAAGTATGGCAAACTGTCAAAGCTGGCAGAGACGCTCTATGACAC	6114
Db	1561	CCGCAGGGTGATATACAAGTATGGCAAACTGTCAAAGCTGGCAGAGACGCTCTATGACAC	1620
QY	6115	CACCAAGGTCAGTTTCACCTATGACGAGACGGCAGGCATGCTGAAGACCAATCAACCTACA	6174
Db	1621	CACCAAGGTCAGTTTCACCTATGACGAGACGGCAGGCATGCTGAAGACCAATCAACCTACA	1680
QY	6175	GAATGAGGGCTTCACCTGCACCATCCGCTACCGTCAGATTGGGCCCCCTGATTGACCGACA	6234
Db	1681	GAATGAGGGCTTCACCTGCACCATCCGCTACCGTCAGATTGGGCCCCCTGATTGACCGACA	1740
QY	6235	GATCTTCCGCTTCACTGAGGAAGGCATGGTCAACGCCCGCTTTTGACTACAACTATGACAA	6294
Db	1741	GATCTTCCGCTTCACTGAGGAAGGCATGGTCAACGCCCGCTTTTGACTACAACTATGACAA	1800
QY	6295	CAGCTTCCGGGTGACCAAGCATGCAGGCTGTGATCAACGAGACCCCACTGCCCATTGATCT	6354
Db	1801	CAGCTTCCGGGTGACCAAGCATGCAGGCTGTGATCAACGAGACCCCACTGCCCATTGATCT	1860
QY	6355	CTATCGCTATGATGTGTGAGGCAAGACAGAGCAGTTTGGGAAGTTTGGTGTCAATTTA	6414
Db	1861	CTATCGCTATGATGTGTGAGGCAAGACAGAGCAGTTTGGGAAGTTTGGTGTCAATTTA	1920
QY	6415	CTATGACATTAACCAGATCATCACCAGCTGTCTATGACCCACACCAAGCATTTTGATGC	6474
Db	1921	CTATGACATTAACCAGATCATCACCAGCTGTCTATGACCCACACCAAGCATTTTGATGC	1980
QY	6475	ATATGGCAGGATGAAGGAAGTGCAGTATGAGATCTTCCGCTCGCTCATGTACTGGATGAC	6534
Db	1981	ATATGGCAGGATGAAGGAAGTGCAGTATGAGATCTTCCGCTCGCTCATGTACTGGATGAC	2040
QY	6535	CGTCCAGTATGATAACATGGGGCGAGTAGTGAAGAAGAGCTGAAGGTAGGACCCCTACGC	6594
Db	2041	CGTCCAGTATGATAACATGGGGCGAGTAGTGAAGAAGAGCTGAAGGTAGGACCCCTACGC	2100
QY	6595	CAATACCACTCGCTACTCTCTATGAGTATGATGCTGACGGCCAGCTGCAGACAGTCTCCAT	6654
Db	2101	CAATACCACTCGCTACTCTCTATGAGTATGATGCTGACGGCCAGCTGCAGACAGTCTCCAT	2160

QY	6655	CAATGACAAAGCCACTCTGGCGCTACAGCTACGACCTCAATGGGAACCTGCACTTACTGAG	6714
Db	2161	CAATGACAAAGCCACTCTGGCGCTACAGCTACGACCTCAATGGGAACCTGCACTTACTGAG	2220
QY	6715	CCCTGGGAACAGTGCACGGCTCACACCACACTACGGTATGACATCCGCGACCGCATCACTCG	6774
Db	2221	CCCTGGGAACAGTGCACGGCTCACACCACACTACGGTATGACATCCGCGACCGCATCACTCG	2280
QY	6775	GCTGGTGACGTGCAATACAAGATGGATGAGGATGGCTTCTAGGACGCGGGCGGTGA	6834
Db	2281	GCTGGTGACGTGCAATACAAGATGGATGAGGATGGCTTCTAGGACGCGGGCGGTGA	2340
QY	6835	TATCTTTGAGTACAACTCAGCTGGCCTGCTCATCAAGGCCTACAAACCGGGCTGGCAGCTG	6894
Db	2341	TATCTTTGAGTACAACTCAGCTGGCCTGCTCATCAAGGCCTACAAACCGGGCTGGCAGCTG	2400
QY	6895	GAGTGTCAAGTACCGCTACGATGGCCTGGGGCGGCGGTGTCCAGCAAGAGCAGCCACAG	6954
Db	2401	GAGTGTCAAGTACCGCTACGATGGCCTGGGGCGGCGGTGTCCAGCAAGAGCAGCCACAG	2460
QY	6955	CCACCACCTGCAGTTCTTCTATGCAGACCTGACCAACCCCAAGGTCAACCCACCTGTA	7014
Db	2461	CCACCACCTGCAGTTCTTCTATGCAGACCTGACCAACCCCAAGGTCAACCCACCTGTA	2520
QY	7015	CAACCACCTCAGCTCTGAGATCACCTCCCTCTACTACGACTTGCAAGGACACCTCTTTGC	7074
Db	2521	CAACCACCTCAGCTCTGAGATCACCTCCCTCTACTACGACTTGCAAGGACACCTCTTTGC	2580
QY	7075	CATGGAGCTGAGCAGTGGTGATGAGTTTACATAGCTTGTGACAAACATCGGGACCCCTCT	7134
Db	2581	CATGGAGCTGAGCAGTGGTGATGAGTTTACATAGCTTGTGACAAACATCGGGACCCCTCT	2640
QY	7135	TGCTGTCTTTAGTGGAAACAGGTTTGATGATCAAGCAAAATCCTGTACACAGCCTATGGGA	7194
Db	2641	TGCTGTCTTTAGTGGAAACAGGTTTGATGATCAAGCAAAATCCTGTACACAGCCTATGGGA	2700
QY	7195	GATCTACATGGATACCAACCCCACTTTTCAGATCATATAGGCTACCATGGTGGCCCTCTA	7254
Db	2701	GATCTACATGGATACCAACCCCACTTTTCAGATCATATAGGCTACCATGGTGGCCCTCTA	2760
QY	7255	TGATCCACTCACAAAGCTTGTCCACATGGGCGGCGAGATTATGATGTGTGGCCGGACG	7314
Db	2761	TGATCCACTCACAAAGCTTGTCCACATGGGCGGCGAGATTATGATGTGTGGCCGGACG	2820
QY	7315	CTGGACTAGCCAGACCAAGCTGTGGAAGCACCTTAGTAGCAGCAACGTCATGCCTTT	7374
Db	2821	CTGGACTAGCCAGACCAAGCTGTGGAAGCACCTTAGTAGCAGCAACGTCATGCCTTT	2880
QY	7375	TAATCTCTATATGTTCAAAAACAAACCCCATCAGCAACTCCCAGGACATCAAGTGCTT	7434
Db	2881	TAATCTCTATATGTTCAAAAACAAACCCCATCAGCAACTCCCAGGACATCAAGTGCTT	2940
QY	7435	CATGACAGATGTTAAACAGCTGGCTGCTCACTTTGGATTCCAGCTACACAACGTCATCCC	7494
Db	2941	CATGACAGATGTTAAACAGCTGGCTGCTCACTTTGGATTCCAGCTACACAACGTCATCCC	3000
QY	7495	TGGTTATCCCAACACAGACATGGATGCCATGGAAACCTCCTACGAGCTCATCCACACACA	7554
Db	3001	TGGTTATCCCAACACAGACATGGATGCCATGGAAACCTCCTACGAGCTTATCCACACACA	3060
QY	7555	GATGAAAACCGCAGGAGTGGGACAAACAGCAAGTCTATCCTCGGGGTACAGTGTGAAGTACA	7614
Db	3061	GATGAAAACCGCAGGAGTGGGACAAACAGCAAGTCTATCCTCGGGGTACAGTGTGAAGTACA	3120
QY	7615	GAAGCAGCTCAAGGCCTTTGTCAACCTTAGAACGGTTTGACCAGCTCTATGGCTCCACAAT	7674
Db	3121	GAAGCAGCTCAAGGCCTTTGTCAACCTTAGAACGGTTTGACCAGCTCTATGGCTCCACAAT	3180
QY	7675	CACCAGCTGCCAGAGGCTCCAAAGACCAAGAGTTTGCATCCAGCGGCTCAGTCTTTGG	7734
Db	3181	CACCAGCTGCCAGAGGCTCCAAAGACCAAGAGTTTGCATCCAGCGGCTCAGTCTTTGG	3240
QY	7735	CAAGGGGTCAAGTTTGCCTTTGAAGGATGGCCGAGTGACCAAGACATCATCAGTGTGGC	7794



Db 3241 CAAGGGGTCAAGTTTCCCTTGAAGGATGGCCGAGTGACCAAGACATCATCACTGTGGC 3300

Qy 7795 CAATGAGGATGGGCGAAGGGTTGCTGCCATCTTGAACCATGCCCACTACCTAGAGAACCT 7854

Db 3301 CAATGAGGATGGGCGAAGGGTTGCTGCCATCTTGAACCATGCCCACTACCTAGAGAACCT 3360

Qy 7855 GCACTTCACCAATTGATGGGTGGATACCCATTACTTTGTGAAACCAGGACCTTCAGAAGG 7914

Db 3361 GCACTTCACCAATTGATGGGTGGATACCCATTACTTTGTGAAACCAGGACCTTCAGAAGG 3420

Qy 7915 TGACCTGGCCATCCTGGGCCTCAGTGGGGCGGCGGAACCCCTGGAGAATGGGTC AACCGT 7974

Db 3421 TGACCTGGCCATCCTGGGCCTCAGTGGGGCGGCGGAACCCCTGGAGAATGGGTC AACCGT 3480

Qy 7975 CACTGTGTCCAGATCAACACAGTACTTAATGGCAGGACTAGACGCTACACAGACATCCA 8034

Db 3481 CACTGTGTCCAGATCAACACAGTACTTAATGGCAGGACTAGACGCTACACAGACATCCA 3540

Qy 8035 GCTCCAGTACGGGGCACTGTCTTGAACACACACGCTACGGGACAACGTTGGATGAGGAGAA 8094

Db 3541 GCTCCAGTACGGGGCACTGTCTTGAACACACACGCTACGGGACAACGTTGGATGAGGAGAA 3600

Qy 8095 GGCACGGGTCCTGGAGCTGGCCCGGCAGAGAGCCGTGCGCCAAAGCGTGGGCCCGCAGCA 8154

Db 3601 GGCACGGGTCCTGGAGCTGGCCCGGCAGAGAGCCGTGCGCCAAAGCGTGGGCCCGCAGCA 3660

Qy 8155 GCAGAGACTGCGGGAAGGGGAGGAAGGCCTGCGGGCCTGGACAGAGGGGGAGACAGCA 8214

Db 3661 GCAGAGACTGCGGGAAGGGGAGGAAGGCCTGCGGGCCTGGACAGAGGGGGAGACAGCA 3720

Qy 8215 GGTGCTGAGCACAGGGCGGTGCAAGGCTACGACGGCTTTTTCGTGATCTCTGTCCAGCA 8274

Db 3721 GGTGCTGAGCACAGGGCGGTGCAAGGCTACGACGGCTTTTTCGTGATCTCTGTCCAGCA 3780

Qy 8275 GTACCCAGAACTGTCAGACAGCGGCCAACACATCCACTTCATGAGACAGAGCGGAGATGGG 8334

Db 3781 GTACCCAGAACTGTCAGACAGCGGCCAACACATCCACTTCATGAGACAGAGCGGAGATGGG 3840

Qy 8335 CCGGAGGTGACAGAGAGGAC 8354

Db 3841 CCGGAGGTGACAGAGAGGAC 3860

RESULT 7

ADQ24356

ID ADQ24356 standard; DNA; 8774 BP.

XX AC ADQ24356;

XX DT 26-AUG-2004 (first entry)

XX DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 7176.

XX KW soft tissue sarcoma; cytotostatic; gene therapy; vaccine; screening; human; ds.

XX OS Homo sapiens.

XX PN WO2004048938-A2.

XX PD 10-JUN-2004.

XX PF 26-NOV-2003; 2003WO-US038193.

XX PR 26-NOV-2002; 2002US-0429739P.

XX PA (PROT-) PROTEIN DESIGN LABS INC.

XX PI Aziz N, Ginsburg WM, Zlotnik A;

XX DR WPI; 2004-441208/41.

PT Early detection of soft tissue sarcoma comprises determining expression of a gene in a first soft tissue sample and a normal soft tissue sample and comparing the gene expression, also useful in treating soft tissue sarcoma.

XX Example 2; SEQ ID NO 7176; 210pp; English.

PS

XX The invention relates to a novel method for detecting soft tissue sarcoma which comprises obtaining a first soft tissue sample from an individual and a normal soft tissue sample from the same or different individual, determining the expression of a gene in both samples and comparing the expression of the gene in both soft tissue samples, where a higher level of protein expression in the first soft tissue sample indicates the presence of soft tissue sarcoma. The method of the invention has cytotostatic applications and may be useful for detecting soft tissue sarcoma, possibly via gene therapy or vaccine production. The nucleic acid sequences may be useful in diagnostic and screening applications. The current sequence is that of a human soft tissue sarcoma-upregulated DNA of the invention. The current sequence is not shown within the specification per se but was submitted in CD format by the inventor.

XX

SQ Sequence 8774 BP; 2210 A; 2279 C; 2190 G; 2060 T; 0 U; 35 Other;

Query Match 43.4%; Score 3621.6; DB 12; Length 8774;

Best Local Similarity 97.4%; Pred. No. 0;

Matches 3758; Conservative 0; Mismatches 14; Indels 88; Gaps 4;

Qy 4578 GTAAAAATGATGCCAACTGTGATTTTCTGGAGACGATGGTTATGCCAAGGATGCAA 4637

Db 1 GTAAAAATGATGCCAACTGTGATTTTCTGGAGACGATGGTTATGCCAAGGATGCAA 60

Qy 4638 AGTTAAATACCCCATCTTCCTTGGCTGTGTGCTGATGGGAGCTCTACGTGGCCGACC 4697

Db 61 AGTTAAATACCCCATCTTCCTTGGCTGTGTGCTGATGGGAGCTCTACGTGGCCGACC 120

Qy 4698 TTGGGAACATCCGAATTCGGTTTATCCGGAAGAAACAGCCTTTCCTCAACACCCAGAACA 4757

Db 121 TTGGGAACATCCGAATTCGGTTTATCCGGAAGAAACAGCCTTTCCTCAACACCCAGAACA 180

Qy 4758 TGTATGAGCTGTCTTACCAATTTGACCAGGAGCTCTATCTGTTTGATACACCGGCAAGC 4817

Db 181 TGTATGAGCTGTCTTACCAATTTGACCAGGAGCTCTATCTGTTTGATACACCGGCAAGC 240

Qy 4818 ACCTGTACACCCAAAGCCTGCCCACAGGAGACTACCTGTACAACTTCACCTACACTGGGG 4877

Db 241 ACCTGTACACCCAAAGCCTGCCCACAGGAGACTACCTGTACAACTTCACCTACACTGGGG 300

Qy 4878 ACGGCGACATCACTCATCAGACAACATGGCAACATGGTAAATGTCCGCCGAGACT 4937

Db 301 ACGGCGACATCACTCATCAGACAACATGGCAACATGGTAAATGTCCGCCGAGACT 360

Qy 4938 CTACTGGGATGCCCTCTGGCTGGTGTCACAGATGGCCAGGTGTACTGGTGACCATGG 4997

Db 361 CTACTGGGATGCCCTCTGGCTGGTGTCACAGATGGCCAGGTGTACTGGTGACCATGG 420

Qy 4998 GCACCAACAGTGCACCTCAAGAGTGTGACCACACAAGGACACGAGTTGGCCATGATGACAT 5057

Db 421 GCACCAACAGTGCACCTCAAGAGTGTGACCACACAAGGACACGAGTTGGCCATGATGACAT 480

Qy 5058 ACCATGGCAATTCGGCCCTTCTGGCAACCAAAAGCAATGAAAACGGATGGACAACATTTT 5117

Db 481 ACCATGGCAATTCGGCCCTTCTGGCAACCAAAAGCAATGAAAACGGATGGACAACATTTT 540

Qy 5118 ATGA----- 5121

Db 541 ATGACAACCTCAGATGGCAGGAATTATCATCCACATTTTACATATGAAGTACAGAGAG 600

Qy 5122 -----GTACGACAGCTTTGGCCGCTTGACAATGTGAC 5154

Db 601 ATTAGATAACAAGCCTGAAACCACACGGTACGACAGCTTTGGCCGCTTGACAATGTGAC 660

Qy 5155 CTTCCCTACTGSCCAGGTGAGCAGTTTCCGAAAGTGATACAGACAGTTTCAGTGCATGTCCA 5214

Db 661 CTTCCCTACTGGCCAGGTGAGCAGTTTCCGAAAGTGATACAGACAGTTTCAGTGCATGTCCA 720

QY 5215 GGTAGAGACCTTCAGCAAGGATGATGTCAACCATAAACCACCAACCTGTCTGCCTCAGGCGC 5274

Db 721 GGTAGAGACCTTCAGCAAGGATGATGTCAACCATAAACCACCAACCTGTCTGCCTCAGGCGC 780

QY 5275 CTTCTACACACTGCTGCTCAAGACCAAGTCCGGAACAGCTACTACATCGGGGCCGATGGCTC 5334

Db 781 CTTCTACACACTGCTGCTCAAGACCAAGTCCGGAACAGCTACTACATCGGGGCCGATGGCTC 840

QY 5335 CTTGGGGTGTGCTGGCCCAACGGCATGGAGGTGGCGCTGCAGACTGAGCCCCACTTTGCT 5394

Db 841 CTTGGGGTGTGCTGGCCCAACGGCATGGAGGTGGCGCTGCAGACTGAGCCCCACTTTGCT 900

QY 5395 GGCTGGCACCGTCAACCCACCGTGGGCAAGAGGAATGTACGCTGCCCATCGACAAACGG 5454

Db 901 GGCTGGCACCGTCAACCCACCGTGGGCAAGAGGAATGTACGCTGCCCATCGACAAACGG 960

QY 5455 CCTCAACCTGTGGAGTGGCCAGCGCAAGAGCAGGCTCGGGGCCAGGTCACTGTCTT 5514

Db 961 CCTCAACCTGTGGAGTGGCCAGCGCAAGAGCAGGCTCGGGGCCAGGTCACTGTCTT 1020

QY 5515 TGGGGCCCGCTGCGGGTGCACAACCGGAATCTCCTATCTCTGGACTTTTGATCGCGTAAC 5574

Db 1021 TGGGGCCCGCTGCGGGTTCACAACCGGAATCTCCTATCTCTGGACTTTTGATCGCGTAAC 1080

QY 5575 ACGCACAGAGAAGATCTATGATGACCAACCGAAGTTTCAACCTTCGGATTCTGTACGACCA 5634

Db 1081 ACGCACAGAGAAGATCTATGATGACCAACCGAAGTTTCAACCTTCGGATTCTGTACGACCA 1140

QY 5635 GCGGGGCCGCCAGCCTCTGGTCAACCCAGCAGCAGGCTGAATGGTGTCAACCGTGACATA 5694

Db 1141 GCGGGGCCGCCAGCCTCTGGTCAACCCAGCAGCAGGCTGAATGGTGTCAACCGTGACATA 1200

QY 5695 CTCCCCCTGGGGTTACATGTCTGGCATCCAGAGGGGCATCATGTCTGAAAGAAATGGAATA 5754

Db 1201 CTCCCCCTGGGGTTACATGTCTGGCATCCAGAGGGGCATCATGTCTGAAAGAAATGGAATA 1260

QY 5755 CGACCAAGGGCCCGCATCACATCCAGGATCTTCGCTGATGGGAAGACATGGAGCTACAC 5814

Db 1261 CGACCAAGGGCCCGCATCACATCCAGGATCTTCGCTGATGGGAAGACATGGAGCTACAC 1320

QY 5815 ATACTTAGAGAAGTCCATGGTGTCTGCTACTACAGCCAGAGGCAGTATATCTTTGAGTT 5874

Db 1321 ATACTTAGAGAAGTCCATGGTGTCTGCTACTACAGCCAGAGGCAGTATATCTTTGAGTT 1380

QY 5875 CGACAAGAATGACCGCCTCTCTTCTGTGACGATGCCAAACGTTGGCGCGGAGACACTAGA 5934

Db 1381 CGACAAGAATGACCGCCTCTCTTCTGTGACGATGCCAAACGTTGGCGCGGAGACACTAGA 1440

QY 5935 GACCATCCGCTCAGTGGGCTACTACAGAAACATCTATCAGCCCCCTGAGGGCAATGCCTC 5994

Db 1441 GACCATCCGCTCAGTGGGCTACTACAGAAACATCTATCAGCCCCCTGAGGGCAATGCCTC 1500

QY 5995 AGTCATACAGGACTTCACTGAGGATGGGCACCTCTTCAACACCTTCTACCTTGGGCACCTGG 6054

Db 1501 AGTCATACAGGACTTCACTGAGGATGGGCACCTCTCTTCAACACCTTCTACCTTGGGCACCTGG 1560

QY 6055 CCGCAGGGTGATATACAAGTATGGCAAACTGTCAAAGCTGGCAGAGACGCTCTATGACAC 6114

Db 1561 CCGCAGGGTGATATACAAGTATGGCAAACTGTCAAAGCTGGCAGAGACGCTCTATGACAC 1620

QY 6115 CACCAAGGTGAGTTTCAACCTATGACGAGACGGCAGGCATGCTGAAGACCATCAACCTTACA 6174

Db 1621 CACCAAGGTGAGTTTCAACCTATGACGAGACGGCAGGCATGCTGAAGACCATCAACCTTACA 1680

QY 6175 GAATGAGGGCTTCACCTGCACCATCCGCTACCGTACAGATTGGGCCCTGATGACCCGACA 6234

Db 1681 GAATGAGGGCTTCACCTGCACCATCCGCTACCGTACAGATTGGG-CCCTGATAGACCGACA 1739

QY 6235 GATCTTCCGCTTCACTGAGGAAGGCATGGTCAACCGCCGTTTTTGACTACAACTATGACAA 6294

Db 1740 GATCTTCCGCTTCACTGAGGAAGGCATGG-CAACCGCCGTTTTTGACTACA---CTATGAC 1795

QY 6295 CAGCTTCCGGGTGACCAGCATGCAGGCTGTGATCAACGAGACCCCACTGCCCATTTGATCT 6354

Db 1796 CCAGTCCGGGTGACCAGCATGCAGGCTGTGATCAACGAGACCCCACTGCCCATTTGATCT 1855

QY 6355 CTATCGCTATGATGTGTCTAGGCAAGACAGAGCAGTTTGGGAAGTTTGGTGTCAATTA 6414

Db 1856 CTATCGCTATGATGTGTCTAGGCAAGACAGAGCAGTTTGGGAAGTTTGGTGTCAATTA 1915

QY 6415 CTATGACATTAACCAAGATCATCAACACAGCTGTCTATGACCCCAACCAAGCATTTTGATGC 6474

Db 1916 CTATGACATTAACCAAGATCATCAACACAGCTGTCTATGACCCCAACCAAGCATTTTGATGC 1975

QY 6475 ATATGGCAGGATGAAGGAAGTGCAGTATGAGATCTTCCGCTCGCTCATGTACTGGATGAC 6534

Db 1976 ATATGGCAGGATGAAGGAAGTGCAGTATGAGATCTTCCGCTCGCTCATGTACTGGATGAC 2035

QY 6535 CGTCCAGTATGATAACATGGGGCAGTAGTGAAGAGGAGCTGAAGGTAGGACCCCTACGC 6594

Db 2036 CGTCCAGTATGATAACATGGGGCAGTAGTGAAGAGGAGCTGAAGGTAGGACCCCTACGC 2095

QY 6595 CAATACCACTCGCTACTCCTATGATGATGCTGACGGCCAGCTGCAGACAGTCTCCAT 6654

Db 2096 CAATACCACTCGCTACTCCTATGATGATGCTGACGGCCAGCTGCAGACAGTCTCCAT 2155

QY 6655 CAATGACAAGCCACTCTGGCGCTACAGCTACGACCTCAATGGGAACCTGCACCTACTGAG 6714

Db 2156 CAATGACAAGCCACTCTGGCGCTACAGCTACGACCTCAATGGGAACCTGCACCTACTGAG 2215

QY 6715 CCCTGGGAACAGTGCACGGTCAACACCTACCGTATGACATCCGGACCGCATCACTCG 6774

Db 2216 CCCTGGGAACAGTGCACGGTCAACACCTACCGTATGACATCCGGACCGCATCACTCG 2275

QY 6775 GCTGGGTGACGTGCAATACAAGATGGATGAGGATGGCTTCTGAGGACGGGGCGGTGA 6834

Db 2276 GCTGGGTGACGTGCAATACAAGATGGATGAGGATGGCTTCTGAGGACGGGGCGGTGA 2335

QY 6835 TATCTTTGAGTACAACTCAGCTGGCCTGCTCATCAAGGCCTACAACCGGCTGGCAGCTG 6894

Db 2336 TATCTTTGAGTACAACTCAGCTGGCCTGCTCATCAAGGCCTACAACCGGCTGGCAGCTG 2395

QY 6895 GAGTGTACGTAACCGTACGATGGCTGGGGCGGCGGTGTCCAGCAAGACAGCCACAG 6954

Db 2396 GAGTGTACGTAACCGTACGATGGCTGGGGCGGCGGTGTCCAGCAAGACAGCCACAG 2455

QY 6955 CCACCACCTGCAGTTCTTCTATGCAGACTGACCAACCCCAACCAAGGTACCCACCTGTA 7014

Db 2456 CCACCACCTGCAGTTCTTCTATGCAGACTGACCAACCCCAACCAAGGTACCCACCTGTA 2515

QY 7015 CAACCACCTGCAGTTCTGAGATCACCTCCCTCTACTACGACTTGCAGGACACCTCTTTGC 7074

Db 2516 CAACCACCTGCAGTTCTGAGATCACCTCCCTCTACTACGACTTGCAGGACACCTCTTTGC 2575

QY 7075 CATGGAGCTGAGCAGTGGTGTGAGTTTACATAGCTTGTGACAAACATCGGGACCCCTCT 7134

Db 2576 CATGGAGCTGAGCAGTGGTGTGAGTTTACATAGCTTGTGACAAACATCGGGACCCCTCT 2635

QY 7135 TGCTGTCTTTAGTGGAAACAGGTTTGTATGATCAAGCAAAATCCTGTACAGACCTATGGGA 7194

Db 2636 TGCTGTCTTTAGTGGAAACAGGTTTGTATGATCAAGCAAAATCCTGTACAGACCTATGGGA 2695

QY 7195 GATCTACATGGATACCAACCCCACTTTCAGATCATATAGGCTACCATGGTGGCCTCTA 7254

Db 2696 GATCTACATGGATACCAACCCCACTTTCAGATCATATAGGCTACCATGGTGGCCTCTA 2755

QY 7255 TGATCCACTCACCAGCTTGTCCACATGGSCGGCGAGATTATGATGTGTGCGCCGACG 7314

Db 2756 TGATCCACTCACCAGCTTGTCCACATGGSCGGCGAGATTATGATGTGTGCGCCGACG 2815

QY 7315 CTGGACTAGCCAGACCAAGCTGTGGAAAGCACTTAGTAGCAGCAACGTATGCCCTT 7374

Db 2816 CTGGACTAGCCAGACCAAGCTGTGGAAAGCACTTAGTAGCAGCAACGTATGCCCTT 2875







XX	Sequence 8964 BP; 2391 A; 2261 C; 2321 G; 1991 T; 0 U; 0 Other;	
SQ	Query Match 42.4%; Score 3544.6; DB 12; Length 8964; Best Local Similarity 65.6%; Pred. No. 0; Matches 5458; Conservative 0; Mismatches 2679; Indels 186; Gaps 12;	
QY	35 ATGGACGTGAAGGAGAGGAAGCCCTTACCGCTCGCTGACCCGGCGC---CGCGACGCCGAG 91 	
Db	50 ATGGATGTGAAGGAACGCAGGCCCTTACTGCTCCTTGACCAAGAGCAGACGGGAAAAGGAA 109 	
QY	92 CGCCGCTACACCAAGCTCGTCCGCGGACAGCGAGGAGGGCAAAAGCCC---CGCAGAAAATCG 148 	
Db	110 AGGCGCTATACAAATTCGTCCGCGGACAATGAGGAGTGTAGGGTCCCCACGCAGAAAGTCC 169 	
QY	149 TACAGCTCCAGCGAGACCCCTGAAGGCCTACGACCAGG--ACGCCCGCCTAGCCTATGGC 205 	
Db	170 TATAGTTCAGTGAACCTTGAAAGCTTTCGATCATGATTATTACGGCTGCTTTATGGA 229 	
QY	206 AGCCGCGTCAAGGACATTTGTCCCGCAGGAGGCCGAGGAATTTCTGCCGCACAGGTGCCAAC 265 	
Db	230 AACAGAGTAAAGGATTTGGTCCACAGAGAAAGCCGACGAGTATACCTAGACAAGACAGAAAT 289 	
QY	266 TTCACCCCTGCGGAGCTGGGGCTGGAAGAAAGTAACGCCCCCTCACGGGACCCCTGTACCGG 325 	
Db	290 TTTACCCCTAAGGCAGTTAGGAGTGTGTGAATCCGAACTCGAAGAGGAGTGGCATTCTGT 349 	
QY	326 ACAGACATTTGGCCTGCCCCCAATGCGGCTACTCCATGGGGCTGGCTCTGATGCCGACATG 385 	
Db	350 GCGGAAATGGGGCTCCCTCACAGAGGTTACTCCATCAGTGCAGGTCAGATGCGGATACG 409 	
QY	386 GAGGCTGACACGCTGTGTCCCTGAGCACCCCGTGGTCTGTGGGGCCGAGACACACGG 445 	
Db	410 GAAACGAAGCAGTGTATGTCCCTGAGCATGCCATGAGACTTTGGGGCAGGGGGTCAAA 469 	
QY	446 TCAGGGCGCAGCTCCTGCCTGTCCAGCCGGGCCCAATTTCCAATCTCACACTCACCGACACC 505 	
Db	470 TCGGGCCGCAAGTTCTGCCTGTCAAGCCGGTCCAACTCGCCCTCACCCCTGACAGACACG 529 	
QY	506 GAGCATGAAAACACTGAGACTGATCATCCGGGGCGCCTGCAGAAACCAACGCGCGCTCCGG 565 	
Db	530 GAGCACGAGAACAGGTCGGAAGTGCAGTGCAGAGCGAGCAACCTTCAAAACAACCCAGGGCAACCC 589 	
QY	566 ACGCCGCCCGCGCTCTCGCACGCCCAACACCCCAACCCAGCACCAACCGCGCCTCCATT 625 	
Db	590 ACCCTGCAGCCTTTGCGGCCATCCCAACAGCAGCACCCCGGCGCAGCATCACCCGTCCATC 649 	
QY	626 AACTCCCTGAACCGGSGCAACTTCACGCCGAGGAGCAACCCAGCCCGGCCCCACCGGAC 685 	
Db	650 ACTTCCCTCAATAGAAACTCCCTGACCAATAGAAGGAACCAAGATCCGGGCCCGCGGCT 709 	
QY	686 CACTCGCTCTCCGGAGAGCCCCCTGCGCGCGGCCAGGAGCCCTGCCCAACGCCCCAGGAG 745 	
Db	710 GCTTTGCCCGCGAGCTGCAAAAC-----CACACCCGAGTCCGTCCAGTGCAGGAC 760 	
QY	746 AACTGGCTGTCAACAGCAACATCCCCCTGGAGACCAAGGAACCTAGGCAAGCAGCCATTTC 805 	
Db	761 AGCTGGGTCTTTGGCAGTAATGTACCACCTGGAAAGCAGGCAATTT----- 804 	
QY	806 CTAGGGACATTCAGGACAACCTCATTTGAGATGGACATTTCTCGGCGCCTCCCGCCATGAT 865 	
Db	805 ----- 804 	
QY	866 GGGGCTTACAGTGACGGGCACCTTCTTCAAGCCTGGAGGCACCTCCCGCTCTCTGTC 925 	
Db	805 -----CCTATTCAAAACAGGSAAGGACGACGCCCACTGTTTCAGT 844 	
QY	926 ACCACATCACCAAGGTATCCCACTGACGTCCAGCACAGTGTACTCTCCTCCGCCCCGACCC 985 	
Db	845 ACGGCAACCCCGGGATACACAATGGCATCTGGCTCTGTTTATTCTCCGCCCTACCCGGCCA 904 	
QY	986 CTGCCCCGACGACCTTCCGCCCGCGCCCTTTAACTCAAGAAAGCCCTCCAGTACTGT 1045 	

Db	905 CTTCTCTAGAAAACACCCCTATCAAGAAAGTGCTTTTAAATTTCAAGAAAGTCTTCAAGTACTGC 964 	
QY	1046 AACTGGAAAGTGGCAGCCCTTGAGCGGCATCGTTCATCTCAGCCACTCTGGTCATCTCTGCTG 1105 	
Db	965 AGCTGGAGTGCACCGCACTGTGTGTGTAGGGGTCTCAGTGTCTCTGGCCATCTCTCCTC 1024 	
QY	1106 GCATACTTTGTGGCCATGCACCTGTTTGGCTTAAACTGGCACCTGCGACCGATGGAGGGG 1165 	
Db	1025 TCCTATTTATAGCAATGCATCTATTTGGCTCAACTGGCACTTACAGCAGACGGAAAAAT 1084 	
QY	1166 CAGATGTATGAGATCAGGGAGGACACAGCCAGCAGTTGGCCCTGTGCCAACCGACGTCTCC 1225 	
Db	1085 GACACATTCGAGA-----ATGGAAGTGAATTCTGACACCGTGCCCAACAAACACTGTA 1138 	
QY	1226 CTATACCCCTCAGGGGGCACTGGCTTAGAGACCCCTGCACAGGAAAGGCAAGGAACCA 1285 	
Db	1139 TCGTTACCTTCTGGCGACA----- 1157 	
QY	1286 GAAGGAAAGCCAGTAGTTTCTTTCCAGAGGACAGTTTTCATAGATTTCTGGAGAAATTGAT 1345 	
Db	1158 -ATGGAATAATTAGGTGGATTACACATGAAATAAACACCATAGATTCCGGAGAACTTGAT 1216 	
QY	1346 GTGGAAAGCGAGCCTCCAGAAAGATTCCTCCTGGCACTTTCTGGAGATCTCAAGTGTTC 1405 	
Db	1217 ATTGGCCGGAGAGCAATTCAAGAGGTTCCCCCGGGATCTTCTGGAGATCGCAGCTCTTT 1276 	
QY	1406 ATAGACCATCCTGTGCATCTGAAATTCATATGTCTCTGGGAAAGGCAGCCCTGGTTGGC 1465 	
Db	1277 ATTGATCAGCCACAGTTTCTTAAGTTCAACATCTCTCTCAGAAGGATGCATTCGGA 1336 	
QY	1466 ATTTATGGCAGAAAAGGCCCTCCCTTCCATACATACACAGTTTGACTTTTGTGGAGCTGCTG 1525 	
Db	1337 GTGTACGGCCGAAAGGGCTTACCGCCCTTCCCATACTCAGTACGACTTTGTGGAACACTG 1396 	
QY	1526 GATGGCAGGAGGCTCCTAACCCAGGAGGCGCGGAGCCTTAGAGGGGACCCCGCCAGTCT 1585 	
Db	1397 GATGGTAGCAGTTAATTGCGAGAGAGCAGCGGAAACCTGGTGGAGTCCGAAAGAGCCGGG 1456 	
QY	1586 CGGGAACTGTGCCCCCTCCAGCCATGAGACAGGCTTCATCCAGTATTTGGATTTCAGGA 1645 	
Db	1457 CGGCAGGCGAGATCTGTCAAGCTGCACGAAAGTGGCTTCATCCAGTACTTGGATTCTGGA 1516 	
QY	1646 ATCTGGCACTTGGCTTTTACAATGACGGAAGGAGTCAAGAGTGGTTTCTTCTCTCAAC 1705 	
Db	1517 ATCTGGCATCTGCTTTTATAACGACGGGAAAAACCCAGAGCAGGTCTCTCTTAAACACG 1576 	
QY	1706 ACTGCCATTGAGTCGGTGGATAACTGCCCCAGCAACTGCTATGGCAATGTTGACTGCATC 1765 	
Db	1577 ATCGTTATAGAGTCTGTGGTGAATGCCCCCGAAATTGCCATGGAAATGGAGAGTGTGTT 1636 	
QY	1766 TCTGGACCTGCCACTGCTTCTCGGGTTTCTGGGCCCCGACTGTGGCAGAGCCTCCTGC 1825 	
Db	1637 TCTGGAACCTTGCCATTGTTTCCCCGGGTTTCTAGGTCCGGATTGTTCAAGAGCAGCCTGT 1696 	
QY	1826 CCCGTGCTCTGAGCGGAAATGGCCAATACATGAAAGGCAGATGCTTGTGCCACAGTGGC 1885 	
Db	1697 CCGGTGCTCTGATGGCAACGGGCAATACTCCAAGGGCCGCTGCCTGTGCTTCAGTGGC 1756 	
QY	1886 TGGAAAGGCGCTGAGTGCATGTGCCCAACCAACCACTGATCGATGTGGCCTGAGCAAC 1945 	
Db	1757 TGGAAAGGCGCACCCGAGTGTGACGTGCCGACGACCCAGTGCATTGACCCCGCAGTGGGGGT 1816 	
QY	1946 CATGGCACCTGCATCAGGGGCACCTGCATCTGCAACCTTGGCTACAAGGGCGAGAGCTGT 2005 	
Db	1817 CGTGGGATTTGCATCATGGGCTCTTGGCTTGTAACTCGGGATACAAAGGAGAAAACTGT 1876 	
QY	2006 GAGGAAGTGGACTGCATGGACCCCAACATGTTTCAGGCCCGGGGTGTCTGCTGAGAGCGGAA 2065 	
Db	1877 GAGGAAGCGGACTGTCTAGACCCCTGGATGTTCTAATCACGGGGTGTGTATCCATGGGGAA 1936 	
QY	2066 TGCCATTGCTTTGTGGGATGGGAGGCAACCACTGCGAGACCCCCAGGGCCACATGCTTA 2125 	
Db	1937 TGTCACTGCAATCCAGGCTGGGGTGGCAGCAACTGTGAAATACTGAAGACTATGTGTGCA 1996 	

Qy	2126	GACCAAGTTTCAGGCCACGGAACCTTCTCCCGACACCGGGCTTTGCAGCTGTGACCCA	2185
Db	1997	GACCAAGTTTCAGGCCACGGAACCTTCTCCCGACACCGGGCTTTGCAGCTGTGACCCA	2056
Qy	2186	AGCTGGACTGGACACGACTGTCTATCGAGATCTGTGCTGCCGACTGTGTTGGCCATGGC	2245
Db	2057	AATTGGACTGGCCCCGACTGTCTCAAAATGAAATATGTTCACTGGACTGCGGCTCACACGGC	2116
Qy	2246	GTGTGCGTAGGGGACCTTCCGCTGCGAGGATGGCTGGATGGGGGCAGCCTGCGACCCAG	2305
Db	2117	GTCTGCATGGGGGGCTCCTGTCTGTGAAGAAGGCTGGACCGGCCCCGGCGTGTAAATCAG	2176
Qy	2306	CGGGCTGCCACCCGCGCTGTGCCGAGCATGGGACCTGCGCGCAGCGGCAAGTGCAGTGC	2365
Db	2177	AGAGCTTGCCACCCCTCGCTGTCTGAGCAGCGGACGCTGCAAGGACGGCAAGTGCAGTGC	2236
Qy	2366	AGCCTGGCTGGAATGGCGAAACACTGCACCATCGCTCACTATCTGGATAGGTAAGTTAAA	2425
Db	2237	AGCCAAGGATGGAAACGAGAGCACTGCACAAATTGCTCACTATTGGATAAGATAAGTTAAA	2296
Qy	2426	GAGGTTGCCCTGGGTTGTGCAATGGCAACGGCAGATGTPACCTTAGACCTGAAATGGTTGG	2485
Db	2297	GAGGTTGCCCCGGCTTGTGCAACAGCAATGGGAGATGCACACTGGACCAAAACGGCTGG	2356
Qy	2486	CACCTGCGTCTCCAGCTGGCTGGAGAGGAGCTGCTGTGACACTTCCATGGAGACTGCC	2545
Db	2357	CACCTGCGTTTCCAGCCAGGTTGGAGAGGAGCAGGCTGTGACGTAGCCATGGAGACCCCTC	2416
Qy	2546	TGCGGTGACAGCAAAAGACAATGATGGAGATGGCCCTGGTGGACTGCATGGACCCCTGACTGC	2605
Db	2417	TGTACAGACAGCAAAAGACAAGAGGAGACGGACTCATTTGACTGATGGATCCCTGATTGC	2476
Qy	2606	TGCCCTCAGCCCCCTGTGCCATATCAACCCGCTGTGCTGGCTTGGCTCCCTAACCCCTCTGGAC	2665
Db	2477	TGCTCCAGAGCTCCTGCCAAAACACGCCCCCTACTGTCTGGCTTGCCTGATCCCTCAGGAT	2536
Qy	2666	ATCATCCAGGAGACACAGGTCCTGTGTCTACAGCAGAAACCTACACTCCTTCTATGACCGC	2725
Db	2537	ATCATTAGCCAAAGCCCTTCAGACACCATCTCAGCAAGCTGTCCAAGTCCCTTCTATGACCCGA	2596
Qy	2726	ATCAAGTTCTCGTGGCAGGACAGCAGCACATAATCCCGGGGAGAACCCCTTTGAT	2785
Db	2597	ATCAGTTTCTTGATTGGATCGGATAGCACCCACGTCGTCTCCCTGGAGAAAGTCCGTTCAAT	2656
Qy	2786	GGAGGGCATGCTTGTGTTATTCTGTGGCCAAAGTGTATGATGACATCAGATGGAACCCCTGGTT	2845
Db	2657	AAGAGTCTTGCTCCGTCATCAGAGGCCAAAGTACTAACAGCTGATGGAACCCCACTTATT	2716
Qy	2846	GGTGTGAACATCAGTTTGTCAATAACCTCTCTTTGGATATACAATCAGCAGGCAAGAT	2905
Db	2717	GGCGTCAACGTGTCGTTTTTACACTACTCGGAATATGGATATACCATTACCCGCCAGGAT	2776
Qy	2906	GGCAGCTTTGACTTGGTGACAAATGGCGGCATCTCCAATCATCTCGGTTTCGACGGGCA	2965
Db	2777	GGAAATGTTGACTTGGTGGCAATGGTGGCGCTTCTCTGACTTTGGTATTTGAGCGGTTCC	2836
Qy	2966	CTTTTCATCACACAGGAGCACACCCTGTGGCTGCCATGGGATCGCTTCTTTGTGATGGAA	3025
Db	2837	CCATTCTCACTCAGTACCACACTGTGTGGATTCCCTTGGAAATGCTTTTATGTGATGGAT	2896
Qy	3026	ACCATCATCATGAGACATGAGGAGAAATGAGATTCCCACTGTGACCTGAGCAATTTTGCC	3085
Db	2897	ACCCTTGTTCATGAAGAAAGAGGAGAACGACATTTCCCACTGTGACCTCAGTGGCTTTGTG	2956
Qy	3086	CGCCCCAACCCAGTCGTCTCTCCATCCCCACTGACGTCCTTCGCCAGCTCCTGTGCAGAG	3145
Db	2957	AGGCCAAGTCCCATCATTTGTGTTTACCGTTATCCACCTTCTTCAGGTCCTTCCCTGAG	3016
Qy	3146	AAAGGCCCCATTGTGCCGGGAAATTCAAGGCTTTTGACAGGAGAAATCTCTATCTCTGGCTGC	3205
Db	3017	GACAGCCCCCATCATCCCCCGAGACACAGGTCCTGTCATGAAGAAACCAATTTCCAGGAACA	3076
Qy	3206	AAGATGAGGCTGAGCTACCTGAGCAGCCGAGACCCCTGGCTACAAATCTGTCTCTGAGGATC	3265
Db	3077	GATTTGAAAACITTTCTTACCTGAGTTCCAGAGCGGAGGTACAAAGTCAGTTCTTAAAGATT	3136
Qy	3266	AGCCTCACCCACCCGACCATCCCCTTCAACCTCATGAAGGTGCACCTCATGGTAGCGGTG	3325
Db	3137	ACCATGACCCAGCGCTCATACCGTTTAACTCATGAAGGTCCATCTGTATGGTGGCCGTG	3196
Qy	3326	GAGGGCCGCTCTTTCAGGAAGTGGTTGCTGTCAGCCCCCAGACCTGTCTTATATTTCATT	3385
Db	3197	GTTGGGAGACTCTTCCAGAAGTGGTTTCCCTGCTCGCCAAACTTGGCCTACACGTTTCATC	3256
Qy	3386	TGGGACAAAGACAGACGTCTACAACCCAGAAAGTGTTTTGGCTTTCAGAAAGCCTTTGTTC	3445
Db	3257	TGGGATAAGACCGACGCGCATATAATCAGAAAGTCTACGGCTTGTTCAGAGGCGAGTTGTTC	3316
Qy	3446	GTGGGTTATGAATATGAATCCTGCCCAGATCTTAATCCTGTGGGAAAAAAGAACCAACAGTG	3505
Db	3317	GTCGGATACGAGTACGAGTCGTGCTTGGACCTGACTCTCTGGGAAAAAGAGACTGCCGTT	3376
Qy	3506	CTGCAGGGCTATGAAATTGACGCGTCCRAAGTTCGAGGATGGAGCCTTAGACAAACATCAT	3565
Db	3377	TTGCAAGGCTATGAGTTGGATGCTTCGAAACATGGGCGCTGGACGTTGGACAAGCACCAT	3436
Qy	3566	GCCCTCAACATTCAAAAGTGGTATCCTGCACAAAAGGGAATGGGGAGAACCAAGTTTGTGTCT	3625
Db	3437	GTACTGGACGTTTCAGAAACGGTATACTATACAAAGGAAAATGGAGAAAATCAGTTTCATCTCT	3496
Qy	3626	CAGCAGCCTCCTGTTCATTGGGAGCATCATGGGCAATGGGCGCCGGAGAAAGCATCTCCTGC	3685
Db	3497	CAGCAGCCTCCGTTGGTCAGCAGCATCATGGGTAAATGGTCGGAGCGTAGCATCTCATGC	3556
Qy	3686	CCCAGCTGCAACGGCCTTGTGACGGCAACAAGCTCCTGGCCCCAGTGGCCCTCACCTGT	3745
Db	3557	CCAAGTTGCAATGGTCAAGCTGACGGGAACAAACTCCTGGCACCCCGTGGCGCTGCTGT	3616
Qy	3746	GGCTCTGACGGGAGCCTCTATGTGGGTGATTTCAACTACATTAGAAAGGATCTTCCCCTCT	3805
Db	3617	GGGATCGACGGCAGTCTATACGTAGGGGATTTCAATTACGTCGGCGGATATTCCCGTCT	3676
Qy	3806	GGAAATGTCACCAACATCCTAGAGCTGAGGAATAAGATTTTCAGACATAGTCACAGTCCA	3865
Db	3677	GGGAATGTGACAAAGTGTTTTAGAACTTAAGAAATAAGATTTTAGACATAGTAGCAACCCA	3736
Qy	3866	GCACACAAATACTACCTGGCCACAGACCCCATGAGTGGGGCGCTCTTCTCTTGACAGC	3925
Db	3737	GCTCACAGATACTACCTGGCTACGGACCCAGTCACCGAGATTTGTACGTCTCTGATACT	3796
Qy	3926	AACAGCCGGCGGCTCTTTAAAATCAAGTCCACTGTGTGGTGAAGGACCTTGTCAAGAAC	3985
Db	3797	AACACCCCGCAGAACTATCGGCCGAAATCACTCACGGGAGCCAAAGACCTGACTAAAAAC	3856
Qy	3986	TCTGAGGTGGTTGCGGGGACAGGTGACCACTGTCCTCCCTTTGATGACACTCGCTGCGGG	4045
Db	3857	GCTGAAGTGGTGGCAGGGACCGGGGAACAGTGCCTTCCCTTTGACGAGGCCAGGTGTGGG	3916
Qy	4046	GATGGTGGGAAGGCCACAGAAAGCCACACTCACCAATCCCAGGGGTATTTACAGTGGACAAG	4105
Db	3917	GATGGAGGCAAGGCTGTGGAAGCAACGCTCATGAGTCCCAAGGAATGGCAATCGATAAG	3976
Qy	4106	TTTGGGCTGATCTACTTCGTGGATGGCACCATGATCAGACGCATCGATCAGATGGGATC	4165
Db	3977	AACGGACTGATCTACTTTGTTGATGGAAACCATGATCAGAAAGGTTGATCAAAATGGAATC	4036
Qy	4166	ATCTCCACCCTGCTCGGCTCTAATGATCTCACATCAGCCCCGCCACTCAGCTGTGATTCT	4225
Db	4037	ATATCAACTCTCTCTGGGCTCCAACGACCTCAGCTCAGCTCGACCTTTAACCTGTGATACT	4096
Qy	4226	GTGATGGATATTTCCAGGTAAGACTGGAGTGGCCCCACAGACTTAGCCATCAACCCCAATG	4285
Db	4097	AGCATGCATATCAGCCAGGTGCGTCTGGAAATGGCCCCACTGACCTCGCGATCAACCCCATG	4156
Qy	4286	GACAACTCACTTTTATGTCTCTCGACAACAATGTGGTCTCTGCAAAATCTCTGAAAAACCCAG	4345



Db 4157 GATAACTCCATCTACGTCCTGGATAATAACGTAAGTTTACAGATCACTGAAAAACCGTCAG 4216  
QY 4346 GTGGCGATTGTCCGGAGGCCCATGCATGCCAGGTCCTTGGCATTTGACCATTCCCTG 4405  
Db 4217 GTCCGCATCGCTGCCGGCGGCCCATGCATGTAGAGTCCCTGGAGTGG--AATACCCG 4273  
QY 4406 CTAAGCAAGGTGGCCATCCACGCAACCCCTGGAGTCAGCCACCGCTTTGGTGTGTTTACAC 4465  
Db 4274 GTGGGGAAGCACGCGGTTAGACCAACCCCTGGAGTCAGCCACGGCCATTGCTGTCTCTAC 4333  
QY 4466 AATGGGGTCCGTATATGCTGAGACTGATGAGAAAAAGATCAACCGCATCAGGCAGGTC 4525  
Db 4334 AGCGGGTCCTTTACATCACGGAACCTGATGAGAAAGATCAACCGAATAAGGCAGGTC 4393  
QY 4526 ACCACTAGTGGAGAGATCTCACTCGTTGCTGGGCCCCAGTGGCTGTGACTGTAAAAAT 4585  
Db 4394 ACGACAGACGGGAGATCTCCTTAGTGGCTGGGATACCTTCGGAATGTGACTGCAAGAAC 4453  
QY 4586 GATGCCAACTGTGATTGTTTTCTGGAGACGATGGTTATGCCAAGGATGCAAAAGTTAAAT 4645  
Db 4454 GACGCCAACTGTGACTGCTACCAAAGCGGAGACGGCTACGCCAAAGATGCCAAACTCAAT 4513  
QY 4646 ACCCCATCTTCCTGGCTGTGTGCTGATGGGAGCTCTACGTGGCCGACCTTGGGAAC 4705  
Db 4514 GCGCGTCTCCTCGCGCCTCGCCAGATGGCACTGTACATTGCAGATCTGGGAAAT 4573  
QY 4706 ATCCGAATTCGGTTTATCCGGAAGAACAAAGCCCTTCCTCAACACCCAGAACATGTATGAG 4765  
Db 4574 ATCAGGATCCGGGCCGTTTCGAAGAATAAAACCTTTACTGAACCTCAATGAACTTTACGAA 4633  
QY 4766 CTGTCTTACCAATTTGACCAGGAGCTCTATCTGTTTGATACCACCGGCAAGCACCTGTAC 4825  
Db 4634 GTTGCCTCTCCAACCTGATCAAGAGCTCTACATCTTTGACATCAACGGTACTCACCAGTAC 4693  
QY 4826 ACCCAAAGCCTGCCACAGGAGACTACCTGTACAACTTCACCTACACTGGGACGGCGAC 4885  
Db 4694 ACGTGAGCCTGGTCACGGGTGACTACCTATATAATTTAGTTACAGCAATGACAATGAC 4753  
QY 4886 ATCACACTCATCAGACAAACAATGGCAACATGGTAAATGTCCGCCGAGACTCTACTGGG 4945  
Db 4754 GTCACCGCTGTAACCTGACAGCAATGGCAACACCCCTCCGAAATCCGAAGGGATCCGAATCGG 4813  
QY 4946 ATGCCCTCTGGCTGGTGGTCCAGATGGCCAGGTGTAAGTGGTGAACCATGGGCACCAAC 5005  
Db 4814 ATGCCGGTGGGTGGTGTCTCCTGTATAACCAGGTGATGGTTGACCATAGGCACCAAC 4873  
QY 5006 AGTGCACTCAAGAGTGTGACCACACAAGGACACGAGTCGAGTTGGCCATGATGACATACCATGGC 5065  
Db 4874 GGGTGTCTGAAAAGCATGACCGCTCAGGGCCTGGAACTGGTTTGTTTACTTACCATGGC 4933  
QY 5066 AATTCCGGCCTTCTGGCAACCAAAAGCAATGAAAACGGATGGACAAACATTTTATGAGTAC 5125  
Db 4934 AACAGTGGGCTTTTAGCCACCAAAAGTGA CGAACTGGATGGACAAACATTTTIGACTAT 4993  
QY 5126 GACAGCTTTGGCCGCTGACAAATGTGACCTTCCCTACTGGCCAGGTGAGCAGTTTCCGA 5185  
Db 4994 GACAGTGAAGGTGCGCTGACGAAATGTTACCTTCCCACTGGGTGGTTACAAACCTGCAC 5053  
QY 5186 AGTGATACAGACAGTTTCAGTGCATGTCCAGGTAGAGACCTCCAGCA--AGGATGATGTC 5242  
Db 5054 GGGGACATGGACAAGGCTATCAGGTGGACATCGAGTCATCCAGCAGAGAGGAAGATGTC 5113  
QY 5243 ACCATAACCAACCAACCTGTCTGCTCAGGCGCCTTCTACACACTGCTGCAAGACCAAGTC 5302  
Db 5114 AGCATCACTTCGAACTGTCTCCTCCATCGATTCTTCTACACCATGGTCCAAAGACCAAGTTA 5173  
QY 5303 CGGAACAGCTACTACATCGGGGCCGATGGCTCCTTGGGGCTGCTGCTGGCCACGGCATG 5362  
Db 5174 AGAAACAGTTACCAGATTGGGTATGATGGCTCCCTTAGAATCTTCTATGCCAGTGGTCTG 5233  
QY 5363 GAGGTGGCGCTGCAGACTGAGCCCCACCTTGTGCTGGCAGCCGTCAACCCACCGTGGGC 5422

Db 5234 GACTCTACTACCAGACAGAGCCCCACGTTCTGGCTGGCACGGCGAATCCCACAGTAGCC 5293  
QY 5423 AAGAGGAATGTACGCTGCCCATCGACAAACGGCCTCAACCTGGTGGAGTGGCGCCAGCGC 5482  
Db 5294 AAAAGAAACATGACTCTTCCCGGTGAGAAACGGGCAGAATCTGGTGGAGTGGAGATCCGA 5353  
QY 5483 AAAGAGCAGGCTCGGGGCCAGGTCACTGTCTTTGGGCGCCGGCTGCGGGTGCAAAACCGA 5542  
Db 5354 AAAGAAACAAGCCAGGGCAAGTCAACGTATTTCGGCCGGAAGCTCAGGGTCAATGGGCGC 5413  
QY 5543 AATCTCCTATCTCTGGACTTTGATCGCGTAAACACGCACAGAGAAGATCTATGATGACCAC 5602  
Db 5414 AACCTACTCTCAGTGGACTTTGATCGGACCAACCAAGACGGAAGATCTATGATGACCAC 5473  
QY 5603 CGCAAGTTCACCCCTTCGGATTCTGTACGACGAGCGGGCGGCCAGCCTCTGTCACCC 5662  
Db 5474 CGGAAATTTCTCTGAGGATCGCTTACGACAGCTCGGGCACCCGACTCTCTGGCTGCCG 5533  
QY 5663 AGCAGCAGGCTGAATGGTGTCAACGTGACATACTCCCCTGGGGGTTACATTGCTGGCATC 5722  
Db 5534 AGTAGCAAGCTAAATGGCAGTGAACGTCACTACTCATCCACCGGTCAAAATGCCAGCATC 5593  
QY 5723 CAGAGGGGCATCATGTCTGAAAAGAAATGGAATACGACCAGGCGGCCGATCAACATCCAGG 5782  
Db 5594 CAGAGAGGGACCACGAGCGAAAAGGTGGACTATGACAGCCAGGGAGGATCGTATCTCGG 5653  
QY 5783 ATCTTCGCTGATGGGAAGACATGGAGCTACACATACTTAGAGAAAGTCCATGCTGCTA 5842  
Db 5654 GTCTTTGCCGATGGGAAAACATGGAGTTACACGTACTTGGAAGAGTCCATGTTCTTCTG 5713  
QY 5843 CTACACAGCCAGAGGCAGTATATCTTTGAGTTTCGACAAGAAATGACCGCCTCTCTTCTGTG 5902  
Db 5714 CTCCATAGCCAGCGGCAGTACATCTTCGAAATACGACATGTGGACCGCCTGTCCGCCATC 5773  
QY 5903 ACGATGCCAAAGCTGGCGGCAGACACTAGAGACCATCCGCTCAGTGGGCTACTACAGA 5962  
Db 5774 ACCATGCCAGTGTGGCTCGCCACACCATGCAGACCATCCGGTCCATTGGCTACTACCGC 5833  
QY 5963 AACATCTATCAGCCCCCTGAGGGCAATGCCTCAGTCATACAGGACTTCTACTGAGGATGGG 6022  
Db 5834 AACATCTACAAATCCCCCAGAAAGCAATGCCTCTATCATCACCGACTACAACGAGGAAGG 5893  
QY 6023 CACCTCCTTCACACCTTCTACCTGGCACTGGCCGAGGTGATATACAAGTATGGCAAA 6082  
Db 5894 CTGCTTCTGCAAAACAGCTTTCCTGGGAACGAGTCGGAGGTCTTATTCAAGTATAGAAG 5953  
QY 6083 CTGTCAAAGCTGGCAGAGACGCTCTATGACACCA CCAAGGTCAGTTTCACCTATGACGAG 6142  
Db 5954 CAGACCAGGCTATCAGAAATTTTATACGACAGCACAAAGATCAGTTTTTACCTACGCGAA 6013  
QY 6143 ACGCAGGCATGCTGAAGACCATCAACCTACAGAAATGAGGGCTTCACTGCACCATCCGC 6202  
Db 6014 ACAGCGGAGTCTGAAAAACAGTAAACCTTCAGAGTGATGGTTTTATTGACCATTAGA 6073  
QY 6203 TACCGTCAGATTGGGCCCCCTGATTGACCGCAGAGATCTTCCGCTTCACTGAGGAAGGCATG 6262  
Db 6074 TACAGGCAAAATGGTCCCCTGATTGACAGACAGATTTTCCGCTTACGCGAGGATGGAATG 6133  
QY 6263 GTCAACGCCCGTTTGTGACTACAACTATGACAAACAGCTTCCGGGTGACCAGCATGCAAGCT 6322  
Db 6134 GTAAATGCGAGATTGACTATAGCTACGACAAACAGCTTTCGAGTGACCAGCATGCAAGGT 6193  
QY 6323 GTGATCAACGAGACCCCACTGCCCATTTGATCTCTATCGCTATGATGTGTCAGGCAAG 6382  
Db 6194 GTCATCAATGAAAAACCACTGCCCATTTGATCTATACCAAGTTTGTGATGACATCTCTGGCAAA 6253  
QY 6383 ACAGAGCAGTTTGGGAAGTTTGGTGTCAATTACTATGACATTAACAGATCATCACCACA 6442  
Db 6254 GTCGAGCAGTTTGGAAAAATTCGAGTGAATATACTACGACATCAACCAAAATCATTTCCACG 6313  
QY 6443 GCTGTCAATGACCCACACCAAGCAATTTTGTATGATATGGCAGGATGAAGGAAGTGCAGTAT 6502  
Db 6314 GCCGTGATGACTTATACAAAGCACTTTGTATGCTCATGGGCGCATCAAGGAGATCCAATAT 6373



QY	6503	GAGATCTTCCGCTCGCTCATGTACTGGATGACCGTCCAGTATGATAACATGGGGCGAGTA	6562	QY	7583	AAGTCTATCCTCGGGGTACAGTGTGAAGTACAGAAGCAGCTCAAGGCCCTTTGTTCACCTTA	7642
Db	6374	GAGATATTTAGGTCACATGTACTGGATTACAATTTCAAATATGATAATATGGSCGGGTA	6433	Db	7439	CCGCCCATCTTTGGAGTTTCAGCAGCAAGTGGCAAGGCAAGCCAAAGGCCCTTCTTGTCCCTG	7498
QY	6563	GTGAAGAAGGAGCTGAAGGTAGGACCTTACGCCCAATPACCACTCGCTACTCCTATGAGTAT	6622	QY	7643	GAACGGTTTGACAGCTCTATGGCTCCACAATCACCAGCTGCCAGCAGGCTCCAAAGACC	7702
Db	6434	ACCAAGAGAGAGATTAAATTTGGCCCTTTTGCCAACACTACCAATACGCGTAGGATAC	6493	Db	7499	GGGAAGATGSCCGAGGTGCAGGTGAGCCGACGCAAAAGCTGGCGCCGAG---CAGTCGTGG	7555
QY	6623	GATGCTACGGCCAGCTGCAGACAGTCTCCATCAATGACAAAGCCACTCTGGCGCTACAGC	6682	QY	7703	AAGAAGTTTGCATCCAGCGGCTCAGTCTTTTGGCAAGGGGTCAAGTTTTCCTTGAAGGAT	7762
Db	6494	GACGTCGATGGACAGCTCCAAACAGTTTACCTAAACGAAAAGATCATGTGGCGGTACAAC	6553	Db	7556	CTGTGGTTTCGCCACGGTCAAGTCGCTCATCGCAAGGGCGTCTATGCTGGCCGTGAGCCAA	7615
QY	6683	TACGACCTCAATGGGAACCTGCACTTACTGAGCCCTGGGAACAGTGCACGGCTCACACCA	6742	QY	7763	GGCCGAGTGACACAGACATCATCAGTGTGSCCAATGAGGATGGGCGAAGGGTTGCTGCC	7822
Db	6554	TACGACCTAAATGGAAACCTCCACTTGTCTCAACCCACAGCAGCGGCCCTGACCCCT	6613	Db	7616	GGCCGCGTGCAGACCAACGTGCTCAACATCGCCAACGAGGACTGCATCAAGGTGGCGGCG	7675
QY	6743	CTACGGTATGACATCCGGACCGCATCACTCGGCTGGGTGACGTGCAATACAAGATGGAT	6802	QY	7823	ATCTTGAAACCATGCCCACTACCTAGAGAACCTTGCACTTCACCATTTGATGGSGTGGATACC	7882
Db	6614	CTGCGCTATGACCTGCGGACAGAAATCACCCGCTGGCGCATGTTTCAGTACCGGCTGGAT	6673	Db	7676	GTGCTCAACAAACGCCCTTCTACCTGGAGAACCTGCACCTTCACCATCGAGGGCAAGGACACA	7735
QY	6803	GAGGATGGCTTCCTGAGGACGGGGCGGTGATATCTTTGAGTACAACTCAGCTGGCCTG	6862	QY	7883	CATTACTTTGTGAAACCAAGGACCTTCAGAAAGTGACCTTGGCCATCCTGGGCTCAGTGGG	7942
Db	6674	GAAGATGGTTTCCTGCGTCAGAGGGGCACTGAAATTTTGAATACAGCTCCAAAGGGCTT	6733	Db	7736	CACACTTTTCATCAAGACCACCAACCCGAGAGCGACCTGGGCACACTGCGGCTGACGAGC	7795
QY	6863	CTCATCAAGGCCTACAACCGGCTGGCAGCTGGAGTGTGAGGTACCGCTACGATGGCCTG	6922	QY	7943	GGCGGCGAAACCCCTGGAGAATGGGGTCAACGTCACCTGTGTCCAGATCAACACAGTACTT	8002
Db	6734	CTGACTCGAGTCTACAGTAAAGCAGTGGCTGGACAGTATCTATCGGTACGACGGCCTG	6793	Db	7796	GGTCGCAAGGCCCTGGAGAACGGGATCAACGTGACCGTGTCTCAGTCCACCACGGTGGTG	7855
QY	6923	GGCGGCGCGTGTCCAGCAAGAGCAGCCACAGCCACCCTGCAGTTCTTCTATGCAGAC	6982	QY	8003	AATGGCAGGACTAGACGCTACACAGACATCCAGCTCCAGTACGGGGCACCTGTGCTTGAAC	8062
Db	6794	GGAAGACGTGTTTCTAGCAAAACACAGCCTGGGACAGCACTTCAGTTTCTACGCGGAC	6853	Db	7856	AACGGCAGGACTCGCAGGTTCCCGACGCTGGAGATGCAGTTCGGTGCCCTGGCACTGCAT	7915
QY	6983	CTGACCAACCCCAACCAAGTCAACCACTGTACAACCACTCCAGCTCTGAGATCACTCC	7042	QY	8063	ACACGCTACGGGACAAACGTTGGATGAGGAGAAGSCACGGGTCTCTGGAGCTGSCCGGCAG	8122
Db	6854	CTGACATACCCCACGAGAAATTACTACGTCTACAACCAATCCAGTTCAGAAATCACTCC	6913	Db	7916	GTGCGCTATGGCATGACGCTGGACGAGGAGAAGGCGCGCATTTCTGGAGCAGGCGGCCAG	7975
QY	7043	CTCTACTACGACTTGCAAGGACACCTCTTTTGCCATGGAGCTGAGCTGAGCAGTGGTATGAT	7102	QY	8123	AGAGCCGTGCGCCAAGCGTGGGCCCCGGAGCAGCAGAGACTGCGGGAAGGGAGGAAGGC	8182
Db	6914	CTGTACTATGACCTCCAAGGACATCTCTTCGCCATGGAGATCAGCAGTGGGATGAGTTC	6973	Db	7976	CGCGCGTTCGCCCGGCGTGGGCACGGGAGCAGCAGCGCTGCGCGACGGCGAGAGGGT	8035
QY	7103	TACATAGCTTGTGACAAACATCGGACCCCTCTTGTGCTCTTTAGTGGAAACAGGTTTGATG	7162	QY	8183	CTGCGGGCCTGGACAGAGGGGGAGAAGCAGCAGGTGCTGAGCACAGGGCGGGTGCAAGGC	8242
Db	6974	TACATCGCCTCGGACNAACACGGGGACACCGCTGGCTGTTTTCAGCAGCAACGGGCTCATG	7033	Db	8036	GCGCGCCTCTGGACGGAGGGTGAGAAACGGCAGCTGCTGAGCGCTGGCAAGGTGCAGGGC	8095
QY	7163	ATCAAGCAAAATCCTGTACACAGCCTATGGGAGATCTACATGGATACCAACCCCACTTT	7222	QY	8243	TACGACGGCTTTTTCGTGATCTCTGTGAGCAGTACCCAGAACTGTTCAGACAGGCCAAC	8302
Db	7034	CTGAACACAGACCCAGTACACTGCCTATGGTGAGATCTACTTTGACTCCAACGTCGACTTT	7093	Db	8096	TACGATGGGTACTACGTACTGTCCGTGGAGCAGTACCCCGAGCTGGCTGACAGTGCCAAC	8155
QY	7223	CAGATCATATAGGCTACCATGGTGGCCTCTATGATCCACTCACCAAGCTTGTCCACATG	7282	QY	8303	AACATCCACTTCATGACACAGAGCGAGATGGGCCGGAGGTTGAC	8345
Db	7094	CAGCTGTTAATTGGATTCCACGGGGGCTTGATGACCCGCTCACCAACTAATCCACTTT	7153	Db	8156	AACATCCAGTTCTTTCGCACAAAGTGAGATCGGCCAAGAGGTTAAC	8198
QY	7283	GGCCGGCGAGATTATGATGTGCTGGCCGGACGCTGGACTAGCCACAGACCACGAGCTGTGG	7342	RESULT 9			
Db	7154	GGAGAAAGAGATTATGACATTTTGGCGGGAAGATGGACCACACCGGACATTTGAAATCTGG	7213	ABQ82344			
QY	7343	AAGCACCTTAGTAGCAGCAACGTCATGCGCTTTTAAATCTCTATATGTTCAAAAACAACAC	7402	ID	ABQ82344	standard; cDNA; 8645 BP.	
Db	7214	A---AAAGATCGGAAAGGACCCCTGCTCCTTTTAACTGTATATGTTTCGGAATAACAC	7270	XX	AC	ABQ82344;	
QY	7403	CCCATCAGCAACTCCAGGACATCAAGTCTTCATGACAGATGTTAAACAGCTGGTGCTC	7462	XX	AC	ABQ82344;	
Db	7271	CCCCGAGCAAAATCCATGATGTGAAAGATTACATCACGGATGTTAAACAGCTGGTGTTG	7330	DT	17-DEC-2002	(first entry)	
QY	7463	ACCTTTGGATTCCAGCTACACAACGTGATCCCTGGTTATCCCAAAACAGACATGGATGCC	7522	XX	Human	NOV15b encoding cDNA SEQ ID NO:37.	
Db	7331	ACGTTTGGCTTCCATCTGCACAATGCTATTCTCCCTGGATTCCCTGTTCCCAAAATTGATTTA	7390	KW	Human; NOVX;	cytostatic; neuroprotective; anticonvulsant; cardiovascular;	
QY	7523	ATGGAACCTCTCTACGAGCTCATCCACACACAGATGAAAACGGCAGGAGTGGACAACAGC	7582	KW	cerebroprotective;	nootropic; antidiabetic; antiinflammatory; fungicide;	
Db	7391	ACTGAGCCTTCTATGAGCT-----TGTAAGAGTCAACAGTGGGAAGATGTG	7438	KW	antirheumatic;	antiarthritic; immunosuppressive; antiallergic; virucide;	
				KW	antianaemic;	antibacterial; protozoacide; antihelminthic; gene therapy;	
				KW	cancer;	leukaemia; lymphoma; melanoma; neurological disorder; epilepsy;	
				KW	stroke;	ischaemic cerebrovascular disease; Alzheimer's disease; allergy;	
				KW	Pick's disease;	vesicular transport disease; gastrointestinal disorder; goitre;	
				KW	diabetes mellitus;	Grave's disease; gastrointestinal disorder; infection;	
				KW	ulcerative colitis;	gastric disorder; duodenal disorder; infection;	
				KW	autoimmune disease;	allergic reaction; autoimmune haemolytic anaemia;	

KW	rheumatoid arthritis; gene; chromosome 4; ss.
XX	
OS	Homo sapiens.
XX	
FH	Key Location/Qualifiers
FT	151..8316
FT	/*tag= a
FT	/product= "NOV15b"
XX	
PN	WO200262999-A2.
XX	
PD	15-AUG-2002.
XX	
PF	31-DEC-2001; 2001WO-US049976.
XX	
PR	29-DEC-2000; 2000US-0258928P.
PR	02-JAN-2001; 2001US-0259415P.
PR	04-JAN-2001; 2001US-0259785P.
PR	20-FEB-2001; 2001US-0269814P.
PR	09-MAR-2001; 2001US-0279863P.
PR	29-MAR-2001; 2001US-0279832P.
PR	29-MAR-2001; 2001US-0279833P.
PR	13-APR-2001; 2001US-0283889P.
PR	18-APR-2001; 2001US-0284447P.
PR	25-APR-2001; 2001US-0286683P.
PR	29-MAY-2001; 2001US-0294080P.
PR	16-AUG-2001; 2001US-0312915P.
PR	17-AUG-2001; 2001US-0313325P.
PR	17-SEP-2001; 2001US-0322699P.
PR	26-NOV-2001; 2001US-0333350P.
XX	
PA	(CURA-) CURAGEN CORP.
XX	
PI	Spytek KA, Li L, Wolenc AR, Vernet CAM, Eisen A, Liu X;
PI	Malyankar U, Shinkets RA, Tchernev VT, Spaderna SK, Gorman L;
PI	Kekuda R, Patturajan M, Gusev V, Gangolli EA, Guo X, Shenoy S;
PI	Rastelli L, Casman SJ, Boldog F, Burgess CE, Edinger S, Ellerman K;
PI	Gunther E, Smithson G, Millet I, Macdougall JR;
XX	
DR	WPI; 2002-732706/79.
DR	P-PSDB; ABP53587.
XX	
PT	New NOVX polypeptides and polynucleotides useful for treating NOVX-
PT	associated disorders, such as cancers, neurological disorders, disorders
PT	of vesicular transport, gastrointestinal disorders, and autoimmune
PT	diseases.
XX	
PS	Claim 8; Page 114-117; 444pp; English.
XX	
CC	The present invention describes novel human proteins designated NOVX,
CC	where X is 1 to 20 e.g. NOV1. NOVX sequences can have neuroprotective,
CC	cytostatic, anticonvulsant, cerebroprotective, nootropic, cardiovascular
CC	antidiabetic, antiinflammatory, antirheumatic, antiarthritic, virucide,
CC	immunosuppressive, antiallergic, antianaemic, antibacterial, fungicide,
CC	protozoacide and antihelminthic activities, and can be used in gene
CC	therapy. The NOVX proteins, nucleotides or antibodies can be used in the
CC	manufacture of a medicament for treating a syndrome associated with a
CC	human disease selected from NOVX-associated disorder, such as cancers
CC	(e.g. leukaemia, lymphoma, melanoma or cancer of the liver, lung, muscle
CC	ovary, testis and uterus), neurological disorders (e.g. epilepsy, stroke
CC	ischaemic cerebrovascular disease, Alzheimer's disease or Pick's
CC	disease), disorders of vesicular transport (e.g. cystic fibrosis,
CC	diabetes mellitus, Grave's disease, or goitre), gastrointestinal
CC	disorders (e.g. ulcerative colitis, or gastric and duodenal disorders),
CC	autoimmune diseases (e.g. allergic reactions, autoimmune haemolytic
CC	anaemia, or rheumatoid arthritis), viral, bacterial, fungal, helminthic
CC	and protozoal infections. The NOVX proteins can be used as immunogens to
CC	produce antibodies and as vaccines. The NOVX nucleotide sequences may be
CC	used in chromosome mapping, identifying individuals from minute
CC	biological samples (tissue typing), and in forensic identification of a
CC	biological sample. The present sequence encodes human NOV15b, which is
CC	located on chromosome 4
XX	



QY	1046	AACTGGAAGTCGCAGCCCTGAGCGCCATCGTCACTCTCAGCCACTCTGGTCACTCCTGCTG	1105
Db	1066	AGCTGGAATGCACCTGCACTGTGTGCCGTAGGGTCTCGGTGCTCCTGGCAATACCTCTG	1125
QY	1106	GCATACCTTTGTGGCCATGCACCTGTTTGGCCATAACTGGCACCTGCAGCCGATGGAGGG	1165
Db	1126	TCTTATTTATAGCAATGCATCTCTTTGGCCCTCAACTGGCAGCTACAGCAGACTGAAAT	1185
QY	1166	CAGATGATGAGATCACGGAGGACACAGCCAGCAGTTGGCCCTGTGCCAACCGACGTCTCC	1225
Db	1186	GACACATTTGAGA-----ATGGAAAAGTGAATTCCTGATACCATGCCAACAAACACTGTG	1239
QY	1226	CTATACCCCTCAGGGGGCACTGGCTTAGAGACCCCTGACAGGAAAGGCAAAAGGAACCACA	1285
Db	1240	TCATTACCTTCTGGAGACA-----	1258
QY	1286	GAAGGAAAGCCAGTAGTTTCTTTCCAGAGGACAGTTTTCATAGATTCTGGAGAAATTGAT	1345
Db	1259	-ATGGAAAAATTAGGTGGAATTTACGCAAGAAAAATAACACATAGATTCGGAGAACTTGAT	1317
QY	1346	GTGGGAAGCGAGCCCTCCAGAAGATTCTCTGGCACTTCTGGAGATCTCAAGTGTTC	1405
Db	1318	ATTGCCGAAGAGCAATTCAAGAGATTCTCCCGGGATCTTCTGGAGATCACAGCTCTTC	1377
QY	1406	ATAGACCATCCTGTGCATCTGAAATTCAATGTGTCTCTGGGAAAGGCAGCCCTGGTTGGC	1465
Db	1378	ATTGATCAGCCACAGTTTCTTAAATTCAATACTCTCTCAGAAAGGATGCAATTGATTGGA	1437
QY	1466	ATTTATGGCAGAAAAGGCCTCCCTCTTCACATACACAGTTTGACTTTGTGGAGCTGCTG	1525
Db	1438	GTATATGGCCGGAAGGCTTACC GCCTTCCATACTCACTAGTATGACTTCGTGGAGCTCCTG	1497
QY	1526	GATGGAGGAGGCTCCTAACCCAGGAGCGCGGAGCCCTAGAGGGGACCCCGCCCACTCT	1585
Db	1498	GATGGCAGCAGGCTGATTGCCAGAGAGCAGCGGAGCCCTGCTTGAGACGGAGAGCCGGG	1557
QY	1586	CGGGAACTGTGCCCCCTCCAGCCATGAGACAGGCTTCAATCCAGTATTTGGATTCAGGA	1645
Db	1558	CGGACGGCAGATCCGTACGCCCTTCATGAGGCCGGCTTATCCAGTACTTGGATTCTGGA	1617
QY	1646	ATCTGGCACTGGCTTTTACAAATGACGGAAAGGAGTCAGAAGTGGTTTCTTCTCACC	1705
Db	1618	ATCTGGCATCTGGCTTTTATAATGATGGGAAAAATGCAAGCAGGTGTCTTTTAATACC	1677
QY	1706	ACTGCCATTGAGTCGGTGGATAACTGCCCCAGCAACTGCTATGGCAATGGTACTGCATC	1765
Db	1678	ATTGTTATAGAGTCTGTGGTGGAAATGTCCTCCGAAATTGCCATGGAAATGGAGAATGCGT	1737
QY	1766	TCTGGGACCTGCCACTGCTTCTCTGGTTTCTTGGCCCGGACTGTGGCAGAGCCCTCCTGC	1825
Db	1738	TCTGGAATTGCCATTGTTTCCAGGATTTCTGGGTCCGGATTGTTCAAGAGCCGCCCTGT	1797
QY	1826	CCCGTGCTCTGTAGCGGAAATGGCCCAATACATGAAAGGCAGATGCTTGTGCCACAGTGSC	1885
Db	1798	CCAGTGTATGTAGTGGCAACGGGGCAGTACTCCAAGGGCCGCTGCCTGTGTTCAGCCGC	1857
QY	1886	TGGAAGCGCTGAGTCGATGTGCCACCAACCAGTGTATCGATGTGGCCTGCAGCAAC	1945
Db	1858	TGGAAGGCGACCGAGTGTGATGTGCCGACTACCCAGTGTATTGACCCACAGTGTGGGGT	1917
QY	1946	CATGGCACCTGCATCACGGGCACCTGCATCTGCAACCTTGGCTACAAAGGCGGAGAGCTGT	2005
Db	1918	CGTGGGATTTGTATCATGGGCTCCTGTGCTTGCACTCAGGATACAAAGGAGAAAGTTGT	1977
QY	2006	GAGGAAGTGGACTGCATGGACCCCACTATGTTCAGGCCGGGTGTCTGCGTGAAGGCGAA	2065
Db	1978	GAAGAAGCTGACTGTATAGACCTGGGTGTTCTAATCATGGTGTGTGTATCCACGGGGA	2037
QY	2066	TGCCATTGCTTTGTGGATGGGGAGGCACAACTGCGAGACCCCAAGGCGGCACATGCTTA	2125
Db	2038	TGTCACCTGCAGTCCAGGATGGGGAGGTAGCAATTGTGAAATACTGAAGACCATGTGTCCA	2097
QY	2126	GACCAGTGTTCAGGCCACGGAAACCTTCTCTCCGGACACCGGGCTTTTGACGCTGTGACCCA	2185
Db	2098	GACCAGTGTCTCGGCCACGGAAACGTATCTTCAAGAAAGTGGCTCCTGCACGTGTGACCCCT	2157
QY	2186	AGCTGGACTGGACACGACTGTTCTATCGAGATCTGTGTGCCGACTGTGGTGGCCATGGC	2245
Db	2158	AACTGGACTGGCCCAGACTGCTCAAACGAAATATGTTCTGTGGACTGTGGCTCACACGGC	2217
QY	2246	GTGTGCGTAGGGGACACCTGCCGCTCGAGGATGGCTGGATGGGGCAGCTGCGACCAAG	2305
Db	2218	GTTTGCATGGGGGGACGTGTGCTGTGAAGAAGGCTGGACGGGCCAGCCTGTAATCAG	2277
QY	2306	CGGGCCTGCCACCCGCGCTGTGCCGAGCATGGGACCTGCCGCGACGGCAAGTGGCAGTGC	2365
Db	2278	AGAGCCTGCCACCCCGCTGTGCCGAGCAGCGGACCTGCAAGGATGGCAAGTGTGAATGC	2337
QY	2366	AGCCTGGCTGGAATGGGGAACAACCTGCACCATCGCTCACTATCTGGATAGGCTAGT---	2421
Db	2338	AGCCAGGCTGGAATGGAGAGCACTGCACATATCGCTCACTATTTGGATAAGATAGTTAAA	2397
QY	2422	-----TAAAGAGGGTTGCCCTGGGTTGTGCAATGGCAACGGCAGATGTACC	2467
Db	2398	GACAAGATAGGATATAAGAGGGTTGTCTCGTCTGTGCAACAGCAATGGAAGATGTACC	2457
QY	2468	TTAGACCTGAATGTTGGCACTGCGTCTGCCAGCTGGCTGGAGAGGAGCTGGCTGTGAC	2527
Db	2458	CTGGACCAAAATGCGGACATTTGTGTGTGCCAGCTGGATGGAGGAGCAGGCTGTGAC	2517
QY	2528	ACTTCCATGGAGACTGCTGCGGTGACAGCAAAAGACAATGATGGAGATGGCCTGGTGGAC	2587
Db	2518	GTAGCCATGGAGACTCTTTGCACAGATAGCAAGGACAATGAAGGGATGGACTCATTGAC	2577
QY	2588	TGCATGGACCTGACTGCTGCCCTCCAGCCCCCTGTGCCATATCAACCCGCTGTGCCCTGGC	2647
Db	2578	TGCATGGATCCCAGATTGCTGCTACAGAGTTCTCTGCCAGAATCAGCCCTATTCTCGGGA	2637
QY	2648	TCCCCTAACCTCTGGACATCATCCAGGAGACAGAGTCCCTGTGTCAACAGCAGAACCTA	2707
Db	2638	CTGCCGATCCTCAGACATCATTAGCCAAAGCCTTCAATCGCCTTCTCAGCAAGCTGCC	2697
QY	2708	CACCTCTTCTATGACCGCATCAAGTTCTCTGTTGGCAGGGACAGCACGCACATAATCCCC	2767
Db	2698	AAATCCTTTTATGATCGAATCAGTTTCTTATAGGATCTGATAGCACCCCATGTTATACCT	2757
QY	2768	GGGAGAAACCCCTTTGATGGAGGGCATGCTTGTGTATTTCGTGGCCAAAGTATGACATCA	2827
Db	2758	GGAGAAAGTCCCTTCAATAAAGAGCCTTGTCATCTGTCTCATAGAGGCCAAAGTACTGCT	2817
QY	2828	GATGAAACCCCTTGTGGTGTGAACATCAGTTTGTCAATAAACCTCTCTTTTGGATAT	2887
Db	2818	GATGAAACTCCACTTATGGAGTAAATGTCTCGTTTTCATTACCAGAAATATGGATAT	2877
QY	2888	ACAATCAGCAGGCAAGATGGCAGCTTTGACTTGTGACAAAATGGGGCATCTCCATCATC	2947
Db	2878	ACTATTACCCCGCAGGACGGAATGTTTGACTTGGTGGCAAAATGGTGGGCCCTCTCTAACT	2937
QY	2948	CTGGGTTTCGAGCGGGCACCTTTCATCACACAGGAGCACACCCCTGTGGCTGCCATGGGAT	3007
Db	2938	TTGGTATTTGAACGATCCCCATTCTCACTCAGTATCATACTGTGTGGATTCCATGGAAT	2997
QY	3008	CGCTCTTTTGTATGGAACCATCATCATGAGACATGAGGAAATGAGATTTCCCAGCTGT	3067
Db	2998	GTCTTTTATGTATGGATACCTAGTCTATGGAGAAAGAGAAATGACATTTCCCAGCTGT	3057
QY	3068	GACCTGAGCAATTTTGCCCGCCCAACCCAGTGTCTCTCCATCCCCACTGACGTCCTTC	3127
Db	3058	GATCTGAGTGGATTCTGTGAGGCCAAATCCCATCATTTGTGTATCACCTTTATCCACCTTT	3117
QY	3128	GCCAGCTCCTGTGCAGAGAAAGGCCCCCATTTGTCCGGAAATTCAGGCTTTGCAGGAGGAA	3187
Db	3118	TTCAGATCTTCTCCTGAAGACAGTCCCATCATTTCCCGAAACACAGGTACTCCACGAGGAA	3177
QY	3188	ATCTCTATCTCTGGCTGCAAGATGAGGCTGAGCTACCTTGAGCAGCCGACCCCTGGCTAC	3247



Db 3178 ACTACAAATCCAGGAACAGATTTGAAACTCTCCTACTTGAGTTCAGAGCTGCAGGGTAT 3237

QY 3248 AAATCTGTCTGAGGATCAGCCTCACCCACCCGACCATCCCCTTCAACCTCATGAAGGTG 3307

Db 3238 AAGTCAGTCTCAAGATCACCATGACCCAGTCTATTATTCATTTAATTAATGAAGGTT 3297

QY 3308 CACCTCATGGTAGCGGTGAGGGCCGCTCTTCAGGAAGTGGTTCGCTGCAGCCCCAGAC 3367

Db 3298 CATCTTATGGTAGCTGTAGTAGGAAGACTCTTCCAAAAGTGGTTTCCCTGCCTCACCAAC 3357

QY 3368 CTGTCCTATTATTTCATTTGGGACAAGACAGAGCTTACAACCAGAAAGTGTGTTGGGCTT 3427

Db 3358 TTGGCCTATACITTCATATGGGATAAAACAGATGCATATAATCAGAAAAGTCTATGGTCTA 3417

QY 3428 TCAGAAAGCCTTTGTTCCGTGGGTTATGAATATGAATCCTGCCCAGATCTPAATCCTGTGG 3487

Db 3418 TCTGAAGCTGTTGTGTCAGTTGGATATGAGTATGAGTCGTGTTTGGACCTGACTCTGTGG 3477

QY 3488 GAAAAAGAACAAACAGTGTGCAGGGCTATGAATTTGACGCGTCCAAGCTTGGAGGATGG 3547

Db 3478 GAAAAGAGGACTGCGCAATCTGCAGGGCTATGAATTGGATGCGTCCAACATGGGTGGCTGG 3537

QY 3548 AGCCTAGACAAACATCATGCCCTCAACATTCAAAAGTGGTATCCTGCAACAAAGGAAATGGG 3607

Db 3538 ACATTAGATAAACATCACGTGCTGGATGTACAGAACGGTATACTGTACAAGGAAACGGG 3597

QY 3608 GAGAACCAAGTTTGTGCTCAGCAGCCTCCTGTCAATGGGAGCATCATGGCAATGGCGC 3667

Db 3598 GAAAACCAGTTTCATCTCCAGCAGCCTCCAGTCGTGAGTAGCATCATGGGCAATGGCGGA 3657

QY 3668 CGGAGAAGCATCTCCTGCCCCAGCTGCAACCGGCCTTGCTGACGGCAACAAGCTCCTGGCC 3727

Db 3658 AGGCGCAGCATTTCCCTGCCCCAGTTGCAATGGTCAAGCTGATGGTAAACAAGTTACTGGCC 3717

QY 3728 CCAGTGGCCCTCACTGTGGCTCTGACGGAGCCCTCTATGTGGGTGATTTCAACTACATT 3787

Db 3718 CCAGTGGCGTAGCTTTGTGGGATCGATGGCAGTCTGTACGTAGGCGATTTCAACTACGTG 3777

QY 3788 AGAAGGATCTTCCCCTCTGGAAATGTCAACAACTCCTAGAGCTGAGGAAATAAGATTTTC 3847

Db 3778 CGGCGGATATTCCCCTCTGGAAATGTAAACAAGTGTCTAGAACTAAGAAATAAAGATTTT 3837

QY 3848 AGACATAGTCACAGTCCAGCACACAATACTACCTGGCCACAGACCCCATGAGTGGGGCC 3907

Db 3838 AGACATAGCAGCAACCCAGCTCATAGATACTACCTTGCACGGATCCAGTCACGGGAGAT 3897

QY 3908 GTCTTCCTTTCTGACGACCAACAGCCGGGGTCTTTAAAAATCAAGTCCCACTGTGGTGGTG 3967

Db 3898 CTGTACGTTTCTGACACAAACACCCGCAGAAATTTATCGCCCCAAAGTCATTCAGGGGGCA 3957

QY 3968 AAGGACCTTGTCAAGAACTCTGAGGTGGTTGGGGACAGGTGACCAAGTCCCTCCCTTT 4027

Db 3958 AAAGACTTGACTTAAAAATGCAGAAAGTCGTGCGCAGGACAGGGAGCAATGCCTTCCGTTT 4017

QY 4028 GATGACACTCGCTCGGGGATGGTGGGAAGGCCACAGAAGCCACACTCACCAATCCCAGG 4087

Db 4018 GACGAGGCGAGATGTGGGGATGGAGGGAAGGCCGTGGAAGCCACACTCATGAGTCCCAA 4077

QY 4088 GGTATTACAGTGGACAAGTTTGGGCTGATCTACTTCTGTGGATGGCACCATGATCAGACGC 4147

Db 4078 GGAATGGCAGTTGATTAAGAAATGGATTAACTACTACTTTGTTGATGGAACCATGATTAGAAA 4137

QY 4148 ATCGATCAGAAATGGGATCATCTCCACCCTGCTCGGCTCTAATGATCTCACATCAGCCCCG 4207

Db 4138 GTTGACCAAAATGGAATCATATCAACTCTTCTGGGCTCTAACGATTTGACITTCAGCCAGA 4197

QY 4208 CCACTCAGCTGTGATTTCTGTCAATGGATATTTCCAGGTAAGACTGGAGTGGCCACAGAC 4267

Db 4198 CCTTTAACTTGTGACACCAGCATGCACATCAGCCAGGTACGTCTGGAATGGCCCACTGAC 4257

QY 4268 TTAGCCATCAACCCCAATGGACAACCTCACTTTTATGTCCTCGACAACAATGTGGTCTGCAA 4327

Db 4258 CTAGCCATTAAACCCTATGGATAAECTCCATTTATGTCTCTGGATAATAATGTAGTTTTACAG 4317

QY 4328 ATCTCTGAAAAACCAACAGGTGGCATTTGTGCGCGGAGGCCCATGCACCTGCCAGGTCCCT 4387

Db 4318 ATCACTGAAAAATCGTCAAGTNCGCAATGCTGCTGGACGGCCCATGCACTGTCAAGTTCCC 4377

QY 4388 GGCAATTGACACATTCCTGTCTAAGCAAGGTGGCCATCCACGCAACCTGGAGTCAGCCACC 4447

Db 4378 GGAGTGG--AATATCCTGTGGGAAGCAGCGGTCAGACAACTGGAATCAGCCACT 4434

QY 4448 GCTTTGGCTGTTTACACAATGGGCTCCTGTATATTGCTGAGACTGATGAGAAAAAGATC 4507

Db 4435 GCCATTGCTGTCTCTACAGTGGGTCCTGTACATTACTGAAACTGATGAGAAAAAATT 4494

QY 4508 AACCGCATCAGGCAGGTCAACCACTAGTGGAGAGATCTCACTCGTTGCTGGGCCCCCACT 4567

Db 4495 AACCGGATAAGGCAGGTCAACAACAGATGGAGAAATCTCCTTAGTGGCCGGAATACCTTCA 4554

QY 4568 GGCTGTGACTGTAAAAAATGATGCCAACTGTGATTTCTGGAGACGATGGTTATGCC 4627

Db 4555 GAGTGTGACTGCAAAAAATGATGCCAACTGTGACTGTTACCAGAGTGGAGATGGCTACGCC 4614

QY 4628 AAGGATGCAAAATTAATAATACCCATCTTCCCTTGGCTGTGTGTGATGGGAGCTCTAC 4687

Db 4615 AAGGATGCCAAACTCAGTGCCCCATCCTCCTGGCTGCTTCTCCAGATGGTACACTGTAT 4674

QY 4688 GTGGCCGACCTTGGGAACATCCGAATTCGGTTTATCCGGAAGAACAAAGCCTTCTCTCAAC 4747

Db 4675 ATTGACAGATCTAGGGAATATCCGGATCCGGCTGTGTCAAAGAATAAGCCTTTACTTAAC 4734

QY 4748 ACCAGAACATGTATGAGCTGTCTTCACCAATTGACCAGGAGCTCTATCTGTTTGATACC 4807

Db 4735 TCTATGAACCTCTATGAAGTTGCGTCTCCAACTGATCAAGAACTCTACATCTTTGACATC 4794

QY 4808 ACCGGCAAGCACCTGTACACCCAAAGCCTGCCCCACAGGAGACTACCTGTACAACCTTCACC 4867

Db 4795 AATGGTACTCACCAATATACTGTAAGTTTAGTCACTGGTGAATTACCTTTACAATTTTAGC 4854

QY 4868 TACACTGGGACGGCGACATCACACTCATCAACAGACAACAATGGCAACATGGTAAATGTC 4927

Db 4855 TACAGCAATGACAAATGATATTACTGTCTGTGACAGACAGCAATGGCAACACCCCTTAGAATT 4914

QY 4928 CGCCGAGACTCTACTGGGATGCCCTCTGGCTGGTGGTCCCAGATGGCCAGGTGACTGG 4987

Db 4915 AGACGGGACCCAAATCGCATGCCAGTTCGAGTGGTGTCTCCTGATAACCAAGTATATGG 4974

QY 4988 GTGACCATGGGCACCAACAGTGCACTCAAGAGTGTGACCACACAAGGACACAGATTGGCC 5047

Db 4975 TTGACAAATAGGAACAAATGGATGTTTGAAGGCATGACTGCTCAAGGACTGGAATTAGTT 5034

QY 5048 ATGATGACATACCATGGCAATTCGGCCTTCTGGCCACACCAAAAGCAATGAAAACGGATGG 5107

Db 5035 TTGTTTACTTACCATGGCAATAGTGGCCTTTTAGCCACTAAAAGTGAATGAAACTGGATGG 5094

QY 5108 ACAACATTTTATGAGTACGACAGCTTTGGCGCCTTGACAAAATGTGACCTTCCCTACTGGC 5167

Db 5095 ACAACGTTTTTTGACTATGACAGTGAAGGTGCTGTGACAAATGTTACGTTTCCAACTGGA 5154

QY 5168 CAGGTGAGCAGTTTCCGAAGTATACAGACAGTTCAGTGCAATGTCCAGGTAGAGACCTCC 5227

Db 5155 GTGGTCACAAACCTGCATGGGACATGGACAAGGCTATCACAGTGGACATTTAGTCACT 5214

QY 5228 AGC--AAGGATGATGTCAACCATAAACCAACCACTGTCTGCCTCAGGCGCTTCTACACA 5284

Db 5215 AGCCGAGAAAGAGATGTCAAGATCACTTCAAAATCTGTCTCGATCGATTCCTTCTACACC 5274

QY 5285 CTGCTGCAAGACCAAGTCCGGAAACAGCTACTACATCGGGGCCGATGGTCTCTGCGGCTG 5344

Db 5275 ATGGTTCAAGATCAGTTAAGAAACAGCTACAGATTTGGTTATGACGGCTCCTCCTCAGAATT 5334

QY 5345 CTGCTGGCCAAACGSCATGGAGGTGGCGCTGCAGACTGAGCCCCACTTGTGCTGGCTGGCACC 5404

Db 5335 ATCTACGCCAGTGGCTGGACTCACACTACCACTACCAAAACAGAGCCGACCGTTCTGGCTGGCACC 5394

QY	5405	GTCAACCCACCGTGGGCAAGAGGAATGTCA	CGCTGCCCATCGACAACGGCCTCAACCTG	5464	QY	6485	ATGAAGGAAGTGCAGTATGAGATCTTCCGCT	CGCTCATGTACTGGATGACCGTCCAGTAT	6544			
Db	5395	GCTAATCCGACGGTTGCCAAAAGAAACAT	GACTTTGGCTGGCGAGAACGGTCAAAACTTG	5454	Db	6475	ATCAAGGAGATTCAATATGAGATATTCA	GCTCGCTCATGTACTGGATTACAATTCAGTAT	6534			
QY	5465	GTGGAGTGGCGCCAGCGCAAGAGCAGGCT	CGGGCCAGGTCACTGTCTTTGGGCGCCGG	5524	QY	6545	GATAACATGGGCGAGTAGTGAAGAGGAGCT	GAAAGGTAGGACCTTACGCCAATACCACT	6604			
Db	5455	GTGGAATGGAGATTCCGAAAAGAGCAAGCC	CAAGCCCAAGGGAAGTCAATGTCTTTGGCCGCAAG	5514	Db	6535	GATAACATGGGTGGGTAAACCAAGAGAGAG	ATTAAAAATAGGGCCCTTTGCCAACACCCACC	6594			
QY	5525	CTGCGGGTGCAAAACCGAAATCTCCTATCT	CTGGAATTTGATCGCGTAACACGACAGAG	5584	QY	6605	CGTACTCCTATGAGTATGATGCTGACGGCC	AGCTGCAGACAGTCTCCATCAATGACAAG	6664			
Db	5515	CTCAGGGTTAATGGCAGAAACCTCCTTTCA	GTGACTTGATCGAACAACAAGACAGAA	5574	Db	6595	AAATATGCTTATGAATATGATGTTGATGG	ACAGCTCCAAACAGTTTACCTCAANTGAAAAG	6654			
QY	5585	AAGATCTATGATGACCAACCGCAAGTTTCA	CCCTTCGGATTTCTGTACGACCGCGGGCGG	5644	QY	6665	CCACTCTGGCGCTACAGCTACGACCTCAAT	CGGAACCTGCACCTTACTGAGCCCTGGGAAC	6724			
Db	5575	AAGATCTATGACGACCAACCGTAAATTTCT	ACTGAGGATCGCCTACGACACGCTCTGGGCAC	5634	Db	6655	ATAATGTGGCGGTACAACTACGATCTGAAT	CGAACCCTCCATTTACTGAACCCCAAGTAAC	6714			
QY	5645	CCCAGCCTCTGGTCA	CCCGACGAGCGGTGAATGGTGTCAACGTG	ACATATCCTCCCTGGG	5704	QY	6725	AGTGACCGGCTCACACCACTACGGTATGAC	ATCCGCGCATCACTCGGCTGGGTGAC	6784		
Db	5635	CCGACTCTCTGGCTGCCAAGCAGCAAGCTG	ATGGCCGTTCAATGTCAACCTATTATCCACA	5694	Db	6715	AGTGCGCGTCTGACACCCCTTCGCTATGAC	CTCGGAGACAATCACTCGACTGGGTGAT	6774			
QY	5705	GGTTACATTGCTGGCATCCAGAGGGGCAT	CATGTCTGAAAGAAATGGAATACGACCGCG	5764	QY	6785	GTGCAATACAAGATGGATGAGGATGGCTT	CCTGAGGCGAGCGGGCGGTGATATCTTTGAG	6844			
Db	5695	GGTCAAAATGCCAGCATCCAGCGAGGCACC	ACTAGCGA	AAAGTAGATTATGACGGACAG	5754	Db	6775	GTTC	CAATATCGGTTGGATGAAGATGGTTTCT	ACGTC	CAAGGGGCACGGAATCTTTGAA	6834
QY	5765	GGCCGATCATCCAGGATCTTCGCTGATGG	GAAGACATGGAGCTACACATATCTTAGAG	5824	QY	6845	TACAACTCAGCTGGCCTGCTCATCAAGGC	CTACAAACCGGGCTGGCAGCTGGAGTGT	CAGG	6904		
Db	5755	GGGAGGATCGTGTCTCGGGTCTTTGCTGAT	GGTAAACATGGAGTTACACATATTTAGAA	5814	Db	6835	TATAGCTCCAAGGGGCTTCTAACTCGAG	TTTACAGTAAAGGCAGTGGCTGGACAGT	GATC	6894		
QY	5825	AAGTCCATGGTGTCTACTACACAGCCAG	AGGCAGTATATCTTTGAGTT	TCGACAAGAAT	5884	QY	6905	TACCGCTACGATGGCCTGGGGCGGCGGT	CTCAGCAAGAGCAGCCACAGCCACCACT	CC	7024	
Db	5815	AAGTCCATGGTCTTCTGCTTATAGCCAG	CGCAGTACATCTTCGAATACGATATGTGG	5874	Db	6895	TACCGTTATGACGGCCTGGGAAGGCGT	GTCTTAGCAAAACCCAGTCTAGGACAG	CACCTG	6954		
QY	5885	GACCGCTCTCTTCTGTGACGATGCCCAAC	CGTGGCGCGGAGACACTAGAGACCATCCGC	5944	QY	6965	CAGTTCTTCTATGCAGACCTGACCAACCC	CAACCAAGGTCACCCACCTGTACAACCACT	CC	7044		
Db	5875	GACCGCTGTCTGCCATCACCATGCCAGT	GTGGTCTGCCACACCATGCAGACCATCCGA	5934	Db	6955	CAGTTTTTTTATGCTGACTTAACTTATC	CCCACTAGGATTACTCATGTCTACAACCAT	TCG	7014		
QY	5945	TCAGTGGGCTACTACAGAAACATCTATC	AGCCCCCTGAGGGCAATGCCTCAGTCATACAG	6004	QY	7025	AGCTCTGAGATCACCTCCCTCTACTACG	ACTTGCAAGGACACCTCTTTGCCATGGAGCTG	7084			
Db	5935	TCCATTGGCTACTACCGCAACATATA	CAACCCCCCGGAAGCAACGCCTCCATCATCAGG	5994	Db	7015	AGTTCAGAAATTACCTCCCTGTATTATG	ATCTCCAAGGACATCTTTTGGCATGGAAATC	7074			
QY	6005	GACTTCACTGAGGATGGGCACCTCCTTCA	CACCTTCTACTGGGCACTGGCGCGAGGGTG	6064	QY	7085	AGCAGTGGTGATGAGTTTTTACATAGCT	TGTGAACAACATCGGGACCCCTCTTGCTGTCTTTT	7144			
Db	5995	GACTACAACGAGGAAGGGTGCTTCTACA	AAACAGCTTTCTTGGGTACAAGTCGAGGGGTC	6054	Db	7075	AGCAGTGGGATGAATTTCTATATTGCA	TCGGATAAACACAGGGACACCACTGGCTGTGTTC	7134			
QY	6065	ATATACAAGTATGGCAAACTGTCAAAGCT	GGCAGAGACGCTCTATGACACCCAAAGGTC	6124	QY	7145	AGTGAACACAGGTTTGATGATCAAGCA	AAATCCTGTACACAGCCTATGGGGAGATCTACATG	7204			
Db	6055	TTATTCAAATACAGAAGGCAGACTAGGCT	CTCAGAAATTTTATATGATAGCAAAAGATC	6114	Db	7135	AGTAGCAATGGGCTTATGCTGAAACAG	ATTTCAGTACACTGCATATGGGAAATCTATTTT	7194			
QY	6125	AGTTTCACTATGACGAGACGGCAGGCAT	GCTGAAGACCATCAACCTACAGAAATGAGGGC	6184	QY	7205	GATACCAACCCCAACTTTCAGATCATCA	TAGGCTTACCATGGTGGCCTCTATGATCCACTC	7264			
Db	6115	AGTTTTACCTATGATGAACACGAGGAGT	CTCTAAAGACAGTAAACCTCCAGAGTGATGGT	6174	Db	7195	GACTCTAATATTGACTTTCAACTGGTA	ATTGGAATTCATGGTGGCCTGTATGACCCACTC	7254			
QY	6185	TTCACTGCACCATCCGCTACCGT	CAGATTGGGCCCCCTGATTGACCGACAGATCTTCCGC	6244	QY	7265	ACCAAGCTTGTCACATGGGCGGCGAGAT	TATGATGTGCTGGCCGACGCTGGACTAGC	7324			
Db	6175	TTTATTTGCACCATTAGATACAGGC	AAATTTGGTCCCCCTGATTGACAGGCAAGATTTCCGC	6234	Db	7255	ACCAAAATTAATCCACTTTGGAGAAAG	AGATTATGACATTTTGGCAGGACGGTGGACAACA	7314			
QY	6245	TTCACTGAGGAAGGCATGGTCAACGCCCG	TTTTGACTACAACCTATGACAACAGCTTCCGG	6304	QY	7325	CCAGACCAAGCTGTGGAAGCA	CCTTAGTAGCAGCAACGTCATGCCTTTTAACTCTAT	7384			
Db	6235	TTTAGTGAAGATGGGATGGTAAATGCAAG	ATTTGACTATAGCTATGACAACAGCTTTTCGA	6294	Db	7315	CCTGACATAGAAATCTGGA	--AAAGAA	TTGGGAAGGACCCAGCTCCTTTTAACTTTGTAC	7371		
QY	6305	GTGACCAAGCATGCAGGCTGTGATCAACG	AGACCCCACTGCCATTTGATCTCTATCGCTAT	6364	QY	7385	ATGTTCAAAAACAACACCCCATCAGCA	AACTCCAGGACATCAAGTGTCTTCATGACAGAT	7444			
Db	6295	GTGACCAAGCATGCAGGCTGTGATCAATGA	AAACGCCACTGCGCTATTGATCTGTATCAGTTT	6354	Db	7372	ATGTTTAGGAATAACAACCCCTGCAAGC	AAAAATCCATGACGCTGAAAGATTACATCACAGAT	7431			
QY	6365	GATGATGTGTGAGGCAAGACAGAGCAGTT	TTGGGAAGTTTGGTGTCATTTACTATGACATT	6424	QY	7445	GTTAACAGCTGGCTGCTCACCTTTTGGAT	TTCCAGCTTACAGTACACAACGTCATCCCTGGTTATCCC	7504			
Db	6355	GATGACATTTCTGGCAAAGTTGAGCAGTT	TTGGAAAGTTTGGAGTTATATATTTATGATAT	6414	Db	7432	GTTAACAGCTGGCTGGTGACATTTGGTT	TTTCCATCTGCACAATGCTATTTCTCTGGATTCCCT	7491			
QY	6425	AACCAGATCATCACCACAGCTGTGATGAC	CCCAACCAAGCAATTTTGATGCATATGGCAGG	6484	QY	7505	AAACCAGACATGGATGCCATGGAACCC	CTCCTACGAGCTCATCCACACACAGATGAAAACG	7564			
Db	6415	AACCAGATCATTTCTACAGCTGTAAATG	ACCTATACGAAGCACTTTGATGCTCATGGCCGT	6474	Db	7492	GTTCCCAAAATTTGATTTAA	CAGAACCTTCTTACGA-----ACTTGTGAAGAGT	7539			
					QY	7565	CAGGAGTGGGACAACACAGCAAGTCTAT	CTCCTCGGGGTACAGTGTGAAGTACAGAAGCAGCTC	7624			

Db 7540 CAGCAGTGGGATGATATACCGCCCATCTTCGGAGTCCAGCAGCAAGTGGCGGCAGGCC 7599

Qy 7625 AAGGCCTTTGTCACTTAGAACGGTTTGACCAGTCTATGGCTCCACATCACCAGCTGC 7684

Db 7600 AAGCCTTCCTGTCTGTGGGAAGATGGCCGAGGTGCAGGTGAGCCGGCCGGCCGGC 7659

Qy 7685 CAGCAGGCTCCAAAGACCAAGAAAGTTTGCATCCAGCGGCTCAGTCTTTGGCAAGGGGTC 7744

Db 7660 ---GGCGGCAGTCTGGCTGTGGTTGCGCAACGGTCAAGTCGTGATCGCAAGGGCGTC 7716

Qy 7745 AAGTTTGCCTTGAAGGATGGCCGAGTGACCAACATCATCAGTGTGGCAATGAGGAT 7804

Db 7717 ATGCTGGCCGTCAGCCAGGGCCGCGTGCAGACCAACGCTGCTCAACATCGCCAACGAGGAC 7776

Qy 7805 GGGCGAAGGTTGCTGCCATCTTGAACCATGCCCACTACCTAGAGAACCTGCACCTTCACC 7864

Db 7777 TGCATCAAGGTGGCGCGCTGCTCAACAACGCCCTTCTACCTGGAGAACCTGCACCTTCACC 7836

Qy 7865 ATTGATGGGGTGATACCCATTACTTTGTGAACACAGGACCTTCAGAAAGGTGACCTGGCC 7924

Db 7837 ATCGAGGGCAAGGACACGCACACTACTTCATCAAGACCACCAACGCCCGAGACCGACCTGGGC 7896

Qy 7925 ATCCTGGGCCTCAGTGGGGGGCGGCGAACCCCTGAGAAATGGGTCAACGTCACCTGTGTCC 7984

Db 7897 ACGTGCGGTTGACCAGCGGCGCGCAAGGCGCTGGAGAACGGCATCAACGTGACGGTGTCTG 7956

Qy 7985 CAGATCAACACAGTACTTAATGGCAGGACTAGCGCTACACAGACATCCAGTCCAGTAC 8044

Db 7957 CAGTCCACCACCGTGTGAAACGGCAGGACCGCGAGGTCGCGGACGTGGAGATGCAGTTC 8016

Qy 8045 GGGGCACTGTGCTTGAACACACACGCTACGGGACAAAGTTGGATGAGGAGAGGCACGGGTC 8104

Db 8017 GGGCGCTGGCGCTGCACGTGCGCTACGGCATGACCTTGGAYGAGGAGAGCGCGCATC 8076

Qy 8105 CTGGAGCTGGCCCGSCAGAGAGCCGTGCGCCCAAGCGTGGGCCCGGAGCAGCAGAGACTG 8164

Db 8077 CTGGAGCAGGCGCGCAGCGCGCGCTCGCCCCGGCCTGGCGCGCAGCAGCAGCGCGTG 8136

Qy 8165 CGGGAAGGGAGGAAAGCCCTGCGGGCCTGGACAGAGGGGGAGAAAGCAGCAGGTGCTGAGC 8224

Db 8137 CGCAGCGCGAGGAGGGCGCGCCCTCTGGACGGAGGGCGAGAAAGCGGACGTGCTGAGC 8196

Qy 8225 ACAGGGCGGGTGCAAGGCTACGACGGCTTTTTCGTGATCTCTGTGAGCAGTACCCAGAA 8284

Db 8197 GCGGCAAGGTGCAGGGCTACGACGGGTACTACGTACTCTCGGTGGAGCAGTACCCCGAG 8256

Qy 8285 CTGTCAAGACAGCGCCAAACAACATCCACTTCATGACACAGAGCGAGATGGCGGAGGTGA 8344

Db 8257 CTGGCCGACAGCGCCCAACAACATCCAGTTCTCTGGCGAGAGCGAGATCGSCAGAGGTAA 8316

Qy 8345 C 8345

Db 8317 C 8317

RESULT 10

ADH41968  
ID ADH41968 standard; DNA; 8645 BP.

XX

AC ADH41968;

XX

DT 25-MAR-2004 (first entry)

XX  
DE Novel human nucleic acid NOV40s.

XX  
KW ds; gene; cardiovascular; antiarteriosclerotic; hypotensive; cytostatic;  
KW anorectic; antidiabetic; immunosuppressive; anti-HIV; neuroprotective;  
KW nootropic; antiparkinsonian; antiasthmatic; antiinfertility;  
KW cardiomyopathy; atherosclerosis; hypertension; cancer; obesity; diabetes;  
KW AIDS; multiple sclerosis; graft-versus-host disease; Alzheimer's disease;  
KW Parkinson's disease; asthma; fertility disorder; chromosome mapping;  
KW tissue typing; preventive medicine; pharmacogenomic; vaccine.

XX  
OS Homo sapiens.  
XX  
PN WO2003102159-A2.  
XX  
PD 11-DEC-2003.  
XX  
PF 04-JUN-2003; 2003WO-US017573.  
XX  
PR 04-JUN-2002; 2002US-0385490P.  
PR 04-JUN-2002; 2002US-0385615P.  
PR 04-JUN-2002; 2002US-0385755P.  
PR 05-JUN-2002; 2002US-0386041P.  
PR 06-JUN-2002; 2002US-0386355P.  
PR 06-JUN-2002; 2002US-0386357P.  
PR 06-JUN-2002; 2002US-0386447P.  
PR 06-JUN-2002; 2002US-0386459P.  
PR 06-JUN-2002; 2002US-0386465P.  
PR 06-JUN-2002; 2002US-0386864P.  
PR 07-JUN-2002; 2002US-0386701P.  
PR 07-JUN-2002; 2002US-0386796P.  
PR 07-JUN-2002; 2002US-0386931P.  
PR 07-JUN-2002; 2002US-0387078P.  
PR 07-JUN-2002; 2002US-0387081P.  
PR 07-JUN-2002; 2002US-0387083P.  
PR 10-JUN-2002; 2002US-0387429P.  
PR 10-JUN-2002; 2002US-0387540P.  
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PR 12-JUN-2002; 2002US-0388432P.  
PR 12-JUN-2002; 2002US-0388479P.  
PR 13-JUN-2002; 2002US-0389123P.  
PR 14-JUN-2002; 2002US-0389120P.  
PR 14-JUN-2002; 2002US-0389146P.  
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PR 18-JUN-2002; 2002US-0389604P.  
PR 18-JUN-2002; 2002US-0389884P.  
PR 19-JUN-2002; 2002US-0390006P.  
PR 19-JUN-2002; 2002US-0390144P.  
PR 19-JUN-2002; 2002US-0390209P.  
PR 25-JUN-2002; 2002US-0391726P.  
PR 06-AUG-2002; 2002US-0401628P.  
PR 09-AUG-2002; 2002US-0402268P.  
PR 12-AUG-2002; 2002US-0402822P.  
PR 13-AUG-2002; 2002US-0403458P.  
PR 15-AUG-2002; 2002US-0403617P.  
PR 15-AUG-2002; 2002US-0403732P.  
PR 26-AUG-2002; 2002US-0406182P.  
PR 12-SEP-2002; 2002US-0410085P.  
PR 13-SEP-2002; 2002US-0410505P.  
PR 23-SEP-2002; 2002US-0412955P.  
PR 30-SEP-2002; 2002US-0415195P.  
PR 23-OCT-2002; 2002US-0420627P.  
PR 23-OCT-2002; 2002US-0420718P.  
PR 24-OCT-2002; 2002US-0420852P.  
PR 31-OCT-2002; 2002US-0422750P.  
PR 01-NOV-2002; 2002US-0423095P.  
PR 05-NOV-2002; 2002US-0423748P.

(CURA-) CURAGEN CORP.

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PA

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PI

PI

Alsobrook JP, Anderson DW, Baumgartner JC, Berghs C, Boldog FL;  
Burgess CE, Casman SJ, Catterton E, Dhanabal M, Edinger SR;  
Ellerman K, Ettenberg S, Gangolli EA, Gerlach VL, Gorman L;





Db 1618 ATCTGGCATCTGGCTTTTATAATGATGGGAAAAATGCAGAGCAGGTGTCTTTAATACC 1677

Qy 1706 ACTGCCATTGAGTCGGTGGATAACTGCCCCAGCAACTGCTATATGGCAATGCTGACTGCATC 1765

Db 1678 ATTGTTATAGAGTCGTGGTGGAAATGTCCCCGGAATTGCCATGGAAATGGAGAATGCGTT 1737

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Db 1738 TCTGGAACCTTGCCATTGTTTCCAGGATTTCCTGGTCCGGATTGTTCAAGAGCCGCCTGT 1797

Qy 1826 CCCGTGCTCTGTAGCGGAANAATGGCCAAATACATGAAGGCAGATGCTTTGTGCCACAGTGGC 1885

Db 1798 CCAGTGTATGTAGTGGCAACGGGCAGTACTCCAAGGGCCGCTGCCCTGTGTTTCAGCGGC 1857

Qy 1886 TGGAAAGGCGCTGAGTGGCATGTGCCACCAACCAAGTGTATCGATGTGGCCTGCAGCAAC 1945

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Qy 1946 CATGGCACCTGCATCAGGGCACCTTGCATCTGCAACCTTGGCTACAAGSGCAGAGCTGT 2005

Db 1918 CGTGGGATTTGTATCATGGGCTCCTGTGCTTGAGCTCAGGATACAAGGAGAAAGTTGT 1977

Qy 2006 GAGGAAGTGGACTGCATGGACCCCCACATGTTTACGGCCGGGTGTCTGCGTGAGAGGGCAA 2065

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Qy 2066 TGCCATTGCTTTGTGGATGGGAGGCACCAACTGCGAGACCCCCAGGGCCACATGCTTA 2125

Db 2038 TGTCACTGCAGTCCAGGATGGGAGGTAGCAATTGTGAAAATACTGAAGACCATGTGTCCA 2097

Qy 2126 GACCAGTGTTCAGGCCACGGAACCTTCCTCCCGGACACCGGGCTTTGCAGCTGTGACCCA 2185

Db 2098 GACCAGTGCTCCGGCCACGGAACGTATCTTCAAGAAAGTGGCTCCTGCACGCTGACCCCT 2157

Qy 2186 AGCTGGACTGGACACGACTGTTCTATCGAGATCTGTGCTGCCGACTGTGGTGGCCATGGC 2245

Db 2158 AACTGGACTGGCCCCAGACTGCTCAACGAAATATGTCTGTGGACTGTGGCTCACACGGC 2217

Qy 2246 GTGTGCGTAGGGGGCACTGCCGCTGCGAGGATGGCTGGATGGGGGCGACCTTCGACCCAG 2305

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Qy 2306 CGGGCCTGCCACCCGCTGTGCCGAGCATGGGACCTGCCCGCAGCGGCAAGTGCAGTGC 2365

Db 2278 AGAGCCTGCCACCCCGCTGTGCCGAGCACGGGACCTGCAAGGATGGCAAGTGTGAATGC 2337

Qy 2366 AGCCCTGGCTGGAATGGGAACACTGCACCATCGCTCACTATCTGGATAGGGTAGT---- 2421

Db 2338 AGCCAGGGCTGGAATGGAGAGCACTGCACATATCGCTCACATATTGGATAAGATAGTAAA 2397

Qy 2422 -----TAAAGAGGGTTGCCCTGGGTTGTGCAATGGCAATGGCAACGGCAGATGTACC 2467

Db 2398 GACAAGATAGGATATAAAGAGGGTTGTCTGCTGTGCAACAGCAATGGAAAGATGTACC 2457

Qy 2468 TTAGACCTGAAATGGTTGGCACTGCGCTGCCAGCTGGGCTGGAGAGGAGCTGGCTGTGAC 2527

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Qy 2528 ACTTCCATGGAGACTGCTGCGGTGACAGCAAAAGACAATGATGGAGATGGCCTGGTGGAC 2587

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Qy 2828 GATGGAACCCCTCGTGTGGTGTGAACATCAGTTTGTCAATAACCCCTCTCTTTTGGATAT 2887

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Db 2998 GTCTTTTATGTGATGGATACCCCTAGTCACTGGAGAAAGAGAGAATGACATTCCCAGCTGT 3057

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Qy 3128 GCCAGCTCCTGTGCAGAGAAAGGCCCAATGTGTCCCGGAAATTCAGGCTTTGCAGGAGGAA 3187

Db 3118 TTCAGATCTTCTCCTGAAGACAGTCCCCTCATTTCCGGAACACAGGTACTCCACGACGAA 3177

Qy 3188 ATCTCTATCTCTGGCTGCAAGATGAGGCTGAGCTACCTGAGCAGCCGCAACCTGGCTAC 3247

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Db 3238 AAGTCAGTTCTCAAGATCACCATGACCCAGTCTATTATTCATTTAATTAATGAAGGTT 3297

Qy 3308 CACCTCATGGTAGCGGTGGAGGGCCGCTCTTTCAGGAAGTGGTTGCTGCGTGCAGCCCCAGAC 3367

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Db 3778 CGGCGGATATTCCCTTCTGGAAATGTAAACAAAGTGTCTTAGAACTAAGAAATAAAGATTTC 3837



QY	3848	AGACATAGTCACAGTCCAGACACAAATACTACCTGGCCACAGACCCCATAGTGGGGCC	3907	QY	4928	CGCCGAGACTCTACTGGGATGCCCTCTGGCTGGTGGTCCCAGATGCCCAGGTGTACTGG	4987
Db				Db			
QY	3838	AGACATAGCAGCAACCCAGCTCATAGATACTACCTTGCAACGGATCCAGTCACGGGAGAT	3897	QY	4988	GTGACCATGGSCACCAACAGTGCACCTCAAGAGTGTGACCACACAAGGACACGAGTTGGCC	5047
Db				Db			
QY	3908	GTCTTCCTTTCTGACAGCAACAGCCGGCGGTCTTTAAAAATCAAGTCCACTGTGGTGGTG	3967	QY	4975	TTGACAATAGGAACAAATGGATGTTTGAAGGCATGACTGCTCAAGGACTGGAATTAGTT	5034
Db				Db			
QY	3968	AAGGACCTTGTCAAGAACTCTGAGGTGGTTGCGGGGACAGGTGACCAGTGCCTCCCTTT	4027	QY	5048	ATGATGACATACCATGGCAATTCCGGCCTTCTGGCAACCAAAAGCAATGAAAAACGGATGG	5107
Db				Db			
QY	3958	AAAGACTTGACTAAAAATGCAGAAAGTCGTGCGAGGGACAGGGAGCAATGCCCTTCGGTTT	4017	QY	5035	TTGTTTACTTACCATGGCAATAGTGGCCTTTTAGCCACTAAAAGTGATGAAAACTGGATGG	5094
Db				Db			
QY	4028	GATGACACTCGCTGCGGGGATGGTGGGAAGGCCACAGAAAGCCACACTCACCAATCCCAGG	4087	QY	5108	ACAACTTTTATGAGTACGACAGCTTTTGGCCGCTTGACAAATGTGACCTTCCCTACTGGC	5167
Db				Db			
QY	4018	GACGAGCGGAGATGTGGGGATGGAGGAAGGCCGTGGAAGCCACACTCATGAGTCCCAAA	4077	QY	5095	ACAACTTTTGTGACTATGACAGTGAAGGTGCTGTGACAAATGTTACGTTTCCAACCTGGA	5154
Db				Db			
QY	4088	GGTATTACAGTGGACAAAGTTTGGGCTGATCTACTTCGTGGATGGCACCATGATCAGACGC	4147	QY	5168	CAGGTGAGCAGTTTCCGAAGTGATACAGACAGTTTCAAGTTCAGTGCATGTCCAGGTAGACCTCC	5227
Db				Db			
QY	4078	GGAAATGGCAGTTGATAAGAAATGGATTAAATCTACTTTGTTGATGGAACCATGATTAGGAAA	4137	QY	5155	GTGGTCACAAACCTGCATGGGACATGGACAAAGGCTATCACAGTGGACATTGAGTCACT	5214
Db				Db			
QY	4148	ATCGATCAGAATGGGATCATCTCCACCCTGCTCGGCTCTAAATGATCTCACATCAGCCCGG	4207	QY	5228	AGC--AAGGATGATGTCACCATAACCAACCAACCTGTCTGCCCTCAGGCGCCTTCTACACA	5284
Db				Db			
QY	4138	GTTGACCAAAATGGAATCATATCAACTCTTCTGGGCTCTAAACGATTTGACTTCAGCCAGA	4197	QY	5215	AGCCGAGAAGAAGATGTGAGCATCACTTCAAATCTGTCTCTCGATCGATTCGATTCCTTCTACACC	5274
Db				Db			
QY	4208	CCACTCAGCTGTGATTCTGTATGGATATTTCCAGGTAAGACTGGAGTGGCCACAGAC	4267	QY	5285	CTGCTGCAAGACCAAGTCCGGAACAGCTACTACATCGGGCCGATGGCTCCTTGGCGCTG	5344
Db				Db			
QY	4198	CCTTTAACTTGTGACACCCAGCATGCACATCAGCCAGGTACGTCTGGAATGGCCCACTGAC	4257	QY	5275	ATGGTTCAAGATCAGTTAAGAAACAGCTACCAGATTGGTTATGACGGCTCCCTCAGAATT	5334
Db				Db			
QY	4268	TTAGCCATCAACCCAAATGGACAACTCACTTTATGTCTCGACAACAATGTGGTCCCTGCAA	4327	QY	5345	CTGCTGGCCAAACGGCATGGAGGTGGCGCTGCAGACTGAGCCCCACTTGTGGCTGGCCACC	5404
Db				Db			
QY	4258	CTAGCCATTAAACCTATGGATAAATCCATTTATGTCTGGATAATAATGTAGTTTACAG	4317	QY	5335	ATCTACGCCAGTGGCCTGGACTCACACTACCAAAACAGAGCCGACCGTTCCTGGCTGGCACC	5394
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QY	4328	ATCTCTGAAAAACCAACAGGTGGCATTTGTCCCGGGAGGCCCATGCACCTGCCAGGTCCCT	4387	QY	5405	GTCAACCCCAACCGTGGGCAAGAGGAATGTACCGCTGCCCATCGACAAACGGCCTCAACCTG	5464
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QY	4318	ATCACTGAAAAATCGTCAAGTTCCGATTGCTGTGGACGSCCATGCATGTCAAGTTCCC	4377	QY	5395	GCTAATCCGACGGTTGCCAAAAGAAACATGACTTTGCCTGGCGAGAACGGTCAAAACTTG	5454
Db				Db			
QY	4388	GGCAATTGACCACTTCCTGTCTAAGCAAGGTGGCCATCCAGCAACCTCGAGTCAGCCACC	4447	QY	5465	GTGGAGTGGCGCCAGCGCAAAAGAGCAGGCTCGGGCCAGGTCACTGTCTTTGGGCGCCGG	5524
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QY	4378	GGAGTGG--AATATCCTGTGGGGAAGCACGCGGTGCAGACAACTGGAATCAGCCACT	4434	QY	5455	GTGGAATGGAGATTCGGAAGAGCAAGCCCAAGGGAAGTCAATGTCTTTGGCCGCAAG	5514
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QY	4448	GCTTTGGCTGTTTCACACAAATGGGGTCCCTGTATATTGCTGAGACTGATGAGAAAAAGATC	4507	QY	5525	CTGCGGGTGACAAACCGGAAATCTCCTATCTCTGACTTTGACTCGGTAAACACGCACAGAG	5584
Db				Db			
QY	4435	GCCATTGCTGTCTCTACAGTGGGTCTGTACATTACTGAAACTGATGAGAAGAAAAAT	4494	QY	5515	CTCAGGGTTAATGGCAGAAACCTCCTTTAGTTGACTTTGATCGAAACAACAAGACAGAA	5574
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QY	4495	AACCGGATAAGGCAGGTCAACAACAGATGGAGAAATCTCCTTAGTGGCCGGAATACCTTCA	4554	QY	5575	AAGATCTATGACGACCAACCGTAAATTTCTACTGAGGATCGCCTACGACACGTCTGGGCAC	5634
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QY	4568	GGCTGTGACTGTAAAAATGATGCCAACTGTGATTGTTTCTGGAGACGATGGTTATGCC	4627	QY	5645	CCAGCCTCTGGTCACCCAGCAGCAGGCTGAATGTTCAACGTGACATACTCCCTGGG	5704
Db				Db			
QY	4555	GAGTGTGACTGCAAAAAATGATGCCAACTGTGACTGTTACAGAGTGGAGATGGCTACGCC	4614	QY	5635	CCGACTCTCTGGCTGCCAAGCAGCAAGCTGATGSGCGTCAATGTCACTATTCATCCACA	5694
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QY	4628	AAGGATGCAAAAGTTAAATACCCCATCTTCCCTTGGCTGTGTGCTGATGGGAGCTCTAC	4687	QY	5705	GGTTACATTGCTGGCATCCAGAGGGGCATCATGTCTGAAAAGAAATGGAATACGACCAGCG	5764
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QY	4615	AAGGATGCCAAAATCAGTGCCCCCATCCCTCCCTGGCTGCTTCTCCAGATGGTACACTGTAT	4674	QY	5695	GGTCAAAATTGCCAGCATCCAGCGAGGCCACCACTAGCGAGAAAAGTAGATTATGACGGACAG	5754
Db				Db			
QY	4688	GTGGCCGACCTTGGGAACATCCGAATTCCGTTTATCCGGAAGAACAAAGCCTTTCCCTCAAC	4747	QY	5765	GGCCGCATCACATCCAGGATCTTTCGTGATGGGAAGACATGGAGCTACACATACATTAGAG	5824
Db				Db			
QY	4675	ATTGCAGATCTAGGGAATATCCGGATCCGGCTGTGTCAAAGAAATAAGCCTTTACTTTAAC	4734	QY	5755	GGGAGGATCGTGTCTCGGCTCTTGTGTATGGTAAAAATGGAGTTACACATATTTAGAA	5814
Db				Db			
QY	4748	ACCCAGAACATGTATGAGCTGTCTCACCAATTTGACCAGGAGCTCTATCTGTTTGTATACC	4807	QY	5825	AAGTCCATGGTGTCTGCTACTACACAGCCAGAGGCGAGTATATCTTTGAGTTTCGACAAGAA	5884
Db				Db			
QY	4735	TCTATGAACTTCTATGAAGTTGCGTCTCCAACCTGATCAAGAACTCTACATCTTTGACATC	4794	QY	5815	AAGTCCATGGTTCCTTCTGCTTCATAGCCAGCGGAGTACATCTTCGAATACGATATGTGG	5874
Db				Db			
QY	4808	ACCGGAAGCACCTGTACACCCAAAGCCTGCCACAGGAGACTACCTGTACAACCTTCACC	4867	QY	5885	GACCGCCTCTCTTCTGTGACGATGCCCAACCGTGGCGGCGCAGACACTAGAGACCATCCGC	5944
Db				Db			
QY	4795	AATGGTACTACCAATATACTGTAAAGTTAGTCACTGTTGATACCTTTACAATTTTAGC	4854	QY	5875	GACCGCCTGTCTGCCATCACCATGCCAGTGTGGCTCGCCACACCATGCAGACCATCCGA	5934
Db				Db			
QY	4868	TACACTGGGACGGCGACATCACTCATCAGACACAACAAATGGCAACATGGTAAATGTC	4927	QY	5945	TCAGTGGGCTACTACAGAAACATCTATCAGCCCCCTGAGGGCAATGCCCTCAGTCAATACAG	6004
Db				Db			
QY	4855	TACAGCAATGACAATGATATTACTGCTGTGACAGACAGCAATGGCAACACCCCTTAGAATT	4914	QY	5935	TCCATTGGCTACTACCGCAACATATACAAACCCCCCGGAAGCAACGCCTCCATCATCAG	5994
Db				QY	6005	GACTTCACTGAGGATGGGACCTCCTTCAACACCTTCTACCTGGGCACTGGCCCGCAGGTTG	6064



Db 5995 GACTACAACGAGGAAGGCTGCTTCTACAAACAGCTTCTTGGGTACAAGTCGGAGGGTC 6054

Qy 6065 ATATACAAAGTATGGCAAACTGTCAAAGCTGGCAGAGACGCTCTATGACACCAACCAAGGTC 6124

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Db 6115 AGTTTTACCTATGATGAACACAGCAGGAGTCCCTAAAGACAGTAAACCTCCAGAGTGATGGT 6174

Qy 6185 TTCACTGCAACCATCCGCTACCGTACCGTCAAGATTGGGCCCTGATTGACCGACAGATCTTCCGC 6244

Db 6175 TTTATTGCACCATTAGATACAGGCCAAATTGGTCCCTGATTGACAGGCAGATTTTCCGC 6234

Qy 6245 TTCACTGAGGAAGGCATGGTCAACGCCCGTTTGTGACTACAACATATGACAAACAGCTTCCGG 6304

Db 6235 TTTAGTGAAGATGGGATGGTAAATGCAAGATTTTGACTATAGCTATGACAAACAGCTTTCGA 6294

Qy 6305 GTGACCAGCATGCAGGCTGTGATCAACGAGACCCCACTGCCCATTTGATCTCTATCGCTAT 6364

Db 6295 GTGACCAGCATGCAGGCTGTGATCAATGAACGCCCACTGCCATTGATCTGTATCAGTTT 6354

Qy 6365 GATGATGTGTCAGGCAAGACAGAGCAGATTTTGGGAAGTTTGGTGTCAATTTACTATGACATT 6424

Db 6355 GATGACATTTCTGGCAAAGTTTGAGCAGTTTGGAAAGTTTGGAGTTATATATTATGATATT 6414

Qy 6425 AACCAGATCATCACACAGCTGTATGATCAACGAGACCCCACTGCCCATTTGATCTCTATCGCTAT 6484

Db 6415 AACCAGATCATTTCTACAGCTGTAATGACCTATACGAAGCACTTTGATGCTCATGGCCGT 6474

Qy 6485 ATGAAGGAAGTGCAGTATGAGATCTTCCGCTCGCTCATGTACTGGATGACCGTCCAGTAT 6544

Db 6475 ATCAAGGAGATTCAATATAGAGATATTCAAGTCGCTCATGTACTGGATTACAAATTCAGTAT 6534

Qy 6545 GATAACATGGGGCGAGTAGTGAAGAGGAGCTGAAGTAGGACCCCTACGCCCAATACCCT 6604

Db 6535 GATAACATGGGTGGGTAAACCAAGAGAGATTAAATAGGGCCCTTTGCCCAACACCACC 6594

Qy 6605 CGCTACTCCTATGAGTATGATGCTGACGGCCAGCTGCAGACAGTCTCCATCAATGACAAG 6664

Db 6595 AAATATGCTTATGAATATGATGTTGATGGACAGCTCCAAACAGTTTACCTCAATGAANAAG 6654

Qy 6665 CCACTCTGGCGCTACAGCTACGACCTCAAATGGGAACCTGCACCTTACTGAGCCCTGGGAAC 6724

Db 6655 ATAAATGTGGCGGTACAACTACGATCTGNAATGGAAACCTCCATTTACTGAACCCAAAGTAAAC 6714

Qy 6725 AGTGACGGCTCACACCACTACGGTATGACATCCGGACCGCATCACTCGGCTGGGTGAC 6784

Db 6715 AGTGGCGTCTGACACCCCTTCGCTATGACCTCGGAGACAGAATCACTCGACTGGGTGAT 6774

Qy 6785 GTGCAATACAAGATGGATGGATGGCTTCCCTGAGGCAGCGGGCGGTGATATCTTTGAG 6844

Db 6775 GTTCAATATCGGTTGGATGAAGATGGTTTCTTACGTCAAAGGGGCACGGAATCTTTGAA 6834

Qy 6845 TACAACTCAGCTGGCCTGCTCATCAAGGCCCTACAACCGGGCTGGCAGCTGGAGTGTCAAG 6904

Db 6835 TATAGCTCCAAGGGGCTTTAACTCGAGTTTACAGTAAAGGCAGTGGCTGGACAGTGATC 6894

Qy 6905 TACCGCTACGATGGCCTGGGCGCGCGTGTCCAGGAAGAGCAGCCACAGCCACCACCTG 6964

Db 6895 TACCGTTATGACGGCCTGGGAAGGCGTGTCTTAGCAAAACCAAGTCTAGGACAGCACCTG 6954

Qy 6965 CAGTCTTCTATGACAGACCTGACCAACCCCAAGGTCAACCCACCTGTACAAACCACTCC 7024

Db 6955 CAGTTTTTTATGCTGACTTAACCTATCCCACTAGGATTAATCATGTCTACAAACCATCG 7014

Qy 7025 AGCTCTGAGATCAACCTCCCTCTACTACGACTTGCAAGGACACCTCTTTTGCCATGGAGCTG 7084

Db 7015 AGTTCAGAAATTACCTCCCTGTATTATGATCTCCAAGGACATCTTTTGGCCATGGAATC 7074

Qy 7085 AGCAGTGGTATGAGTTTATCATAGCTTGTGACAAACATCGGGACCCCTCTTTGCTGCTTTT 7144

Db 7075 AGCAGTGGGATGAATTTCTATATTGGCATCGGATAAACACAGGGACACCACCTGGCTGTGTTT 7134

Qy 7145 AGTGGAAACAGGTTTGATGATCAAGCAAATCCTGTACACAGCCTATGGGGAGATCTACATG 7204

Db 7135 AGTAGCAATGGGCTTATGCTGAAACAGATTCAGTACACTGCATATGGGGAATCTATTTT 7194

Qy 7205 GATACCAACCCCAACTTTTCAAGATCATCATAGGCTACCATGGTGGCCTCTATGATCCACTC 7264

Db 7195 GACTCTAATATTGACTTTCAACTGGTAATTGGATTTTCAATGGTGGCCTGTATGACCCACTC 7254

Qy 7265 ACCAAGCTTTGTCACATGGCCGGCGGAGATTATGATGTGCTGGCCGGACGCTGGACTAGC 7324

Db 7255 ACCAAATTAAATCCACTTTGGAGAAAGAGATTATGACATTTTGGCAGGACGGTGGACAACA 7314

Qy 7325 CCAGACCACGAGCTGTGGAAGCACCTTTAGTAGCAGCAACGTCATGCCCTTTTAATCTCTAT 7384

Db 7315 CCTGACATAGAAATCTGGA--AAAGAAATTTGGGAAGGACCCAGCTCCTTTTAACTTGTA 7371

Qy 7385 ATGTTCAAAAACAACAACCCCATCAGCAACTCCAGGACATCAAGTGCCTTCATGACAGAT 7444

Db 7372 ATGTTTAGGAATAACAACCCCTGCAAGCAAAATCCATGACGTGAAGATTACATCACAGAT 7431

Qy 7445 GTTAACAGCTGGCTGCTCACCTTTGGATTCCAGCTACAAACGTCATCCCTGGTTATCCC 7504

Db 7432 GTTAACAGCTGGCTGGTGACATTTGGTTTCCATCTGCACAAATGCTATTTCCTGGATTCCCT 7491

Qy 7505 AAACCAGACATGGATGCCATGGAAACCCCTCCTACGAGCTCATCCACACACAGATGAANAACG 7564

Db 7492 GTTCCCAAATTTGATTTAAACAGAACCTTCTTACGA-----ACTTGTGAAGAGT 7539

Qy 7565 CAGGAGTGGGACAAACAGCAAGTCTATCCTCGGGTACAGTGTGAAGTACAGAAAGCAGCTC 7624

Db 7540 CAGCAGTGGGATGATATACGCCCATCTTTCGAGTCCAGCAGCAAGTGGCGCGCAGGCC 7599

Qy 7625 AAGGCCTTTGTCACTTAGAACGGTTTGACCAGCTCTATGGCTCCACAATCACCAGCTGC 7684

Db 7600 AAGGCCTTCTGTCTGGGGAAGATGGCCGAGGTGAGCGCGGCCCGGCCGCGC 7659

Qy 7685 CAGCAGGCTCCAAAGACCAAGAAGTTTGCATCCAGCGGCTCAGTCTTTGGCAAGGGGGTC 7744

Db 7660 ---GGCGCGCAGTCTCTGGCTGTGGTTTCGCCACGGTCAAGTCGCTGATCGGCAAGGGCGTC 7716

Qy 7745 AAGTTTGCCTTTGAAGATGGCCGAGTGACCAACAGACATCATCAGTGTGGCCAAATGAGGAT 7804

Db 7717 ATGCTGGCCGTCAGCCAGGGCCGCGTGCAGACCAACGTCGCTCAACATCGCCCAACGAGGAC 7776

Qy 7805 GGGCGAAGGGTTGCTGCCATCTTGAACCATGCCCACTACCTAGAGAACCTGCACCTTCACC 7864

Db 7777 TGCATCAAGGTGGCGCGGTGCTCAACAACGCTTCTACCTGGAGAACCTGCACCTTCACC 7836

Qy 7865 ATTGATGGGGTGGATACCCATTACTTTGTGTAACCAAGGACCTTTCAGAAGGTTGACCTGGCC 7924

Db 7837 ATCAGAGGCAAGGACACGCACACTACTTTCATCAAGACCACCAACCCGAGAGCGACCTGGGC 7896

Qy 7925 ATCTTGGGCTCAGTGGGGGGCGCGGAACCTTGAGAAATGGGGTCAACGTCACCTGTGTCC 7984

Db 7897 ACGTTCGGTTGACCAGCGGCCGCAAGGGCGCTGGAGAACGGCATCAACGTCACGGTGTGCG 7956

Qy 7985 CAGATCAACACACAGTACTTAATGGCAGGACTAGACGCTACACAGACATCCAGCTCCAGTAC 8044

Db 7957 CAGTCCACCACGCTGGTGAACGGCAGGACCGCGAGGTCGCGGACGCTGGAGATGCAAGTTC 8016

Qy 8045 GGGGCACCTGTGCTTGAACACACAGCTACGGGACAACTTGGATGAGGAGAAGGCACGGGTC 8104

Db 8017 GGCGCGCTGGCGTGCACGTGCGCTACGGCATAACCTTGACGAGGAGAAGGCGCGCATC 8076

Qy 8105 CTGGAGCTGGCCCGCAGAGAGCCGTCGCGCCCAAGCTTGGGCCCGCGCAGCAGAGACTG 8164

Db 8077 CTGGAGCAGGCGCGCAGCGCGGCTCGCCCGGGCCCTGGCGCGCGCAGCAGCAGCGCGTG 8136

Qy 8165 CGGGAAGGGGAGGAAGCCCTGCGGGCCTGGACAGAGGGGGAGAAGCAGCAGGTCGTGAGC 8224

Db 8137 CGCGACGGCGAGGAGGGCGCGCGCTCTCTGGACGGAGGGCGAGAAGCGGCAGCTGCTGAGC 8196

QY	8225	ACAGGGCGGTGCAAGGCTACGACGGCTTTTTCGTGATCTCTGTCGAGCAGTACCCAGAA	8284
Db	8197	GCCGGCAAGGTGCAGGGCTACGACGGGTACTACGTACTCTCGTGGAGCAGTACCCCGAG	8256
QY	8285	CTGTCCAGACGCGCCCAACAACATCCACTTCATGACACAGAGCGAGATGGGCGGAGGTGA	8344
Db	8257	CTGGCCGACAGCGGCCCAACAACATCCAGTTCCTGCGCAGAGCGAGATCGGCAGGAGGTAA	8316
QY	8345	C	8345
Db	8317	C	8317
RESULT 11			
ADH41972			
ID	ADH41972 standard; DNA; 8204 BP.		
XX			
AC	ADH41972;		
XX			
DT	25-MAR-2004 (first entry)		
XX			
DE	Novel human nucleic acid NOV40u.		
XX			
KW	ds; gene; cardiovascular; antiarteriosclerotic; hypotensive; cytostatic;		
KW	anorectic; antidiabetic; immunosuppressive; anti-HIV; neuroprotective;		
KW	nootropic; antiparkinsonian; antiasthmatic; antiinfertility;		
KW	cardiomyopathy; atherosclerosis; hypertension; cancer; obesity; diabetes;		
KW	AIDS; multiple sclerosis; graft-versus-host disease; Alzheimer's disease;		
KW	Parkinson's disease; asthma; fertility disorder; chromosome mapping;		
KW	tissue typing; preventive medicine; pharmacogenomic; vaccine.		
XX			
OS	Homo sapiens.		
XX			
PN	WO2003102159-A2.		
XX			
PD	11-DEC-2003.		
XX			
PF	04-JUN-2003; 2003WO-US017573.		
XX			
PR	04-JUN-2002; 2002US-0385490P.		
PR	04-JUN-2002; 2002US-0385615P.		
PR	04-JUN-2002; 2002US-0385755P.		
PR	05-JUN-2002; 2002US-0386041P.		
PR	06-JUN-2002; 2002US-0386355P.		
PR	06-JUN-2002; 2002US-0386357P.		
PR	06-JUN-2002; 2002US-0386447P.		
PR	06-JUN-2002; 2002US-0386459P.		
PR	06-JUN-2002; 2002US-0386465P.		
PR	06-JUN-2002; 2002US-0386864P.		
PR	07-JUN-2002; 2002US-0386701P.		
PR	07-JUN-2002; 2002US-0386796P.		
PR	07-JUN-2002; 2002US-0386931P.		
PR	07-JUN-2002; 2002US-0387078P.		
PR	07-JUN-2002; 2002US-0387081P.		
PR	07-JUN-2002; 2002US-0387083P.		
PR	10-JUN-2002; 2002US-0387429P.		
PR	10-JUN-2002; 2002US-0387540P.		
PR	10-JUN-2002; 2002US-0387866P.		
PR	11-JUN-2002; 2002US-0387606P.		
PR	11-JUN-2002; 2002US-0387610P.		
PR	11-JUN-2002; 2002US-0387659P.		
PR	11-JUN-2002; 2002US-0387668P.		
PR	11-JUN-2002; 2002US-0387696P.		
PR	11-JUN-2002; 2002US-0387859P.		
PR	12-JUN-2002; 2002US-0387934P.		
PR	12-JUN-2002; 2002US-0387960P.		
PR	12-JUN-2002; 2002US-0388022P.		
PR	12-JUN-2002; 2002US-0388096P.		
PR	12-JUN-2002; 2002US-0388432P.		
PR	12-JUN-2002; 2002US-0388479P.		
PR	13-JUN-2002; 2002US-0389123P.		
PR	14-JUN-2002; 2002US-0389120P.		

PR	14-JUN-2002;	2002US-0389146P.
PR	17-JUN-2002;	2002US-0389742P.
PR	18-JUN-2002;	2002US-0389604P.
PR	18-JUN-2002;	2002US-0389884P.
PR	19-JUN-2002;	2002US-0390006P.
PR	19-JUN-2002;	2002US-0390144P.
PR	19-JUN-2002;	2002US-0390209P.
PR	25-JUN-2002;	2002US-0391726P.
PR	06-AUG-2002;	2002US-0401628P.
PR	09-AUG-2002;	2002US-0402268P.
PR	12-AUG-2002;	2002US-0402822P.
PR	13-AUG-2002;	2002US-0403458P.
PR	15-AUG-2002;	2002US-0403617P.
PR	15-AUG-2002;	2002US-0403732P.
PR	26-AUG-2002;	2002US-0406182P.
PR	12-SEP-2002;	2002US-0410085P.
PR	13-SEP-2002;	2002US-0410505P.
PR	23-SEP-2002;	2002US-0412955P.
PR	30-SEP-2002;	2002US-0415195P.
PR	23-OCT-2002;	2002US-0420627P.
PR	23-OCT-2002;	2002US-0420718P.
PR	24-OCT-2002;	2002US-0420852P.
PR	31-OCT-2002;	2002US-0422750P.
PR	01-NOV-2002;	2002US-0423095P.
PR	05-NOV-2002;	2002US-0423748P.
XX	(CURA-) CURAGEN CORP.	
PA		
XX		
PI	Alsobrook JP, Anderson DW, Baumgartner JC, Berghs C, Boldog FL;	
PI	Burgess CE, Casman SJ, Catterton E, Dhanabal M, Edinger SR;	
PI	Ellerman K, Ettenberg S, Gangolli EA, Gerlach VL, Gorman L;	
PI	Grosse WM, Gunther E, Guo X, Gusev VV, Herrmann JL, Ji W, Kekuda R;	
PI	Khramtsov NV, Larochele WJ, Li L, Liang H, Low K, Macdougall JR;	
PI	MacIachlan T, Malyankar UM, McQueeney K, Mezick AJ, Miller CE;	
PI	Millet I, Padigar M, Patturajan M, Peyman JA, Qian X, Rastelli L;	
PI	Rieger DK, Rothenberg ME, Shenoy SG, Shimkets RA, Smithson G;	
PI	Spytek KA, Stone DJ, Sukumaran S, Szekeres ES, Vernet CAM, Voss EZ;	
PI	Wolenc AR, Zhong M, Zhong H;	
XX		
DR	WPI; 2004-053467/05.	
DR	P-PSDB; ADH41973.	
XX		
PT	New NOVX polypeptides and nucleic acid molecules useful for preventing or	
PT	treating NOVX-associated disorders, e.g. cancer, cardiomyopathy,	
PT	atherosclerosis or diabetes, in chromosome mapping, tissue typing or in	
PT	pharmacogenomics.	
XX		
PS	Claim 20; SEQ ID NO 525; 1503pp; English.	
XX		
CC	The invention relates to 566 new isolated human polypeptides and their	
CC	encoding genes, sequences that are at least 95% identical to these or	
CC	sequences comprising one or more conservative substitutions in these. The	
CC	polypeptide, polynucleotide and antibodies against the polypeptides are	
CC	useful in diagnosing, treating or preventing NOVX-associated disorders,	
CC	e.g. cardiomyopathy, atherosclerosis, hypertension, cancer, obesity,	
CC	diabetes, AIDS, multiple sclerosis, graft-versus-host disease,	
CC	Alzheimer's disease, Parkinson's disease, asthma, or fertility disorders.	
CC	The nucleic acids are further used as hybridization probes, in chromosome	
CC	mapping, tissue typing, preventive medicine, and pharmacogenomics. The	
CC	polypeptides are also useful as vaccines. This sequence represents an	
CC	example of the nucleic acid sequence of the invention.	
XX		
SQ	Sequence 8204 BP; 2220 A; 1950 C; 2087 G; 1947 T; 0 U; 0 Other;	
Query Match 41.6%; Score 3473.8; DB 12; Length 8204;		
Best Local Similarity 65.2%; Pred. No. 0;		
Matches 5445; Conservative 0; Mismatches 2692; Indels 216; Gaps 14		
QY	35	ATGGACGTGAAGGAGAGAGCGCTTACCGCTCGCTGACCCGGCGC---CGCGACGCCGAG 91
Db	4	ATGGATGTGAAGAACCGCAGGCTTACTGCTCCCTGACCAAGAGCAGACGAGAAGGAA 63
QY	92	CGCCGCTACACCAGCTCGTCCGCGGACAGCGAGGGGCAAG---CCCCGAGAAATCG 148

Db 64 CGGCGCTACACAAATTCTCCGCAGACAAATGAGGAGTGCCGGGTACCCACACAGAAGTCC 123

QY 149 TACAGCTCCAGGAGACCCCTGAAGGCCTACGACCAGGA---CGCCCGCCTAGCCTATGGC 205

Db 124 TACAGTTCAGCGAGACATTGAAAGCTTTTGATCATGATTCCTCGCGCTGCTTTACGGC 183

QY 206 AGCCGCGTCAAGACATTTGTCCGCAGGAGGCCGAGGAATTTCTGCCGACACAGGTGCCAAC 265

Db 184 AACAGAGTGAAGGATTTGGTTACAGAGAAGCAGACGAGTTCACTAGACAAGGACAGAAAT 243

QY 266 TTCACCCCTGCGGAGCTGGGGCTGGAAGAAGTAAACGCCCCCTCACGGGACCCTGTACCGG 325

Db 244 TTTACCCCTAAGGCAGTTAGGAGTTTGTGMACCAGCAACTCGAAGAGGACTGGCATTTTGT 303

QY 326 ACAGACATTTGGCCTGCCCAATCGCGCTACTCCATGGGGCTGGCTCTGATGCCGACATG 385

Db 304 GCGGAAATGGGCTCCCTCACAGAGGTTACTCTATCAGTGCAGGCTCAGATGCTGATACT 363

QY 386 GAGGCTGACACGGTCTGTCCCTTGAGCACCCCGTGCCTGTGTGGGSCCGGAGCACACGG 445

Db 364 GAAATGAAGCATGATGTCCCAGAGCATGCCATGAGACTTTGGGGCAGGGGGTCAAA 423

QY 446 TCAGGGCGCAGCTCTGCTGCCCTGTCCAGCCGGGCAATTCAAATCTCACACTCACCGACAC 505

Db 424 TCAGGCCGCAGCTCCTGCCTGTCAAGTCGGTCCAACTCAGCCCTCACCCCTGACAGATACG 483

QY 506 GAGCATGAAACACTGAGACTGATCATCCGGGGCGCCTGCAGAAACCAAGCGCGGCTCCGG 565

Db 484 GAGCACGAAACAAAGTCCGACAGTGAGATGAGCAACCTGCAAGCAATCAAGGCCAGTCT 543

QY 566 ACGCCGCGCGCGCTCTCGCACGCCCCACACCCCCAAACAGCACCAACCGCGCCTCCATT 625

Db 544 ACCCTGCAGCCCTTGCCGCTTCCCATAAGCAGCACTCTGCACAGCATCATCCATCCATC 603

QY 626 AACTCCCTGAACCGGGCAACTTTCAGCCCGAGGAGCAACCCAGCCCGCCCCCACGGAC 685

Db 604 ACTTCTCTCAACAGAAACTCCCTGACCAATAGAAGGAACAGAGTCCGGCCCCCGCGCT 663

QY 686 CACTCGTCTCCGGAGAGCCCCCTGCCGGCGGCCAGGAGCCTGCCACAGCCCCAGGAG 745

Db 664 GCTTTGCCCGCGAGCTGCAAAAC-----CACACCGAGTCCGTCCAGCTGCAGGAC 714

QY 746 AACTGGCTGCTCAACAGCAACATCCCCCTGGAGACCAGGAACCTTAGGCAAGCAGCCATT 805

Db 715 AGCTGGGTCCTTGGCAGTAATGTACCACCTGGAAGCAGGCATTT----- 758

QY 806 CTAGGGACATTCAGGACAAACCTCATTTGAGATGAGACATTCCTCGGCGCCTCCGCCCATGAT 865

Db 759 ----- 758

QY 866 GGGGCTTACAGTGACGGGCACTTCTCTTCAAGCCTGGAGGCACCTCCCCGCTCTTCTGC 925

Db 759 -----CCTATTCAAAACAGGAACAGGTACAAACGCCACTGTTTCAGT 798

QY 926 ACCACATCACAGGTTACCCACTGACGTCCAGCACAGTGTACTCTCCTCCGCCCCGACCC 985

Db 799 ACTGCAACCCAGGATACACAATGGCATCTGGCTCTGTTTATTACCAACCTACTCGGCCA 858

QY 986 CTGCCCCGACAGCCTTCGCCCGCGGCTTTAACTCAAGAAGCCCTCAAGTACTGT 1045

Db 859 CTACCTAGAAACACCCCTATCAAGAAGTGTCTTTAAATTCAGAAGTCTTCAAAAGTACTGT 918

QY 1046 AACTGGAAGTGCAGCGCCTGAGCGCCATCGTCACTCAGCCACTCTGGTCACTCTGCTG 1105

Db 919 AGCTGGAATGCACCTGCACTGTGTGCCGTAGGGGTCTCGGTCTCCTGGCAATACTCCTG 978

QY 1106 GCATACTTTGTGGCCATGCACCTGTTTGGCCTAAACTGGCACCTGCAGCCCGATGGAGGG 1165

Db 979 TCTTATTTATAGCAATGCATCTCTTTGGCCTCAACTGGCAGCTACAGCAGACTGAAAT 1038

QY 1166 CAGATGTATGATTCAGGAGGACACAGCCAGTGTGGCCTGTGCCAACCGACGTCTCC 1225

Db 1039 GACACATTTGAGA-----ATGGAAGAGTGAAATTTCTGATACCATGCCAACAAACACTGTG 1092

QY 1226 CTATACCCCTCAGGGGGCACTGGCTTAGAGACCCCTGACAGGAAGGCAAAGGAACCACA 1285

Db 1093 TCATTACCTTCTGGAGACA----- 1111

QY 1286 GAAGGAAAGCCCAGTAGTTTCTTTCCAGAGGACAGTTTCTATAGATTTCTGGAGAAATTTGAT 1345

Db 1112 -ATGGAAGAAATTAGGTGGATTTACGCAAGAAAAATAACACCATAGATTTCCGAGAACTTTGAT 1170

QY 1346 GTGGAAAGCGAGCCTCCCAGAAAGATTCTCTCTGGCACTTTCTTGAGATCTCAAAGTGTTC 1405

Db 1171 ATTGSCCGAAGAGCAATTCAAGAGATTCTCCCGGATCTTCTCGAGATCACAGCTCTTC 1230

QY 1406 ATAGACCATCTGTGCATCTGAATTTCAATGTGTCTCTGGGAAAGGCAGCCCTGTTGGC 1465

Db 1231 ATTGATCAGCCACAGTTTCTTTAAATTTCAATATCTCTCTTCAGAAAGGATGCATTTGATTGA 1290

QY 1466 ATTTATGGCAGAAAAAGGCCCTCCCTCTTTCACATA-----CACAGTTTGACTTT 1513

Db 1291 GTATATGGCCGGAAGAAGTTTACCGCTTCCCATACTCAGTCTCTCCCCCAGTATGACTTC 1350

QY 1514 GTGAGCTGCTGGATGGCAGGAGGCTCTAAACCAGGAGCGCGGAGCCTAGAGGGGACC 1573

Db 1351 GTGAGCTCCTGGATGGCAGCAGGCTGATTGCCAGAGAGCAGCGGAGCCTGCTTGAGACG 1410

QY 1574 CCGCGCCAGTCTCGGGGAACGTGCCCCCTCCAGCCCATGAGACAGGCTTCATCCAGTAT 1633

Db 1411 GAGAGAGCGGGCGGAGGAGATCCGTGAGCTTTCATGAGCGCGCTTATCCAGTAC 1470

QY 1634 TTGGATTCAGGAATCTGGCACTTGGCTTTTACAATGACGGAAAGGAGTCAGAAAGTGGTT 1693

Db 1471 TTGGATTCGGAATCTGGCATCTGGCTTTTATAATGATGGGAAAAATGCAGAGCAGGTG 1530

QY 1694 TCCTTTCTCACCACTGCCATTGAGTCGGTGGATAACTGCCCCCAGCAACTGCTATGGCAAT 1753

Db 1531 TCTTTTAAATACCATTTGTATAGAGTCTGTGGTGAATGTCCCCGAAATTGCCATGGAAAT 1590

QY 1754 GGTGACTGCATCTCTGGGACCTGCCACTGCTTCTGGGTTTCTGGGCCCCGACTGTGGC 1813

Db 1591 GGAGAAATGCGTTTCTGGAACCTTGCCATTGTTTCCAGGAATTTCTGGTCCGGATTGTTCA 1650

QY 1814 AGAGCCTCCTGCCCCGTGCTCTGTAGCGGAAATGGCCAATACATGAAAGGCAGATGCTTG 1873

Db 1651 AGAGCCGCTGTCCAGTGTATGTAGTGCAACGGGCAGTACTCCAAGGGCCGCTGCCTG 1710

QY 1874 TGCCACAGTGGCTGGAAGGGCGCTGAGTCGATGTGCCCAACCAACCAAGTGTATCGATGTG 1933

Db 1711 TGTTTCAGCGGCTGGAAGGGCACCGAGTGTGATGTGCCGACTACCCAGTGTATTGACCCA 1770

QY 1934 GCCTGCAGCAACCATGGCACCTGCATCAAGGGCACCTGCATCTGCAACCCCTGGCTACAAG 1993

Db 1771 CAGTGTGGGGTCGTGGGATTTGTATCATGGGCTCCTGTGCTTGCAGCTCAGGATACAA 1830

QY 1994 GCGAGAGCTGTGAGGAAGTGGACTGCATGGACCCCCACATGTTTCAGGCCGGGGTGTCTGC 2053

Db 1831 GGAGAAAGTTGTGAAGAAAGCTGACTGTATAGACCCCTGGGTGTTCTAATCATGTTGTGTGT 1890

QY 2054 GTGAGAGGCGAATGCCATTGCTTTGTGGATGGGAGGCACCAACTGCGAGACCCCCAGG 2113

Db 1891 ATCCACGGGGAATGTCACTGCAGTCCAGGATGGGAGGTAGCAATTTGTGAAATACTGAAG 1950

QY 2114 GCCACATGCTTAGACCAAGTGTTCAGGCCACGGAACCTTCTCCCGGACACCGGGCTTTGC 2173

Db 1951 ACCATGTGTCCAGACCAGTGCTCCGGCCACGGAACGTA TCTTCAAGAAAGTGGCTCCTGC 2010

QY 2174 AGCTGTGACCCAAAGCTGGACTGGACACGACTGTTCTATCGAGATCTGTGCTGCCGACTGT 2233

Db 2011 ACGTGTGACCCCTAACTGGACTGGCCCCAGACTGCTCAAACGAAATATGTCTGTGGACTGT 2070

QY 2234 GGTGGCCATGGCCTGTGCGTAGGGGGCACTGCCGCTGCGAGGATGGCTGGATGGGGGCA 2293

Db 2071 GGCTCACACGGCGTTTGCATGGGGGGGACGTGTCGTGTGAAGAAAGGCTTGACGGGCCCCA 2130



Qy	2294	GCCTGCGACGAGCGGCCTGCCACCCCGCTGTGTCCGAGCATGGGACTTGC CGGACGGC	2353	Qy	3356	GCAGCCCCAGACCTGTCTATTATTTTCATTTGGGACAAGACAGACGTCTACAACCCAGAAG	3415
Db	2131	GCCTGTAATCAGAGAGCCTGCCACCCCGCTGTGTCCGAGCACGGGACCTGCAAGGATGGC	2190	Db	3211	GCCTCACCAAACTTGGCCTATACTTTTCATATGGGATAAAAACAGATGCATATAATCAGAAA	3270
Qy	2354	AAGTGCAGTGCAGCCCTGGCTGGAAATGGCGAACTGCACCATCGCTCACTATCTGGAT	2413	Qy	3416	GTGTTTGGGCTTTCAGAAAGCCTTTGTTTCCGTGGGTATGAATATGAATCCTGCCCAGAT	3475
Db	2191	AAGTGTGAATGCAGCCAGGGCTGGAATGGAGAGCACTGCACATATCGCTCACTATTTGGAT	2250	Db	3271	GTCTATGGTCTATCTGAAGCTGTGTGTAGTTGGATATGAGTATGAGTCGTGTTGGAC	3330
Qy	2414	AGGGTAGT-----TAAAGAGGTTGCCCTGGGTTGGTTGTGCAATGGCAAC	2455	Qy	3476	CTAATCCTGTGGGAAAAAAGAAACAAACAGTGTGTCAGGGCTATGAAATTGACGCGTCCAAG	3535
Db	2251	AAGATAGTTAAAGACAAGATAGGATATAAAAGAGGGTTGTCTGGTCTGTGCAACAGCAAT	2310	Db	3331	CTGACTCTGTGGGAAAAGAGGACTGCCATTCTGCAGGGCTATGAATTGGATGCGTCCAAC	3390
Qy	2456	GGCAGATGTACCTTAGACCTGAATGGTTGGCACTGCGTCTGCCAGCTGGCTGGAGAGGA	2515	Qy	3536	CTTGAGGATGGAGCCCTAGACAAACATCATGCCCCCTCAACATTCAAAGTGGTATCCTGCAC	3595
Db	2311	GGAAGATGTACCCCTGGACCAAAATGGCGGACATTTGTGTGCCAGCCTGGATGGAGAGGA	2370	Db	3391	ATGGGTGGCTGGACATTAGATAAACATCACGTGCTGGATGTACAGAAACGGTATACTGTAC	3450
Qy	2516	GCTGGCTGTGACACTTCCATGGAGACTGCCCTGCGGTGACAGCAAGACAATGATGGAGAT	2575	Qy	3596	AAAGGAATGGGGAGAAACCAAGTTGTGTCTCAGCAGCCTCCTGTCTATTTGGGAGCATCATG	3655
Db	2371	GCAGGCTGTGACGTAGCCATGGAGACTCTTTGCAACAGATAGCAAGGACAATGAAGGGGAT	2430	Db	3451	AAGGAAACGGGGAAAAACCAAGTTTCATCTCCAGCAGCCTCCAGTCGTGAGTAGCATCATG	3510
Qy	2576	GGCCTGGTGGACTGCATGGAACCTGACTGCTGCCCTCAGCCCCCTGTGCCATPATCAACCCG	2635	Qy	3656	GGCAATGGCGCCGGAGAAAGCATCTCCTCTGCCAGCTGCCAGTGCAACGGCCTTCTGTACGGCAAC	3715
Db	2431	GGACTCATGTACTGCATGGATCCCGATTGCTGCCATACAGAGTTCTTGCCAGAAATCAGCCC	2490	Db	3511	GGCAATGGCGGAAGCGCAGCATTTCTGCCCCAGTTGCAATGGTCAAGCTGATGGTAAC	3570
Qy	2636	CTGTGCCCTTGGCTCCCTTAACCTCTTGGACATCATCCAGGAGACACAGGTCCCTGTGTCA	2695	Qy	3716	AAGCTCCTGGCCCCAGTGGCCCTCACCTGTGGTCTGACGGAGCCTCTATGTGGGTGAT	3775
Db	2491	TATTGTGGGGACTGCCCGATCCTCAGGACATCATTAGCCAAAGCCTTCAATCGCCTTCT	2550	Db	3571	AAGTTACTGGCCCCAGTGGCGCTAGCTTGTGGGATCGATGGCAGTCTGTACGTAGCGAT	3630
Qy	2696	CAGCAGAACTTACACTCCTTCTATGACCGCATCAAGTTCTCGTGGCAGGACAGCAGCAG	2755	Qy	3776	TTCAACTACATTAGAAGGATCTTCCCCTCTTGAAATGTCAACACATCCTTAGAGCTGAGG	3835
Db	2551	CAGCAAGCTGCCAAATCCCTTTATGATCGAATCAAGTTCTTATAGGATCTGATAGCACC	2610	Db	3631	TTCAACTACGTGCGGGGATATTCCCTTCTTGAAATGTAAACAAGTGTCTTAGAACTAAGA	3690
Qy	2756	CACATAATCCCGGGAGAAACCCCTTTGATGGAGGGGATGCTTGTGTTATTTCGTGGCCAA	2815	Qy	3836	AATAAAGATTTCAGACATAGTCAAGTCCAGCACACAAATACTACCTGGCCACAGACCCC	3895
Db	2611	CATGTTATACCTGGAGAAAGTCTTTCAATAAGAGCCTTGCATCTGTCTATCAGAGGCCAA	2670	Db	3691	AATAAAGATTTAGACATAGCAGCAACCCAGCTCATAGATACTACCTTGCAACGGATCCA	3750
Qy	2816	GTGATGACATCAGATGGAACCCCGCTGGTTGGTGTGAACATCAGTTTTTGTCAATAACCTT	2875	Qy	3896	ATGAGTGGGGCGCTCTTCCCTTCTGACAGCAACAGCCGGCGGTCTTTAAAAATCAAGTCC	3955
Db	2671	GFACTGACTGCTGATGGAACTCCACTTATTGGAGTAATGTCTCGTTTTTCCATTACCCA	2730	Db	3751	GTACCGGGAGATCTGTACGTTTTCTGACACAAACACCCGCAGAAATTTATCGCCCAAAGTCA	3810
Qy	2876	CTCTTTGGATATACAATCAGCAGGCAAGATGGCAGCTTTGACTTGGTGACAAATGCGCGC	2935	Qy	3956	ACTGTGTGTGAAGGACCTTGTCAAGAACTCTGAGGTGTTGCGGGGACAGGTGACCAG	4015
Db	2731	GAATATGATATACTATTACCCGCGCAGGACGGAAATGTTTGAATTTGGTGCAAAATGGTGGG	2790	Db	3811	CTTACGGGGCAAAAGACTTGACTAAAAATGCAGAACTCGTCGCAGGSAACAGGGAGCAA	3870
Qy	2936	ATCTCCATCATCCTGCGGTTGAGCGGGCACCTTTATATCACACAGGAGCACACCTGTGG	2995	Qy	4016	TGCCTCCCTTTGATGACACTCGCTGCGGGGATGGTGGGAAGGCCACAGAAAGCCACACTC	4075
Db	2791	GCCTCTCTAACTTTGGTATTTGAACGATCCCCATTCCTCACTCAGTATCATCTGTGTGG	2850	Db	3871	TGCTTCCGTTTGACGAGCGGAGATGTGGGGATGGAGGAAAGGCCGTGGAAGCCACACTC	3930
Qy	2996	CTGCCATGGATCGCTTCTTTGTATGGAACCATCATCATGAGACATGAGGAGAAATGAG	3055	Qy	4076	ACCAATCCCAGGGGTATTACAGTGGACAAAGTTTGGGCTGATCTACTTCGTGGATGGCACC	4135
Db	2851	ATTCCATGGAATGTCTTTTATGTGTGATACCTTAGTCAATGAGGAAAGAGAGATGAC	2910	Db	3931	ATGAGTCCCAAGGAATGGCAGTTGATAAGAAATGGATTAATCTACTTTTGTGTGGAACC	3990
Qy	3056	ATTCCCAGCTGTGACCTGAGCAAATTTTGCCCGCCCCCAACCCAGTCGTCTCTCCATCCCCA	3115	Qy	4136	ATGATCAGACGCGCATCGATCAGAAATGGGATCGATCTCCACCTGCTCGGCTCTAATGATCTC	4195
Db	2911	ATTCCCAGCTGTGATCTGAGTGGATTCTGTAGGCCAAATCCCATCATTTGTCTCATCACCT	2970	Db	3991	ATGATTAGGAAAGTTGACCAAAATGGAATCATATCAACTCTTCTGGGCTCTAACGATTTG	4050
Qy	3116	CTGACGCTCCTTCGCCAGCTCCTGTGCAGAGAAAGGCCCCCATTTGTCCCGGAAATTCAGGCT	3175	Qy	4196	ACATCAGCCCCGCCACTCAGCTGTGATTCTGTCTCATGGATATTTCCAGGTAAAGACTGGAG	4255
Db	2971	TTATCCACCTTTTTCAGATCTTCTCCTGAAGACAGATTTGAAACTCTCCTACTTGAGTTCAGA	3030	Db	4051	ACTTCAGCCAGACCTTTAACTTGTGACACCCAGCATGCACATCAGCCAGGTACGTCTGGAA	4110
Qy	3176	TTGCAGGAGGAAATCTCTATCTCTGGCTGCAAGATGAGGCTGAGCTACCTGAGCAGCCGG	3235	Qy	4256	TGGCCACAGACTTAGCCCATCAACCCCAATGGACAACACTCACTTTATGTCTCGACACAAT	4315
Db	3031	CTCCACGAGGAAACTACAATTCAGGAACAGATTTGAAACTCTCCTACTTGAGTTCACAGA	3090	Db	4111	TGCCCCACTGACCTAGCCATTAAACCTTATGGATAACTCCATTATGTCTCTGGATAAAT	4170
Qy	3236	ACCCCTGGCTACAAATCTGTCTGAGGATCAGCCTCACCCACCCGACCATCCCCTTCAAC	3295	Qy	4316	GTGGTCTGCAAATCTCTGAAAAACCCAGGTGCGATTGTCCCGGGAGGCCCATGAC	4375
Db	3091	GCTGCAGGGTAAAGTCAGTTCTCAAGATCACCATGACCCAGTCTATTATTCCATTTAAT	3150	Db	4171	GTAGTTTTACAGATCACTGAAAAATCGTCAAGTTTCGATTGCTGTGGACGGCCCATGAC	4230
Qy	3296	CTCATGAAGGTGCACCTCATGGTAGCGGTGGAGGGCCGCTCTTCAGGAAGTGGTTCGCT	3355	Qy	4376	TGCCAGGTCCCTGGCATTGACCACTTCCCTGTCTAAGCAAGGTGGCCATCCACGCAACCTG	4435
Db	3151	TTAATGAAGGTTTCATCTTATGGTAGCTGTAGTGAAGAGACTCTTCCAAAAGTGGTTTCCT	3210	Db	4231	TGTCAGGTTCCCGGAGTGG--AATATCCTGTGGGGAAGCACCGGTCAGACAACACTG	4287
				Qy	4436	GAGTCAGCCACCGCTTTGGCTGTTTTTACACAATGGGGTCTCTGTATATTGCTGAGACTGAT	4495

Db 4288 GAATCAGCCACTGCCATTGCTGTGTCCTACAGTGGGTCCCTGTACATTACTGAAACTGAT 4347  
QY 4496 GAGAAAAAGATCAACCGCATCAGGCAGGTCAACCACTAGTGGAGAGATCTCACTCGTTGCT 4555  
Db 4348 GAGAAGAAAAATTAAACGGGATAAGGCAGGTCAACAACAGATGGAGAATCTCCTTAGTGGCC 4407  
QY 4556 GGGGCCCCAGTGGCTGTGACTGTAAAAATGATGCCAACTGTGATTGTTTTTCTGGAGAC 4615  
Db 4408 GGAATACCTTCAGAGTGTGACTGCAAAAAATGATGCCAACTGTGACTGTACCAAGAGTGA 4467  
QY 4616 GATGGTTATGCCAAGGATGCAAAAGTTAAATACCCCATCTTCCCTGGCTGTGTGCTGAT 4675  
Db 4468 GATGGCTACGCCAAGGATGCCAAACTCAGTGGCCCCATCCTCCCTGGCTGCTTCTCCAGAT 4527  
QY 4676 GGGGAGCTCTACGTGGCCGACCTTGGGAACATCCGAATTCGGTTTATCCGGAAGAACAAAG 4735  
Db 4528 GGTACACTGTATATTCAGATCTAGGGAATATCCGGATCCGGGCTGTGTCAAAGAATAAG 4587  
QY 4736 CCTTTCTCAACACCCAGAACATGTATGAGCTGTCTTCCCAATTTGACCAGGAGCTCTAT 4795  
Db 4588 CCTTTACTTAACTTATGAACCTTCTATGAAGTTGGTCTCCAACCTGATCAAGAACTCTAC 4647  
QY 4796 CTGTTTGATACCAACGGCAAGCACCTGTACACCAAAAGCCTGCCCAACAGGAGACTACCTG 4855  
Db 4648 ATCTTTGACATCAATGGTACTCACCAATATATACTGTAAGTTTAGTCACTGGTGATTACCTT 4707  
QY 4856 TACAACTTCACCTACACTGGGACGGCGACATCACACTCATCACAGACAACAATGGCAAC 4915  
Db 4708 TACAATTTTAGCTACAGCAATGACAATGATATTACTGCTGTGACAGACAGCAATGGCAAC 4767  
QY 4916 ATGGTAAATGTCGCGAGACTCTACTGGGATGCCCTCTGGCTGGTGGTCCCAGATGGC 4975  
Db 4768 ACCCTTAGAATTAGACGGGACCCAAATCGCATGCCAGTTCGAGTGGTGTCTCCTGATAAC 4827  
QY 4976 CAGGTGTACTGGGTGACCATTGGGCACCAACAGTGCACCTCAAGAGTGTGACCACACAAGGA 5035  
Db 4828 CAAGTGATATGGTTGACAAATAGGAACAAATGGATGTTTGAAAGGCATGACTGCTCAAGGA 4887  
QY 5036 CACGAGTTGGCCATGATGACATACCATGGCAATTCGGGCCTTCTGGCAACCAAAAGCAAT 5095  
Db 4888 CTGGAATTAGTTTTTGTACTTACCATTGGCAATAGTGGCCTTTTAGCCACTAAAAGTGAT 4947  
QY 5096 GAAAAAGGATGGACAACATTTTATGAGTACGACAGCTTTGGCCGCTTGACAAATGTGACC 5155  
Db 4948 GAAACTGGATGGACAACGTTTTTTGACTATGACAGTGAAGGTCGCTCTGACAAATGTTACG 5007  
QY 5156 TTCCCTACTGGCCAGGTGAGCAGTTTTCCGAAGTGATACAGACAGTTCAGTGCATGTCCAG 5215  
Db 5008 TTTCCAACCTGGAGTGGTCACAAACCTGCATGGGGACATGGACAAGGCTATCACAGTGGAC 5067  
QY 5216 GTAGAGACCTCCAGC---AAGGATGATGTCACCATAAACCACCAACCTGTCTGCCTCAGGC 5272  
Db 5068 ATTGAGTCATCTAGCCGAGAAGAAGATGTCAGCATCACTTCAAATCTGTCTCGATCGAT 5127  
QY 5273 GCCTTCTACACACTGTGCAAGACCAAGTCCGGAAACAGCTACTACATCGGGGCCGATGGC 5332  
Db 5128 TCTTTCTACACCATGGTTCAAGATCAGTTAAGAAACAGCTACCAGATTGGTTATGACGGC 5187  
QY 5333 TCCTTGGCGTGTGCTGSCCAACGGCATGGAGTGGCGCTGCAGACTGAGCCCCACTTG 5392  
Db 5188 TCCCTCAGAAATTATCTACGCCAGTGGCCTGGACTCACACTACCNAACAGAGCCGCACGTT 5247  
QY 5393 CTGGCTGGCACCGTCAACCCACCGTGGGCAAGAGGAATGTCAACGCTGCCCATCGACAAC 5452  
Db 5248 CTGGCTGGCACCGCTAATCCGACGGTTGCCAAAAGAAAACATGACTTTGCCTGGCGAGAAC 5307  
QY 5453 GGCCTCAACCTGGTGGAGTGGCGCCAGCGCAAAAGCAGGCTCGGGGCCAGGTCACTGTC 5512  
Db 5308 GGTCAAAACTTGGTGGAATGGAGATTCCGAAAAGAGCAAGCCCAAGGGAAAGTCAATGTC 5367  
QY 5513 TTTGGGCGCGGCTGGGGTGCACAACCGAAATCTCCTATCTCTGGACTTTGATCGCGTA 5572  
Db 5513 TTTGGGCGCGGCTGGGGTGCACAACCGAAATCTCCTATCTCTGGACTTTGATCGCGTA 5572

Db 5368 TTTGGCCGCAAGCTCAGGGTTAATGGCAGAAACCTCCTTTTCAGTTGACTTTGATCGAACA 5427  
QY 5573 ACACGCACAGAGAAAGATCTATGATGACCACCGCAAGTTTACCCTTCGGATTCTGTACGCAC 5632  
Db 5428 ACAAGACAGAAAAGATCTATGACGACCAACCGTAAATTTTCTACTGAGGATCGCCTACGCAC 5487  
QY 5633 CAGGGGGGCGGCCAGCCTCTGGTCAACCAGCAGCAGGCTGAATGGTGTCAACGCTGACA 5692  
Db 5488 ACGTCTGGGCACCCGACTCTCTGGCTGCCAAGCAGCAAGCTGATGGCCCGTCAATGTCAACC 5547  
QY 5693 TACTCCCTGGGGTTACATTGCTGGCATCCAGAGGGGCAFCATGTCTGAAAAGAAATGGAA 5752  
Db 5548 TATTCAATCCACAGGTCAAATTGCCAGCATCCAGCGAGGCACCACTAGCGAGAAAAGTAGAT 5607  
QY 5753 TACGACCAAGCGGGCCGCATCACATCCAGGATCTTCGCTGATGGGAAGACATGGAGCTAC 5812  
Db 5608 TATGACGACAGGGGAGGATCGTGTCTCGGGTCTTTGCTGATGGTAAAACATGGAGTTAC 5667  
QY 5813 ACATACTTAGAGAAAGTCCATGGTCTGCTACTACACAGCCAGAGGCAGTATATCTTTTGAG 5872  
Db 5668 ACATAATTAGAAAAGTCCATGGTTCTTCTGCTTCATAGCCAGCGGCAGTACATCTTCGAA 5727  
QY 5873 TTCGACAAGAAATGACCGCCTCTCTTCTGTGACGATGCCCAAACGTCGGCGGCAGACACTA 5932  
Db 5728 TACGATATGTGGACCGCCTGTCTGCCATCACCATTGCCAGTGGCTCGCCACACCATG 5787  
QY 5933 GAGACCATCCGCTCAGTGGCTACTACAGAAAACATCTATCAGCCCCCTGAGGGCAATGCC 5992  
Db 5788 CAGACCATCCGATCCATTGGCTACTACCGCAACATATACAACCCCGGAAAAGCAACGCC 5847  
QY 5993 TCAGTCATACAGGACTTCACTAGGATGGGCACCTCCTTCACACCTTCTACCTGGGCACT 6052  
Db 5848 TCCATCATCAGGACTACAACGAGGAAGGCTGCTTCTACAACACAGCTTCTTGGGTACA 5907  
QY 6053 GCGCGCAGGTTGATATACAAGTATGCCAAACTGTCAAAGCTGGCAGAGACGCTCTATGAC 6112  
Db 5908 AGTCGGAGGTCCTTATTCAAATACAGAAGGCAGACTAGGCTCTCAGAAAATTTTATATGAT 5967  
QY 6113 ACCACCAAGGTCAGTTTTACCTATGACGAGACGGCAGGCAATGCTGAAGACCATCAACCTA 6172  
Db 5968 AGCACAAAGATCAGTTTTTACCTATGATGAACACAGCAGGAGTCTTAAGACAGTAAACCTC 6027  
QY 6173 CAGAATGAGGGCTTCACCTGCACCATCCGCTACCGTCAGATTGGGCCCTGATTGACCGA 6232  
Db 6028 CAGAGTGATGGTTTTATTGCAACCATAGATACAGGCNAAATGGTCCCTGATTGACAGG 6087  
QY 6233 CAGATCTTCGCTTCACTGAGGAAGGCATGGTCAACGCCCGTTTTCGACTACAACATATGAC 6292  
Db 6088 CAGATTTTCGCTTTAGTGAAGATGGATGGTAAATGCAAGATTTTGACTATAGCTATGAC 6147  
QY 6293 AACAGCTTCGGGTGACCCAGCATGCAAGCTGTGATCAACGAGACCCCACTGCCCATTTGAT 6352  
Db 6148 AACAGCTTCGAGTGACCCAGCATGCAAGGTGTGATCAATGAACGCCACTGCCATTGAT 6207  
QY 6353 CTCTATCGCTATGATGTGTCAAGCAAGACAGAGCAGTTTGGGAAGTTTGGTGTCAATT 6412  
Db 6208 CTGTATCAGTTTGATGACATTTCTGGCAAAAGTTGAGCAGTTTGGAAAGTTTGGAGTTATA 6267  
QY 6413 TACTATGACATTAACCAGATCATCACACAGCTGTCTATGACCCACACCAAGCATTTTGTAT 6472  
Db 6268 TATTATGATATTAACCAGATCAATTTCTACAGCTGTAATGACCTATACGAAGCAGTCTTGTAT 6327  
QY 6473 GCATATGGCAGGATGAAGGAAGTGCAGTATGAGATCTTCGCTCGCTCATGTACTGGATG 6532  
Db 6328 GCTCATGGCCGTATCAAGGAGATTCRAATATGAGATATTCAGSTCGCTCATGTACTGGATT 6387  
QY 6533 ACCGTCCAGTATGATAACATGGGGCGAGTAGTGAAGAAGGAGCTGAAGGTAGGACCCCTAC 6592  
Db 6388 ACAATTCAGTATGATAACATGGGTCCGGTAAACCAAGAGAGAGATTAAATAGGGCCCTTT 6447  
QY 6593 GCCAATACCACTCGCTACTCCTATGATGATGATGCTGACGGCCAGCTGCAGACAGTCTCC 6652  
Db 6448 GCCAACACCACCAAAATATGCTTATGAATATGATGTTGATGGACAGCTCCAAACAGTTTAC 6507



QY	6653	ATCAATGACAAAGCCACTCTGGCGCTACAGCTACGACCTCAATGGGAACCTGCACCTTACTG	6712	QY	7733	GGCAAGGGGTCAAAGTTTGCCTTGAAGGATGGCCGAGTGACCACAGACATCATCAGTGTG	7792
Db	6508	CTCAATGAAAAGATAATGTGGCGGTACAACCTACGATCTGAATGGAACCTCCATTTACTG	6567	Db	7570	GGCAAGGGGTCTATGCTGGCCGTACGCCAGGGCCGCTGCAGACCACCTGCTCAACATC	7629
QY	6713	AGCCCTGGGAACAGTGACCGGCTCACACCACTACGGTATGACATCCGCGACCGCATCACT	6772	QY	7793	GCCAATGAGGATGGCGAAGGTTGCTGCCATCTTTGAACCATGCCACTACCTACCTAGAGAAC	7852
Db	6568	AACCCAAAGTAACAGTGCAGCTGACACCCCTTCGCTATGACCTCGGAGACAGAATCACT	6627	Db	7630	GCCAACGAGGACTGCATCAAGGTGGCGCGTGCTCAACAAACGCCTTCTACCTGGAGAAC	7689
QY	6773	CGGCTGGGTGACGTGCAATACAAGATGGATGAGGATGGCTTCCAGGCGAGCGGGCGGT	6832	QY	7853	CTGCACCTTCAACCATTTGATGGGTGGATACCCATTACTTTGTGAAACCAGGACCTTCAGAA	7912
Db	6628	CGACTGGGTGATGTTCAATATCGGTTGGATGAAGATGGTTTCCACGTCAAAGGGCAGC	6687	Db	7690	CTGCACCTTCAACCATCGAGGGCAAGGACACGCACCTACTTTCATCAAGACCACCGCCCGAG	7749
QY	6833	GATATCTTTGAGTACAACCTCAGCTGGCCTGCTCATCAAGGCCTACAACCCGGGCTGGCAGC	6892	QY	7913	GGTGACCTGGCCATCCTGGGCCTCAGTGGGGGGCGGAACCCCTGGAGAATGGGTCAAC	7972
Db	6688	GAAATCTTTGAATATAGCTCCAAGGGGCTTCTAACTCGAGTTTACAGTAAAGGCAGTGGC	6747	Db	7750	AGCGACCTGGGCACGCTGCGGTTGACCAAGCGGCCGCAAGGCGCTGGAGAACGGCATCAAC	7809
QY	6893	TGGAGTGTACAGGTACCGCTACGATGGCCTGGGCGCGCGGTGTCAGCAAGAGCAGCCAC	6952	QY	7973	GTCACTGTGTCCAGATCAACACAGTACTTAATGGCAGGACTAGACGCTACACAGACATC	8032
Db	6748	TGGACAGTGATCTACCGTTATGACGGCCTGGGAAGCGGTGTTTCTAGCAAAACCAAGTCTA	6807	Db	7810	GTGACGGTGTCCAGTCCACCAACCGTGGTGAACGGCAGGACGCGCAGGTTCGCGGACGTG	7869
QY	6953	AGCCACCACCTGCAGTTCTTCTATGCAGACCTGACCAACCCCAACCAAGGTACCCACCTG	7012	QY	8033	CAGTCTCAGTACGGGGCACCTGTGCTTGAACACACACGCTACGGGACAAACGTTGGATGAGGAG	8092
Db	6808	GGACAGCACCTGCAGTTTTTTTATGCTGACTTAACTTATCCCACTAGGATTAATCATGTC	6867	Db	7870	GAGATGCAGTTCGGCGCGCTGGCGTGCACGTGCCTACGGCATGACCTCGACGAGGAG	7929
QY	7013	TACAACCACTCCAGCTCTGAGATCACCTCCCTCTACTACGACTTGCAAGGACACCTCTTT	7072	QY	8093	AAGGCACGGTCTCTGGAGCTGGCCCGGCAGAGAGCGTGCGCCAAGCGTGGGCCCCGCGAG	8152
Db	6868	TACAACCATTCGAGTTCAGAAATTACCTCCCTGTATTATGATCTCCAAGGACATCTTTT	6927	Db	7930	AAGCGCGCATCTCTGGAGCAGGCGCGCAGCGCGCTCGCCCCGGCCTGGGCGCGCGAG	7989
QY	7073	GCCATGGAGCTGAGCAGTGGTGATGAGTTTACATAGCTTGTGACAAACATCGGACCCCT	7132	QY	8153	CAGCAGAGACTCGCGGAAGGGGAGGAAGGCGCTCGGGCCTTGACAGAGGGGAGAGAAGCAG	8212
Db	6928	GCCATGGAAATCAGCAGTGGGATGAATTCATATTGATCGGATTAACACAGSGACACCA	6987	Db	7990	CAGCAGCGCGTGGCGACGGCGAGGAGGGCGCGCGCTCTGGACGGAGGCGAGAAGCGG	8049
QY	7133	CTTGCTGTCTTTAGTGGAACAGGTTTGATGATCAAGCAAAATCCTGTACACAGCCTATGGG	7192	QY	8213	CAGGTGCTGACACAGGGCGGGTGTCAAGGCTACGACGGCTTTTTCGTGATCTCTGTCTGAG	8272
Db	6988	CTGGCTGTTCAGTAGCAATGGGCTTATGCTGAAACAGATTCAGTACACTGCATATGGG	7047	Db	8050	CAGCTGCTGAGCGCCGGAAGGTGCAGGGGTACGACGGGTACTACGTACTCTCGGTGGAG	8109
QY	7193	GAGATCTACATGGATACCAACCCCAACTTTTCAGATCATCATAGGCTACCATGGTGGCCTC	7252	QY	8273	CAGTACCCAGAACTGTCAGACAGCGGCCCAACAACATCCACTTCATGAGACAGACGAGATG	8332
Db	7048	GAAATCTATTTTGACTCTAAATATTGACTTTTCAACTGGTAAATTGGATTTTCATGGTGGCCTG	7107	Db	8110	CAGTACCCCGAGCTGGCCGACAGCGGCCCAACAACATCCAGTTCTCTCGGCAGACGAGATC	8169
QY	7253	TATGATCCACTCACCAAGCTTGTCTCCACATGGCGCGCGAGATTATGATGTCTGGCCGGA	7312	QY	8333	GGCCGGAGGTGAC	8345
Db	7108	TATGACCCCACTCACCAAAATTAATCCACTTTTGGAGAAAGAGATTATGACATTTTGGCAGGA	7167	Db	8170	GGCAGGAGGTAAC	8182
QY	7313	CGCTGGACTAGCCAGACCAGAGCTGTGGAAAGCACCTTAGTAGCAGCAACGTATGCT	7372	RESULT 12			
Db	7168	CGGTGGACAACACCTGACATAGAAAATCTGGA---AAAGAAATGGGAAGGACCCAGCTCCT	7224	ADH41990			
QY	7373	TTTAATCTCTATATGTTCAAAAACAACAACCCCATCAGCAACTCCCAGGACATCAAGTGC	7432	ID	ADH41990 standard; DNA; 8657 BP.		
Db	7225	TTTAACTTGTAATGTTTAGGAATAACAACCCCTGCAAGCAAAAATCCATGACGTGAAAGAT	7284	XX	ADH41990;		
QY	7433	TTTCATGACAGATGTTAACAGCTGGCTGCTCACCTTTTGGATTCCAGCTACACAAACGTGATC	7492	AC	25-MAR-2004 (first entry)		
Db	7285	TACATCACAGATGTTAACAGCTGGCTGGTGACATTTTGGTTTCCATCTGCAACAATGCTATT	7344	XX	Novel human nucleic acid NOV40d #2.		
QY	7493	CCTGGTTATCCCAAAACCAGACATGGATGCCATGGAACCCCTCCTACGAGCTCATCCACACA	7552	DE	ds; gene; cardiovascular; antiarteriosclerotic; hypotensive; cytostatic;		
Db	7345	CCTGGATCCCTGTTCCCAAATTTGATTAAACAGAAACCTTCTTACGA-----A	7392	XX	anorectic; antidiabetic; immunosuppressive; anti-HIV; neuroprotective;		
QY	7553	CAGATGAAAACGCAGGAGTGGGACAAACAGCAAGTCTATCTCGGGGTACAGTGTGAAGTA	7612	KW	nootropic; antiparkinsonian; antiasthmatic; antiinfertility;		
Db	7393	CTTGTGAAGAGTCAGCAGTGGGATGATATACCGCCCATCTTCGGAGTCCAGCAGCAAGTG	7452	KW	cardiomyopathy; atherosclerosis; hypertension; cancer; obesity; diabetes;		
QY	7613	CAGAAAGCAGCTCAAGGCCCTTTGTACCTTAGAACGGTTTGAACAGCTCTATGGCTCCACA	7672	KW	AIDS; multiple sclerosis; graft-versus-host disease; Alzheimer's disease;		
Db	7453	GCGCGCAGGCCAAGGCCCTTCCTGTCGCTGGGAAGATGGCGAGGTGCAGGTGAGCCGG	7512	KW	Parkinson's disease; asthma; fertility disorder; chromosome mapping;		
QY	7673	ATCACCAGCTGCCAGCAGGCTCCAAAGACCAAGAAGTTTGCATCCAGCGGCTCAGTCTTT	7732	KW	tissue typing; preventive medicine; pharmacogenomic; vaccine.		
Db	7513	CGCCGGCGCGC---GGCGCGCAGTCCTGGCTGTGGTTTCGCCACGGTCAAGTCGCTGATC	7569	XX	Homo sapiens.		
				OS	WO2003102159-A2.		
				XX	11-DEC-2003.		
				PN	04-JUN-2003; 2003WO-US017573.		
				XX	04-JUN-2002; 2002US-0385490P.		
				PD	04-JUN-2002; 2002US-0385615P.		
				XX			
				PF			
				PR			
				PR			





QY	746	A	A	A	C	T	G	G	T	G	C	T	C	A	A	C	A	C	A	T	C	C	C	C	T	G	G	A	G	A	C	C	T	A	G	G	A	C	C	T	A	G	G	A	C	C	A	T	T	C	805							
Db	862	A	G	T	G	G	T	C	C	T	T	G	C	A	G	T	A	A	T	G	T	A	C	C	A	C	T	G	A	A	G	C	A	G	G	C	A	T	T	-----	-----	-----	-----	-----	-----	-----	-----	905										
QY	806	C	T	A	G	G	A	C	A	T	T	G	C	A	G	A	C	A	C	T	C	A	T	T	G	A	T	G	A	T	G	A	C	A	T	T	C	T	C	G	G	C	C	T	C	C	G	C	A	T	G	865						
Db	906	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	905										
QY	866	G	G	G	C	T	T	A	C	A	G	T	A	C	A	G	G	G	C	A	T	T	C	C	T	T	C	A	A	G	C	T	T	G	A	G	G	C	A	C	C	T	C	C	C	G	C	T	T	T	C	T	G	C	925			
Db	906	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	945										
QY	926	A	C	C	A	T	A	C	C	A	G	G	T	A	C	C	C	A	C	T	G	A	C	G	T	C	A	G	C	A	C	A	G	T	G	T	A	C	T	C	T	C	T	C	C	C	C	C	G	A	C	C	985					
Db	946	A	C	T	C	A	A	C	C	C	C	A	G	A	T	A	C	A	C	A	C	A	A	T	G	G	C	T	G	T	T	A	T	T	A	T	T	A	T	T	A	T	T	A	T	T	A	T	T	A	T	C	G	G	C	C	A	1005
QY	986	C	T	G	C	C	C	C	G	C	A	C	T	T	C	G	C	C	G	C	C	T	T	T	A	A	C	T	T	A	A	C	T	T	A	A	G	A	G	C	C	T	C	A	A	G	T	A	C	T	G	T	1045					
Db	1006	C	T	A	C	C	T	A	G	A	A	C	A	C	C	T	A	T	C	A	A	G	A	G	T	G	C	T	T	T	A	A	A	T	C	A	A	G	A	G	T	C	T	T	C	A	A	A	G	T	A	C	T	G	T	1065		
QY	1046	A	A	C	T	G	A	A	G	T	G	C	G	C	C	T	G	A	C	G	C	C	A	T	C	G	T	C	A	T	C	A	G	C	C	A	T	C	T	C	A	G	C	C	A	T	C	T	G	T	C	T	G	T	1105			
Db	1066	A	G	C	T	G	G	A	A	T	G	C	A	C	T	G	T	G	C	C	G	T	A	G	G	T	C	G	G	T	C	T	C	G	T	C	G	T	C	T	C	T	C	T	C	T	C	T	C	T	C	T	G	T	1125			
QY	1106	G	C	A	T	A	C	T	T	T	G	T	G	C	A	T	G	C	A	C	C	T	G	T	T	G	G	C	T	A	A	A	C	T	G	G	C	A	C	C	T	G	C	A	C	C	G	A	T	G	G	A	G	G	1165			
Db	1126	T	C	T	T	A	T	T	A	T	A	G	C	A	A	T	G	C	A	T	C	T	T	T	G	G	C	T	C	A	A	C	T	G	G	C	A	C	T	A	C	A	G	C	A	C	T	G	A	A	A	T	1185					
QY	1166	C	A	G	A	T	A	G	A	T	C	A	C	G	G	A	G	A	C	A	C	A	G	C	A	G																																

QY	1814	AGAGCCTCCTGCCCCGCTGCTCTGTAGCGGAAATGGCCAAATACATGAAAGGCAGATGCTTG	1877
DB	1798	AGAGCCGCTGTCCAGTGTTATGTAGTGGCAACGGGCAGTACTCCAAGGGCCGCTGCCTG	1857
QY	1874	TGCCACAGTGGCTGGAAGGCGCTGAGTGCAGATGTGCCACCAACCAAGTGTATCGATGTG	1933
DB	1858	TGTTTCAGCGGCTGGAAGGGCACCGAGTGTATGTGCCGACTACCCAGTGTATTGACCCA	1917
QY	1934	GCCTGCAGCAACCATGGCACCTGCATCACGGGCACCTGCATCTGCAACCCCTGGCTACNAAG	1993
DB	1918	CAGTGTGGGGTCTGTGGATTTGTATCATGGGCTCCTGTGCTTGCAGCTCAGGATACAAA	1977
QY	1994	GGCGAGAGCTGTGAGGAAGTGGACTGCATGGACCCCAACATGTTCAAGCCGGGTGTCTGC	2053
DB	1978	GGAGAAAGTTGTGAAGAACTGACTGTATAGACCCCTGGGTGTTCTTAATCATGTTGTGT	2037
QY	2054	GTGAGAGGCGAATGCCATTTGCTTTGTGGATGGGAGGCCAACCACTGCGAGACCCCCAGG	2113
DB	2038	ATCCACGGGGAATGTCACTGCAGTCCAGGATGGGAGGTAGCAATGTTGAAATACTGAAG	2097
QY	2114	GCCACATGCTTAGACCAGTGTTCAGGCCACGGAACCTTCTCCCGGACACCGGGCTTTGC	2173
DB	2098	ACCATGTGTCCAGACCAGTGTCTCCGGCCACGGAACGTATCTTCAAGAAAGTGGCTCCTGC	2157
QY	2174	AGCTGTGACCCAAAGCTGGACTGGACACGACTGTTCTATCGAGATCTGTGCTGCCGACTGT	2233
DB	2158	ACGTGTGACCTTAAGTGGACTGGCCAGACTGCTCAACGAAATATGTTCTGTGGACTGT	2217
QY	2234	GGTGGCCATGGCGTGTGCGTAGGGGGCACCTGCCGCTGCGAGGATGSGCTGGATGGGGCA	2293
DB	2218	GGCTCACACGGCGTTTGCAATGGGGGGGACGTGTGCTGTGAAGAAAGCTGGACGGCCCA	2277
QY	2294	GCCTGGACACAGCGGGCCTGCCACCCGCGCTGTGCCGAGCATGGGACCTGCCCGCAGCGC	2353
DB	2278	GCCTGTAATCAGAGAGCCTGCCACCCCGCTGTGCCGAGCACGGGACCTGCAAGGATGGC	2337
QY	2354	AAGTGCAGTGCAGCCCTGGCTGGAATGGCGAAACACTGCACCATCGCTCACTATCTGGAT	2413
DB	2338	AAGTGTGAATGCAGCCAGGGCTGGAATGGAGAGCACTGCACATCGCTCACTATTTGGAT	2397
QY	2414	AGGGTAGT-----TAAAGAGGGTTGCCCTGGTTGTGCAATGGCAAC	2455
DB	2398	AAGATAGTTAAAGACAAGATAGGATATAAAGAGGGTTGTCTGCTGTGTGCAACAGCAAT	2457
QY	2456	GGCAGATGTACTTAGACCTGAATGGTTGGCACCTGCGTCTGCCAGCTGGGCTGGAGAGGA	2515
DB	2458	GGAAGATGTACCTGGACCACAAATGGCGGCACATTGTGTGTGCCAGCCTGGATGGAGAGGA	2517
QY	2516	GCTGGCTGTGACACTTCCATGGAGACTGCTTCCGCTGCGGTGACAGCAAAAGACAATGAGAGAT	2575
DB	2518	GCAGGCTGTGACGTAGCCATGGAGACTCTTTGCACAGATAGCAAGGACAAATGAAGGGAT	2577
QY	2576	GGCCTGGTGGACTGCATGGACCCCTGACTGCTGCCTCCAGCCCCCTGTGCCATATCAACCCG	2635
DB	2578	GGACTCAATTGACTGTCATGGATCCCGATTGCTGCCTACAGAGTTCTCTGCCAGAAATCAGCCC	2637
QY	2636	CTGTGCCCTTGGCTCCCTAAACCCCTCTGGACATCATCCAGGAGACACAGGTCCCTGTGTCA	2695
DB	2638	TATTGTGGGGACTGCCGGATCCTCAGGACATCATTAGCCAAAGCCTTCAATCGCCTTCT	2697
QY	2696	CAGCAGAACCTACACTCCTTCTATGACCGCATCAAGTTCCTCGTGGCAGGACAGCAGCAG	2755
DB	2698	CAGCAAGCTGCCAAATCCTTTTATGATCGAATCAGTTTCTTATAGGATCTGATAGCACC	2757
QY	2756	CACATAATCCCGGGAGAAACCCCTTTGATGGAGGGCATGCTTGTGTTATTCTGTGGCCAA	2815
DB	2758	CATGTTATACCTGGAGAAAGTCTTTCAATAAGAGCCTTGCATCTGTTCATCAGAGGCCAA	2817
QY	2816	GTGATGACATCAGATGGAAACCCCCCTGGTTGGTGTGAACATCAGTTTTTGTCAATAACCTT	2875
DB	2818	GTACTGACTGCTGATGGAACCTCCACTTATTGGAGTAAATGTCTCGTTTTTCCATTACCCA	2877
QY	2876	CTCTTTGGATATACAATCAGCAGGCAAGATGGCAGCTTTTGACTTGGTGACAAATGGCGGC	2935



Db	2878	GAATATGGATATACTATTACCCGCCAGGACGGAATGTTTGACTTGGTGCCAAATGGTGGG	2937	Db	3958	CTTACGGGGGCAAAAGACTTTGACTAAAAATGCAGAAATCGTCGCAGGGACAGGGGAGCAA	4017
QY	2936	ATCTCCATCATCCTGCGGTTTCGAGCGGGCACCTTTTCATCACACAGGACACACCCCTGTGG	2995	QY	4016	TGCTTCCCCTTTTGATGACACTCGCTGCGGGGATGGTGGGAAGGCCACACAGAAGCCACACTC	4075
Db	2938	GCCTCTCTAACTTTGGTATTTGAACGATCCCATTCCTCACTCAGTATCATACTGTGTGG	2997	Db	4018	TGCTTCCCCTTTTGACGAGCGAGATGTGGGGATGGAGGAAAGCGCGTGGAAAGCCACACTC	4077
QY	2996	CTGCCATGGGATCGCTTCTTTGTCTATGGAAACCATCATCATGAGACATGAGGAGAATGAG	3055	QY	4076	ACCAATCCCAGGGGTATTACAGTGGACAAGTTTGGGCTGATCTACTTCGTGGATGGCAAC	4135
Db	2998	ATTCCATGGAATGTCTTTTATGTGATGGATACCCCTAGTCTATGGAGAAGAAGAGAAATGAC	3057	Db	4078	ATGAGTCCCAAGGAATGGCAGTTGATAAGAATGGATTAATCTACTTTGTGTGTAACAC	4137
QY	3056	ATTCCCAGCTGTGACCTTGAGCAATTTTGCCGCCCCAACCCAGTCGTCCTCCATCCCCCA	3115	QY	4136	ATGATCAGACGCATCGATCAGAAATGGGATCATCTCCACCCTGCTCGGCTCTAATGATCTC	4195
Db	3058	ATTCCCAGCTGTGATCTGAGTGGATTCTGTGAGGCCAAATCCCATCATATTGTGTCAACCT	3117	Db	4138	ATGATTAGGAAAAGTTGACCAAAATGGAATCATATCAACTCTTCTCGGCTCTAACGATTG	4197
QY	3116	CTGACGTCCTTCGCCAGCTCCTGTGCAGAGAAAGGCCCCCATTTGTCCGGAATTCAGGCT	3175	QY	4196	ACATCAGCCCCGCCACTCAGCTGTGATTCTGTCTATGGATATTTCCCAGGTAAGACTGGAG	4255
Db	3118	TTATCCACCCTTTTCAGATCTTCTCCTGAAGACAGTCCCATCATTCCCGAAACACAGGTA	3177	Db	4198	ACTTCAGCCAGACCTTTAACTTTGTGACACCAGCATGCACATCAGCCAGGTACGTCTGGAA	4257
QY	3176	TTGCAGGAGGAATCTCTATCTCTGGCTGCAAGATGAGGCTGAGCTACCTGAGCAGCCGG	3235	QY	4256	TGGCCACAGACTTAGCCATCAACCCAAATGGACAACTCACTTTATGTCTCTCGACAACAAT	4315
Db	3178	CTCCACGAGGAAACTACAATTCAGGAACAGATTTGAAACTCTCCTACTTGAGTTCAGAG	3237	Db	4258	TGGCCCACTGACCTAGCCATTAAACCCTATGGATAACTCCATTTATGTCTGGATAATAAT	4317
QY	3236	ACCCCTGGCTACAAATCTGTCTGAGGATCAGCCTCACCCACCCGACCATCCCTTCAAC	3295	QY	4316	GTGCTCTGCAAAATCTCTGAAAAACCAACAGGTGCGATTGTGCGCGGAGGCCCATGCAAC	4375
Db	3238	GCTGCAGGGTATAAGTCAGTTCTCAAGATCACCATGACCCAGTCTATTATTCCATTTAAT	3297	Db	4318	GTAGTTTACAGATCACTGAAAAATCGTCAAGTTTCGCATTGTCTGTGACGGCCCATGCAC	4377
QY	3296	CTCATGAAGGTGCACCTCTCTATATTATTTTCATTTGGGACAAAGACAGACGCTTACAAC	3415	QY	4376	TGCCAGTCCCTGGCATTGACCCACTTCTCTGCTAAGCAAGGTGGCCATCCACGCAACCCCTG	4435
Db	3298	TTAATGAAGTTTCATCTTATGGTAGCTGTAGTGAAGACTCTTCCAAAAGTGGTTTCCT	3357	Db	4378	TGTCAGGTTCCCGAGTGG--AATATCCTGTGGGAAGCACCGCGGTGCAGACAACACTG	4434
QY	3356	GCAGCCCCAGACCTGTCTTATTTATTTGAGCAAGACAGACGCTTACAAC	3415	QY	4436	GAGTCAGCCACCGCTTTGGCTGTTTCACACAATGGGGTCTCTGTATATTGTGAGACTGAT	4495
Db	3358	GCCTCACCAAACTTGGCCTATACCTTTCATATGGGATAAACAGATGCATATAATCAGAAA	3417	Db	4435	GAATCAGCCACTGCCATTGCTGTGCTACAGTGGGGTCTCTGTACATTACTGAAACTGAT	4494
QY	3416	GTGTTTGGGCTTTCAGAAAGCCTTTGTTTCCGTGGGTTATGAATATGAATCCTGCCAGAT	3475	QY	4496	GAGAAAAGATCAACCGCATCAGGCAAGGTCAACACTAGTGGAGAGATCTCACTCGTTGCT	4555
Db	3418	GTCTATGGTCTATCTGAAGCTGTTGTGTAGTTGGATATGAGTATGAGTCGTGTTGGAC	3477	Db	4495	GAGAAGAAAATTAACCGGATAAGGCAGGTCAACAGATGGAGAAATCTCCTTAGTGGCC	4554
QY	3476	CTAATCCTGTGGGAAAAAGAAACAACAGTGTGAGGGGCTATGAAATGACCGCTCCAAG	3535	QY	4556	GGGGCCCCAGTGGCTGTGACTGTAAAAATGATGCCAACTGTGATGTTTCTTCTGGAGAC	4615
Db	3478	CTGACTCTGTGGGAAAAGAGGACTGCCATTCTGCAGGGCTATGAATGGATGCGTCCAAC	3537	Db	4555	GGAATACCTTCAGAGTGTGACTGCAAAAAATGATGCCAACTGTGACTGTTACCAGAGTGA	4614
QY	3536	CTTGAGGATGGAGCCTPAGACAAAACATCATGCCCTCAACATTCAAAAGTGGTATCCTGCAAC	3595	QY	4616	GATGTTATGCCAAAGGATGCAAAAGTTAAATACCCCATCTTCTTGGCTGTGTGTGCTGAT	4675
Db	3538	ATGGTGGCTGGACATTAGATAAACATCACGTCGTGGATGTACAGAACGGTATACTGTAC	3597	Db	4615	GATGGCTAGCCCAAGGATGCCAAACTCAGTGCCCCCATCTCTCCCTGGCTGCTTCTCCAGAT	4674
QY	3596	AAAGGGAATGGGGAGAACAGATTGTGTCTCAGCAGCCTCCTGTCTATTGGGAGCATCATG	3655	QY	4676	GGGGAGCTCTACGTGGCCGACCTTGGGAACATCCGAAATTCGGTTTATCCGGAAGAACAAAG	4735
Db	3598	AAGGAAAACGGGGAAAACAGTTTCATCTCCAGCAGCCTCCAGTCGTGTAGTATCATG	3657	Db	4675	GGTACACTGTATATGCAGATCTAGGGAATATCCGGATCCGGGTGTGTCAAAGAATAAG	4734
QY	3656	GGCAATGGGGCCCGGAGAAAGCATCTCCTGCCCCAGCTGCAACGGCCCTTGTGACGGCAAC	3715	QY	4736	CCTTTCTCAACACCCAGAACATGTATGAGCTGTCTTACCAAATTTGACCAGGAGCTCTAT	4795
Db	3658	GGCAATGGCGAAGGCGAGCATTTCTTGCCCCAGTTGCAATGGTCAAGCTGATGGTAAC	3717	Db	4735	CCTTTACTTAACTCTATGAACTTCTATGAAGTTGCGTCTCCAACTGATCAAGAACTCTAC	4794
QY	3716	AAGCTCCTGGCCCCAGTGGCCCTCACCTGTGGCTCTGACGGGAGCCTCTATGTGGGTGAT	3775	QY	4796	CTGTTTGATACACCGGCAAGCACCTGTACACCCAAAGCCTGCCACAGGAGACTACCTG	4855
Db	3718	AAGTTACTGGCCCCAGTGGCGCTAGCTTGTGGATTCGATGGCAGTCTGTACGTAGGCGAT	3777	Db	4795	ATCTTTGACATCAATGGTACTCACCAATFATACTGTAAAGTTTAGTCACTGCTGATTACCTT	4854
QY	3776	TTCAACTACATTAGAAAGGATCTTCCCCTCTGGAATGTCAACCAACATCCTPAGAGCTGAGG	3835	QY	4856	TACAACTTCACCTPACACTGGGGACGGCGGACATCACACTCATCACAGACAACAATGGCAAC	4915
Db	3778	TTCAACTACGTGCGGCGGATATTCCTTCTGGAATGTAAACAAGTGTCTTAGAACTAAGA	3837	Db	4855	TACAATTTTAGCTACAGCAATGACAAATGATATTACTGTGTGACAGACAGCAATGGCAAC	4914
QY	3836	AATAAAGATTTTCAGACATAGTCAAGTCCAGCACAACAATACTACCTGGCCACAGACCCC	3895	QY	4916	ATGGTAAATGTCGCCCGAGACTCTACTGGSATGCCCTCTGGCTGGTGTCCAGATGGC	4975
Db	3838	AATAAAGATTTTAGACATAGCAGCAACCCAGCTCTAGATATACTACCTTGCACGGATCCA	3897	Db	4915	ACCTTAGAATTAGACGGGACCCAAATCGCATGCCAGTTTCGAGTGGTGTCTCTGTATAAC	4974
QY	3896	ATGAGTGGGGCCGCTCTTCTTCTGACAGCAACAGCCGGCGGCTCTTTTAAATCAAGTCC	3955	QY	4976	CAGGTGTACTGGGTGACCATGGGCACCAACAGTGCACCTCAAGAGTGTGACCACACAAGGA	5035
Db	3898	GTACAGGGAGATCTGTACGTTTCTGACACAAACACCCGCAGAAATTTATCGCCCCAAAGTCA	3957	Db	4975	CAAGTGATATGGTTGACAAATAGGAACAAATGGATGTTTGAAGGCATGACTGCTCAAGGA	5034
QY	3956	ACTGTGGTGAAGGACCTTGTCAAGAACTCTGAGGTGGTTGCGGGACAGGTGACCAG	4015	QY	5036	CACGAGTTGGCCATGATGACATACCATGGCAATTCGGGCCCTTCTGGCAACCAAAAGCAAT	5095
				Db	5035	CTGGAATTAGTTTGTGTTTACTTACCATGGCAATAGTGGCCTTTTAGCCACTAAAAGTGAT	5094



Qy	5096	GAAAA	CGGATGG	CAACA	CA	TTTTAT	GAGTAC	GACAG	CTTTGG	CCGCTG	ACAAAT	GTGACC	5155	Qy	6173	CAGAA	TGAGG	CTTCA	CTGC	ACCAT	CCGCTA	CCGTCA	GATTTGG	GGCCCT	GATTG	ACC	GA	6232																								
Db	5095	GAA	ACTGG	ATGG	CAAC	AGTTT	TGAC	TATG	ACAG	TGAA	GGTC	GTCTG	ACAA	5154	Db	6175	CAG	ATG	ATGG	TTTAT	TGC	CA	CCATTAG	ATAC	AGCA	AAAT	TGGT	CCCT	GTATG	ACAG	6234																					
Qy	5156	TTCC	CTACT	GGCC	AGT	GAG	CA	GT	TTCC	GAA	GTAT	ACAG	ACAG	5215	Qy	6233	CAG	ATCTT	CCG	CTTCA	CTG	AGGA	GGCAT	GGTCA	ACCC	CGT	TTT	TGACT	ACAA	CTATG	AC	6292																				
Db	5155	TTT	CCA	ACTG	GAG	TGTC	CA	AAAC	CTTG	CA	TGG	GAC	ATGG	5214	Db	6235	CAG	ATTTT	CCG	CTT	AGT	GA	AGAT	GGGAT	GTTAA	TGCA	AGAT	TTT	GACT	ATAG	CTATG	AC	6294																			
Qy	5216	GTAG	AGAC	CTC	CAG	---A	AGG	ATG	ATG	TC	ACCA	ACC	AA	5272	Qy	6293	AA	CAG	CTT	CCG	GTG	AC	CAG	CA	TG	ATCA	ACG	AGAC	CC	CACTG	CCCA	TTGAT	6352																			
Db	5215	ATT	GAG	TCAT	CTAG	CCG	AGA	GA	AGAT	GT	CA	AG	ATG	5274	Db	6295	AA	CAG	CTT	TCG	AGT	GA	CCAG	CA	TG	ATCA	TA	GA	AA	CGCC	CACTG	CCCT	ATTGAT	6354																		
Qy	5273	GCT	TTT	AC	AC	ACTG	CTG	CA	AG	ACCA	AGT	CCG	GA	5332	Qy	6353	CT	CTAT	CG	CTAT	G	ATG	ATG	ATG	ATG	ATG	ATG	ATG	ATG	ATG	ATG	ATG	ATG	ATG	6412																	
Db	5275	TC	TTT	CT	AC	CA	CTG	TT	CA	AG	AT	CA	GT	5334	Db	6355	CT	GTAT	CAG	TTT	GAT	GA	CA	TTT	CT	GG	CA	AG	TTT	GG	AA	AGTT	TGG	AGTTATA	6414																	
Qy	5333	TC	CTT	G	CG	CTG	CTG	TC	GC	CA	AC	CG	CA	5392	Qy	6413	TAC	TATG	AC	ATTAA	CCAG	ATCA	TCA	CCAG	CA	TG	ATCA	CC	CA	CA	CA	CA	CA	CA	CA	6472																
Db	5335	TCC	CT	CAG	AATTA	TCT	AC	GC	AGT	GG	CTG	GA	CT	5394	Db	6415	TAT	TATG	ATTA	TA	CCAG	ATCA	TTT	CTAC	AG	CTG	TA	TG	AG	AT	TCA	TG	ATG	ATG	6474																	
Qy	5393	CTG	G	CTG	GC	CA	CC	CG	TG	GG	CA	AG	GA	5452	Qy	6473	GC	ATAT	G	GC	AG	ATG	AA	AGT	GC	AGT	ATG	AG	AT	CG	CT	CA	TG	TG	ATG	6532																
Db	5395	CTG	G	CTG	GC	CA	CC	CT	TA	AT	CCG	AC	GGT	5454	Db	6475	GC	TCAT	G	GC	CG	GTAT	CA	AT	TG	AG	AT	TCA	TG	AG	AT	TCA	TG	ATG	ATG	6534																
Qy	5453	GG	CT	CA	AC	CTG	G	AGT	GG	CG	CA	AG	CG	5512	Qy	6533	ACC	GT	CC	AGT	ATG	AT	CA	TG	GG	CG	AGT	AGT	AG	AGT	AG	AGT	AG	AGT	6592																	
Db	5455	GGT	CA	AA	ACTT	GGT	G	GA	AT	TC	CG	AA	AG	5514	Db	6535	ACA	ATT	CAG	TATG	AT	TA	CA	TG	GGT	CGG	GTAA	CCA	AG	AG	AG	AT	TA	AA	ATAG	GGCCCTTT	6594															
Qy	5513	TTT	G	CG	CG	CG	CG	CTG	CG	GTG	CA	CA	AC	5572	Qy	6593	G	CCA	AT	AC	CA	CT	CG	TACT	CG	CTAT	G	AGT	ATG	ATG	ATG	ATG	ATG	ATG	ATG	6652																
Db	5515	TTT	G	CG	CG	CA	AG	CT	CA	GGT	TA	TG	GC	5574	Db	6595	G	CCA	AC	CA	CC	AA	ATA	TG	CTT	AT	GA	AT	TAT	G	ATG	ATG	ATG	ATG	ATG	6654																
Qy	5573	AC	AG	CA	CA	AG	AA	GA	ATCT	AT	G	ATG	AC	5632	Qy	6653	AT	CA	ATG	CA	AA	GG	CA	CTCA	CG	CTAT	G	AGT	ATG	ATG	ATG	ATG	ATG	ATG	ATG	6712																
Db	5575	ACA	AG	CA	GA	AA	AG	ATCT	AT	G	AC	CA	CC	5634	Db	6655	CT	CA	ATG	AA	AG	AT	TA	TG	CG	CTAT	G	AGT	ATG	ATG	ATG	ATG	ATG	ATG	ATG	6714																
Qy	5633	CAG	G	CG	GG	CG	CG	CC	AG	CC	CTCT	G	TC	5692	Qy	6713	AG	CC	CT	G	GG	CA	CTCA	CG	CTAT	G	AGT	ATG	ATG	ATG	ATG	ATG	ATG	ATG	6772																	
Db	5635	AC	G	TC	TG	GC	CA	CC	CG	ACT	CT	CT	G	5694	Db	6715	A	CC	CA	AGT	AA	CAGT	GC	GTCT	AC	AC	CC	CT	TC	G	CTAT	G	AGT	ATG	ATG	6774																
Qy	5693	TAC	T	CC	CT	GG	GG	TT	TAC	AT	TG	CT	G	5752	Qy	6773	C	G	G	CT	G	G	GT	CA	AT	TG	AG	ATG	ATG	ATG	ATG	ATG	ATG	ATG	ATG	6832																
Db	5695	TAT	T	CA	TC	CA	CA	AG	TCAA	TT	GC	AG	CA	5754	Db	6775	C	G	A	CT	G	G	GT	CA	AT	CG	GT	G	AG	AT	TA	G	ATG	ATG	ATG	6834																
Qy	5753	TAC	G	AC	CA	AG	CG	CG	CG	CA	TC	AC	AT	5812	Qy	6833	G	A	T	AT	CT	T	T	G	AT	CA	AA	CT	CA	TG	CT	CA	AA	CGG	CGGT	6892																
Db	5755	TAT	G	AC	CG	GA	CA	GG	GAG	ATCG	GT	CT	CG	5814	Db	6835	G	A	A	AT	CT	T	T	G	AA	TAT	AG	CT	CC	AA	GG	CG	CTT	TA	CT	CA	AG	TTT	AC	AGT	GGC	6894										
Qy	5813	AC	A	T	CT	TAG	A	AG	ATCC	AT	GGT	GTG	CT	5872	Qy	6893	T	G	G	AT	GT	CA	CG	CTAC	GA	TG	CG	CG	CG	CG	CG	CG	CG	CG	CG	CG	6952															
Db	5815	AC	A	T	TT	TAG	A	AA	AGTCC	AT	GGT	TC	TC	5874	Db	6895	T	G	G	AC	AGT	AT	CA	CG	CTT	AT	GA	CG	CTT	TA	CT	CA	AG	AA	CG	CTA	6954															
Qy	5873	TT	C	G	CA	CA	AG	AA	ATG	AC	CG	CT	CT	5932	Qy	6953	AG	C	C	CA	CC	CTG	AG	AT	CA	CC	CA	CC	CA	CC	CA	CC	CA	CC	CA	CC	CA	CC	7012													
Db	5875	TAC	G	AT	AT	G	TG	G	AC	CG	CTG	TC	TC	5934	Db	6955	G	G	AC	AG	CA	CC	CTG	AG	AT	CA	CC	CT	TA	CTA	CG	ACT	AGG	AT	TAC	ATG	CT	CA	TG	7014												
Qy	5933	GAG	A	CC	AT	CCG	CT	CAGT	GG	CTACT	AC	AG	AA	5992	Qy	7013	TAC	AA	CC	CA	CTC	AG	AT	CA	CC	CT	TA	CTA	CG	ACTT	GC	AA	AGG	AC	CA	CC	CTTT	7072														
Db	5935	CAG	A	CC	AT	CCG	AT	CC	AT	CC	AT	CC	AT	5994	Db	7015	TAC	AA	CC	AT	TCG	AGT	T	CAG	AA	AT	TAC	CT	CC	CT	CT	CT	CT	CT	CT	CT	CT	7074														
Qy	5993	TC	AGT	CA	TAC	AG	GA	CTTCA	CTG	AG	AT	GG	CA	6052	Qy	7073	G	C	C	AT	G	G	AG	CTG	AT	GA	GT	T	T	T	T	T	T	T	T	T	T	7132														
Db	5995	TCC	AT	CA	TAC	AG	GA	CTA	CA	AC	CG	GG	CT	6054	Db	7075	G	C	C	AT	G	G	AA	AT	TAC	CT	CC	CT	CT	CT	CT	CT	CT	CT	CT	CT	CT	7192														
Qy	6053	G	G	C	G	C	G	AG	GTAT	AC	AA	AG	CTG	6112	Qy	7133	C	T	T	G	C	T	AG	CA	AG	GT	T	T	G	AT	CA	AG	CA	AA	AT	C	T	G	T	TA	C	AG	CC	TAT	GGG	7194						
Db	6055	AGT	C	G	G	AG	GGT	CTT	AT	T	CA	AA	TA	CAG	6114	Db	7135	C	T	G	C	T	AG	CA	AG	GT	T	T	G	AT	CA	AG	GT	T	T	G	AT	T	T	G	AT	T	T	G	AT	GGG	7194					
Qy	6113	ACC	A	CA	AG	GGT	CAGT	TTT	C	AC	CT	TAT	G	6172	Qy	7193	G	A	G	AT	CT	A	C	AT	G	AT	CA	T	C	A	T	G	G	CT	T	C	A	T	G	G	CT	C	7252									
Db	6115	AG	CA	CA	AG	AGT	CAGT	TTT	T	AC	CT	TAT	G	6174	Db	7253	T	A	T	G	AT	CC	AC	T	G	T	CC	AC	AT	T	G	G	CC	CG	CG	AG	AT	T	A	T	G	AT	G	T	G	CT	G	G	CC	CG	GA	7312







Db	1318	ATGGCCGAAGAGCAATTCAAGAGATTCTCCCGGATCTTCTGGAGATCACAGCTCTTC	1377
Qy	1406	ATAGACCAATCCTGTGCATCTGAAATTCAATGTGTCTCTGGGAAAGGCAGCCCTGGTTGGC	1465
Db	1378	ATTGATCAGCACAGTTTCTTAAATTCAATATCTCTCTTCAGAAAGGATGCATTGATTGGA	1437
Qy	1466	ATTATATGSCAGAAAAGCCCTCCCTCCCTTCACATA-----CACAGTTTGACTTT	1513
Db	1438	GTATATGGCCGAAGAAGTTACCGCCTTCCCATACTCAGTCTCTCCCGGATGACTTC	1497
Qy	1514	GTGGAGCTGTGGATGGCAGGAGCTCTTAACCCAGGAGCGCGGAGCCCTAGAGGGGACC	1573
Db	1498	GTGGAGCTCTGGATGGCAGCAGGCTGATGGCCAGAGAGCAGCGGAGCCCTGTGGAGACG	1557
Qy	1574	CCGCGCCAGTCTCGGGGAACCTGTGCCCCCTCCAGCCATGACAGGCTTCATCCAGTAT	1633
Db	1558	GAGAGAGCCGCGCGCAGGCGAGATCCGTGAGCTTCATGAGCGCGCTTTATCCAGTAC	1617
Qy	1634	TTGGATTCCAGGAATCTGGCACTTGGCTTTTACAATGACGGAAGGAGTCAGAAAGTGGT	1693
Db	1618	TTGGATTCTGGAATCTGGCATCTGGCTTTTATAATGATGGGAAAAATGCAGAGCAGGTG	1677
Qy	1694	TCCTTTCTACCACTGCCATTGAGTCGGTGGATAACTGCCCCAGCAACTGCTATGGCAAT	1753
Db	1678	TCCTTTAATACCAATTGTTATAGATCTGTGGTGGAAATGTCCCGGAAATGGCCATGGAAAT	1737
Qy	1754	GGTGACTGATCTCTGGGACCTGCCACTGCTTCTGGGTTTCTGGGCCCCGACTGTGGC	1813
Db	1738	GGAGAAATGCGTTCTGGAACCTTGCCATTGTTTCCAGGATTTCTGGGTCCGATTGTTCA	1797
Qy	1814	AGAGCCTCCTGCCCGTGTCTGTAGCGGAAATGGCCAAATACATGAAAGGCAGATGCTTG	1873
Db	1798	AGAGCCGCTGTCCAGTGTTATGTAGTGSAAACGGGCAGTACTCCAAGGGCCGCTGCCTG	1857
Qy	1874	TGCCACAGTGGCTGGAAAGGCGCTGAGTCGGATGTGCCCAACCAACCAAGTGTATCGATGTG	1933
Db	1858	TGTTTCAGCGGCTGGAAGGGCACCGAGTGTGATGTGCCGACTACCCAGTGATTGACCCA	1917
Qy	1934	GCCTGCAGCAACCATGGCACCTGCATACGGGCACCTGCATCTGCAACCCCTGGCTACAAG	1993
Db	1918	CAGTGTGGGGTGTGGGATTTGTATCATGCGGCTCCTGTGCTTGAGCTCAGGATACAAA	1977
Qy	1994	GGCGAGAGCTGTGAGGAAGTGGACTGCATGAGCAACCCACACATGTTGAGGCCGGGTGTCTGC	2053
Db	1978	GGAGAAAGTTGTGAAGAAGCTGACTGTATAGACCCCTGGGTGTTCTAATCATGTTGTGTGT	2037
Qy	2054	GTGAGAGGCGAATGCCATTGCTTTGTGGGATGGGAGGCACCAACTGCGAGACCCCGGAGG	2113
Db	2038	ATCCACGGGGAATGTCACTGCAGTCCAGATGGGAGGTAGCAATGTGAAATACTGAAG	2097
Qy	2114	GCCACATGCTTAGACCAGTGTTCAGGCCACGGAACCTTCTCTCCCGACACCGGCTTTGC	2173
Db	2098	ACCATGTGTCCAGACCAAGTGTCTCCGGCCACGGAACGTATCTTCAAGAAAGTGGTCTCTGC	2157
Qy	2174	AGCTGTGACCCCAAGCTGGACTGGACACGACTGTTCTATCGAGATCTGTGCTGCCGACTGT	2233
Db	2158	ACGTGTGACCCCTAACTGGACTGGCCCGAGCTGCTCAACGAAATATGTTCTGTGGACTGT	2217
Qy	2234	GGTGGCCATGGCGTGTGCGTAGGGGGCACCTGCCGCTGCGAGGATGCGTGGATGGGGCA	2293
Db	2218	GGCTCACACGGCGTTTGCATGGGGGGGACGTGTGCTGTGAAGAGGCTGGACGGGCCCA	2277
Qy	2294	GCCTGCGACCGAGCGGCCTGCCACCCGCGTGTGCCGAGCATGGGACCTGCCCGCAGCGC	2353
Db	2278	GCCGTGAATCAGAGAGCCTGCCACCCCGCTGTGCTGCGAGCACGGGACCTGCAAGGATGGC	2337
Qy	2354	AAGTGCAGTGCAGCCCTGGCTGGAATGGGAAACACTGCACCATCGCTCACTATCTGGAT	2413
Db	2338	AAGTGTGAATGCAGCAGGCTGGAATGGAGAGCACTGCACATATCGCTCACTATTTGGAT	2397
Qy	2414	AGGGTAGT-----TAAAGGGTTGCCCTGGGTTGTGCAATGGCAAC	2455

QY	3536	CTTGGAGGATGGAGCCTAGACAAAACATCATGCCCCTCAACATTCAAAGTGGTATCCTGCGAC	3595	QY	4616	GATGGTTATGCCAAGGATGCAAAAGTTAAATACCCCATCTTCCTTGGCTGTGTGCTGAT	4675
Db	3538	ATGGGTGGCTGGACATTAGATAAAACATCACGTGCTGGATGTACAGAACGGTATACTGTAC	3597	Db	4615	GATGGCTACGCCAAGGATGCCAAACTCAGTGGCCCATCTCTCCCTGGCTGCTTCTCCAGAT	4674
QY	3596	AAAGGGAATGGGAGAACCAAGTTTGTGTCTCAGCAGCCTCCTGTCTATTTGGGAGCATCATG	3655	QY	4676	GGGAGACTCTACGTGGCCGACCTTGGGAACATCCGAATTCGGTTTATCCGGAAGAAACAAG	4735
Db	3598	AAGGGAAA CGGGGAAACCAAGTTCATCTCCAGCAGCCTCCAGTCGTGAGTAGCATCATG	3657	Db	4675	GGTACACTGTATATTGCAGATCTAGGGAATATCCGGATCCGGGCTGTGTCAAAGAATAAG	4734
QY	3656	GGCAATGGCGCGGAGAAAGCATCTCCTGCCCCAGCTGCAACGGCCCTTGCTGACGGCAAC	3715	QY	4736	CTTTTCTCAACACCCAGAACATGTATGAGCTGTCTTTCACCAATTTGACCAGGAGCTCTAT	4795
Db	3658	GGCAATGGCGGAAGGCGCAGCATTTCTTGCCCCAGTTGCAATGGTCAAGCTGATGGTAAC	3717	Db	4735	CTTTTACTTAACCTCTATGAACTTCTATGAAGTTGCGTCTCCAACCTGATCAAGAACCTTAC	4794
QY	3716	AAGCTCCTGGCCCCAGTGGCCCTCACCTGTGGCTCTGACGGGAGCCTCTATGTGGGTGAT	3775	QY	4796	CTGTTTGATACCACCCGGCAAGCACCTGTACACCCCAAGCCCTGCCACAGGAGACTACCTG	4855
Db	3718	AAGTTACTGGCCCCAGTGGCGCTAGCTTTGIGGGATCGATGGCAGTCTGTACGTAGGCGAT	3777	Db	4795	ATCTTTGACATCAATGGTACTCACCAATATACTGTAACTTAGTCACTGGTGAATACCTT	4854
QY	3776	TTCAACTACATTAGAAAGATCTTCCCCTCTGGAAATGTCACCAACATCTCTAGAGCTGAGG	3835	QY	4856	TACAACTTCACCTACACTGGGGACGGGACATCACTCATCAAGACACAAATGGCAAC	4915
Db	3778	TTCAACTACGTGCGGCGGATATTCCTTCTCGGAAATGTAACAAAGTGTCTTAGAACTAAGA	3837	Db	4855	TACAACTTTTAGCTACAGCAATGACAAATGATATTACTGTCTGTACAGACAGCAATGGCAAC	4914
QY	3836	AATAAAGATTTTCAGACATAGTCACAGTCCAGCACACAAAATACTACCTGGCCACAGACCCC	3895	QY	4916	ATGGTAAATGTCCGCCGAGACTCTACTGGGATGCCCCCTCTGGCTGGTGGTCCCAGATGGC	4975
Db	3838	AATAAAGATTTTAGACATAGCAGCAACCCAGCTCATAGATATACTACCTTGCAACGGATCCA	3897	Db	4915	ACCCTTAGAATTAGACGGGACCCAAATCGCATGCCAGTTTCGAGTGGTGTCTCTCTGATAAC	4974
QY	3896	ATGAGTGGGCGCGTCTTCCCTTCTGACAGCAACAGCGCGGGGTCTTTAAATCAAGTCC	3955	QY	4976	CAGGTGTACTGGGTGACCATGGGCACCAACAGTGCACTCAAGAGTGTGACCACACAAGGA	5035
Db	3898	GTACGGGAGATCTGTACGTTTCTGACACAAACACCCGCAGAAATTTATCGCCCCAAAGTCA	3957	Db	4975	CAAGTGATATGGTTGACAAATAGGAACAAATGGATGTTTGAAGGCATGACTGCTCAAGGA	5034
QY	3956	ACTGTGGTGGTGAAGGACCTTGTCAAGAACTCTGAGGTGGTTGCGGGGACAGSTGACCAG	4015	QY	5036	CACGAGTTGGCCATGATGACATACCATGGCAATTCGGCCCTTCGGCCTTCGGCAACCAAAAGCAAT	5095
Db	3958	CTTACGGGGGCAAAAGACTTGACTAAAAATGCAGAAATCGTCGACGGGACAGGGGAGCAA	4017	Db	5035	CTGGAATTAGTTTGTTTACTTTACCATGGCAATAGTGGCCTTTTAGCCACTAAAAAGTGAT	5094
QY	4016	TGCCTCCCTTTTGATGACATCTGCTGCGGGATGGTGGGAAGGCCACAGAAAGCCACACTC	4075	QY	5096	GAAAAACGGATGGACAAACATTTTATGAGTACGACAGCTTTTGGCCGCTGACAAATGTGACC	5155
Db	4018	TGCCTTCCGTTTGACGAGCGGAGATGTGGGATGGAGGAAGCCGTGGAAAGCCACACTC	4077	Db	5095	GAAACTGGATGGACAAACGTTTTTTGTGACTATGACAGTGAAGGTCGTCTGACAAATGTTACG	5154
QY	4076	ACCAATCCCAGGGGTATTACAGTGGACAAAGTTTGGGCTGATCTACTTCGTGGATGGCACC	4135	QY	5156	TTCCCTACTGGCCAGGTGAGCAGTTTCCGAAAGTGATA CAGACAGTTTCAGTGCATGTCCAG	5215
Db	4078	ATGAGTCCCAAAGGAATGGCAGTTGTAAAGAA TGGATTAAATCTACTTTGTTGATGGAACC	4137	Db	5155	TTTCCAACTGGAGTGGTCACAAACCTGCATGGGACATGGACAAGGCTATCACAGTGGAC	5214
QY	4136	ATGATCAGACGCATCGATCAGAAATGGGATCATCTCCACCTGCTCGGCTCTAATGATCTC	4195	QY	5216	GTAGAGACCTCCAGC-- --AAGGATGATGTCAACCATAAACCAACCTGTCTGCTCTCAGGC	5272
Db	4138	ATGATTAGGAAAGTTTGACCAAAATGGAAATCATATCAACTCTTCTGGGCTCTAACGATTG	4197	Db	5215	ATTGAGTCATCTAGCCGAGAAGAAGATGT CAGCATCACTTCAAATCTGTCTCGATCGAT	5274
QY	4196	ACATCAGCCCGCCACTCAGCTGTGATTTCTGTATGGATAFTTCCAGGTAAGACTGGAG	4255	QY	5273	GCCTTCTACACACTGCTGCAAGACCAAGTCCGGAA CAGCTACTACATCGGGCCGATGGC	5332
Db	4198	ACTTCAGCAGACCTTTTAACTTTGTGACACCAGCATGCACATCAGCCAGGTACGCTCTGGAA	4257	Db	5275	TCCTTCTACACCATGGTTCAAGATCAGTTAAGAAACAGCTACCAGATTGTTATGACGGC	5334
QY	4256	TGGCCCAACAGACTTAGCCATCAACCCAAATGGACAACTCACTTTATGTCTCTCGACAAACAAT	4315	QY	5333	TCCTTGCGGCTGCTGCTGGCCAA CCGCATGGAGGTGGCGCTGCAGACTGAGCCCCACTTG	5392
Db	4258	TGGCCCACTGACCTAGCCATTAAACCTATGGATAACTCCATTATGTCTCTGGATAATAAT	4317	Db	5335	TCCCTCAGAAATTATCTACGCCAGTGGCCTGGACTCACA CTACCAACAGAGCCGCACGTT	5394
QY	4316	GTGGTCTGCAAAATCTCTGAAAACCAACAGGTGCGCATTTGTGCGCGGAGGCCCATGCAC	4375	QY	5393	CTGGTGGCACCGTCAACCCACCCGTCGCGGAAGAGGAATGT CACGCTGCCCATCGACAAC	5452
Db	4318	GTAGTTTTACAGATCACTGAAAATCGTCAAGTTCGCATTTGCTGTGACCGGCCCATGCAC	4377	Db	5395	CTGGTGGCACCCGCTAATCCGACGGTTGCCAAAAGAGCAAGCCCAAGGAAAGTCAATGTC	5454
QY	4376	TGCCAGGTCCCTGGCATTTGACCACTTCTGCTAAGCAAGGTGGCCATCCACGCAACCCCTG	4435	QY	5453	GGCCTCAACCTGGTGGAGTGGCGCAGCGCAAGAGCAGGCTCGGGGCCAGGTCACTGTC	5512
Db	4378	TGTCAGGTTCCGGAGTGG-- --AATATCTGTGGGGAAGCAGCGGGTGCAGACAACACTG	4434	Db	5455	GGTCAAAACCTTGGTGGAAATGGAGATTCCGAAAAGAGCAAGCCCAAGGAAAGTCAATGTC	5514
QY	4436	GAGTCAGCCACCGCTTTGGCTGTTTCACACAAATGGGGTCTGTATATTGCTGAGACTGAT	4495	QY	5513	TTTGGGCGCCGCTGCGGGTGCACAACCCGAAATCTCCTATCTCTGGACTTTGATCGCGTA	5572
Db	4435	GAATCAGCCACTGCCATTGCTGTCTCTACAGTGGGGTCTGTGATTAATCTAGAACTGAT	4494	Db	5515	TTTGGCCGCAAGCTCAGGGTTAATGGCAGAAACCTCTTTCAGTTGACTTTGATCGAACA	5574
QY	4496	GAGAAAAAGATCAACCGCATCAGGCAGGTCAACCACTAGTGGAGAGATCTCACTCGTTGCT	4555	QY	5573	ACAGCACAGAGAAAGATCTATGATGACCAACCGCAAGTTCA CCCCCTTCGGATTCTGTACGAC	5632
Db	4495	GAGAAGAAAAATTAAACCGGATAAGGCAGGTCAACACAGATGGAGAAATCTCCTTAGTGCC	4554	Db	5575	ACAAAGACAGAAAAGATCTATGACGACCAACCCGTA AATTTCTACTGAGGATCGCCTACGAC	5634
QY	4556	GGGGCCCCAGTGGCTGTGACTGTAAAAATGATGCCAACTGTGATTTGTTTCTGGAGAC	4615	QY	5633	CAGCGGGGCGGCCAGCCTCTGGTCACCCAGCAGCAGGCTGAATGGTGTCAACGTGACA	5692
Db	4555	GGAATACCTTCAGAGTGTGACTGCAAAAATGATGCCAACTGTGACTGTACCAGATGGA	4614	Db	5635	ACGTCTGGGCACCCGACTCTCTGGCTGCCAAGCAGCAAGCTGATGGCCGTCAATGTCAACC	5694
				QY	5693	TACTCCCCTGGGGTTACATTGTCTGGCATCCAGAGGGGCATCATGTCTGAAAAGAAATGGAA	5752



Db 5695 TATTCAATCCACAGGTCAAATGGCCAGCATCCAGCGAGGCCACCTAGCGAGAAAGTAGAT 5754  
QY 5753 TACGACCAAGGCGGCGCATCACATCCAGGATCTTCGCTGATGGGAAGACATGGAGCTAC 5812  
Db 5755 TATGACGGACAGGGAGGATCGTGTCTCGGGTCTTTGCTGATGTTAAACATGGAGTTAC 5814  
QY 5813 ACATACTTAGAAGTCCATGGTGTCTACTACACAGCCAGAGCGAGTATATCTTTGAG 5872  
Db 5815 ACATAATTTAGAAAAGTCCATGGTCTTCTGCTTCATAGCCAGCGGAGTACATCTTCGAA 5874  
QY 5873 TTGACAAAGATGACCGCCTCTCTCTGTGACGATGCCAAACGTTGGCGCGGCAGACACTA 5932  
Db 5875 TACGATATGTGGACCGCCTGTCTGCCATCACCATGCCCAGTGTGGCTCGCCACACCATG 5934  
QY 5933 GAGACCATCCGCTCAGTGGGCTACTACAGAAAAACATCTATCAGCCCCCTGAGGGCAATGCC 5992  
Db 5935 CAGACCATCCGATCCATTGGCTACTACCGCAACATATACAACCCCGGAAAGCAACGCC 5994  
QY 5993 TCAGTCATACAGGACTTCAGTGAGGATGGGCACCTCTTCACACCTTCTACCTGGGCAC 6052  
Db 5995 TCCATCATCAGGACTACAACGAGGAAGGGCTGCTTCTACAAACAGCTTCTTGGGTACA 6054  
QY 6053 GGCCGACGGTGATATACAAGTATGGGAAACTGTCAAAGCTGGCAGACGCTCTATGAC 6112  
Db 6055 AGTCGAGGGTCTTATTCAAATACAGAAAGCAGACTAGGCTCTCAGAAAATTTTATATGAT 6114  
QY 6113 ACCACCAAGTCAAGTTTACCTATGACGACGGCAGGCAATGCTGAAGACCATCAACCTA 6172  
Db 6115 AGCACAAGAGTCAGTTTACCTATGATGAACAGCAGGAGTCTTAAAGACAGTAAACCTC 6174  
QY 6173 CAGAATGAGGGCTTCACCTGCACCATCCGCTACCGTACAGATTGGGCCCTGATTGACCGA 6232  
Db 6175 CAGAGTGATGGTTTATTGTCACCATTAGATACAGGCAAAATGGTCCCTGATTGACAGG 6234  
QY 6233 CAGATCTTCCGCTTCACTGAGGAAGGCATGGTCAACGCCCGTTTTGACTACAACTATGAC 6292  
Db 6235 CAGATTTTCCGCTTAGTGAAGATGGGATGGTAAATGCAAGATTTGACTATAGCTATGAC 6294  
QY 6293 AACAGCTTCCGGGTGACAGCATGCAGGCTGTGATCAACGAGACCCCACTGCCCATTTGAT 6352  
Db 6295 AACAGCTTTCAGTGACCCAGCATGCAGGGTGTGATCAATGAACGCCACTGCCTATTGAT 6354  
QY 6353 CTCTATCGCTATGATGATGTGTAGGCAAGACAGAGCAGTTTGGGAAGTTTGGTGTCAAT 6412  
Db 6355 CTGTATCAGTTTGATGACATTTCTGGCAAAGTTGAGCAGTTTGGAAAGTTTGGAGTTATA 6414  
QY 6413 TACTATGACATTAACCCAGATCATCACACAGCTGTGATGACCCACACCAAGCATTTTGTAT 6472  
Db 6415 TATTATGATATTAAACCAGATCATTTCTACAGCTGTAATGACCTATACGAAGCACTTTGAT 6474  
QY 6473 GCATATGGCAGGATGAAGGAAGTGACGTATGAGATCTTCCGCTCGCTCATGTACTGGATG 6532  
Db 6475 GCTCATGGCCGTATCAAGGAGATTCAAATATGAGATATTCAGGTTCGCTCATGTACTGGATT 6534  
QY 6533 ACCGTCCAGTATGATAACATGGGGCGAGTAGTGAAGAGGAGCTGAAGGTAGGACCCCTAC 6592  
Db 6535 ACAATTCAGTATGATAACATGGGTGCGGTAAACCAAGAGAGAGATTAAATAGGGCCCTTT 6594  
QY 6593 GCCAATACCACTCGCTACTCTATGAGTATGATGCTGACGGCCAGCTGCAGACAGTCTCC 6652  
Db 6595 GCCAACACCCACCAATATGCTTATGAATATGATGTTGATGGACAGCTCCAAACAGTTTAC 6654  
QY 6653 ATCAATGACAAGCCACTCTGGCGCTACAGCTACGACCTCAATGGGAACCTGCACCTTACTG 6712  
Db 6655 CTCAATGAAAAGATAATGTGGCGGTACAACTACGATCTGAATGGAAACCTCCATTTACTG 6714  
QY 6713 AGCCCTGGGAACAGTGCAAGGCTCACACCCTACCGGTATGACATCCGCGACCGCATCACT 6772  
Db 6715 AACCCAAGTAACAGTGGCGGTCTGACACCCCTTCGCTATGACCTGCGAGACAGAACTACT 6774  
QY 6773 CGGCTGGGTGACGTGCAATACAAGATGGATGAGGATGGCTTCCTGAGGCGGGGCGGT 6832

Db 6775 CGACTGGGTGATGTTTCAATATCGGTTGGATGAAGATGGTTTCTTCTACGTCAAAGGGGCACG 6834  
QY 6833 GATATCTTTTGTAGTACAACTCAGCTGGCCTGCTCATCAAGGCCCTACAACCGGGCTGGCAGC 6892  
Db 6835 GAAATCTTTTGAATATAGCTCCAAGGGGCTTCTAACTCGAGTTTACAGTAAAGGCAGTGGC 6894  
QY 6893 TGGAGTGTTCAGGTACCGCTACGATGGCCTGGGGCGGCGGTGTCCAGCAAGAGCAGCCAC 6952  
Db 6895 TGGACAGTGATCTACCGTTTATGACGGCCTGGGAAGGCGTGTCTTAGCAAAAACAGTCTA 6954  
QY 6953 AGCCACACCTGCAGTTCCTTCTATGCAGACCTGACCAACCCCAAGGTCACCCACCTG 7012  
Db 6955 GGACAGCACCTGCAGTTTCTTATGCTGACTTAACCTTATCCCCTAGGATTACTCATGTC 7014  
QY 7013 TACAACTACTCCAGCTCTGAGATCACCTCCCTCTACTACGACTTGCAAGGACACCTCTTT 7072  
Db 7015 TACAACCATTCGAGTTCAGAAATTAACCTCCCTGTATTATGATCTCCAAGGACATCTTTT 7074  
QY 7073 GCCATGGAGCTGAGCAGTGGTGATGAGTTTTACATAGCTTTGTGACAAACATCGGGACCCCT 7132  
Db 7075 GCCATGGAAAATCAGCAGTGGGATGAAATCTATATTGCAATCGGATAACACAGGGACACCA 7134  
QY 7133 CTGTGTCTTTTAGTGAACAGGTTTGATGATCAAGCAAACTTCAGATCATATAGGTCACCATGGCCTC 7192  
Db 7135 CTGGCTGTGTTCAGTAGCAATGGGCTTATGCTGAAACAGATTTCAGTACACTGCATATGGG 7194  
QY 7193 GAGATCTACATGGATACCAACCCCAACTTTCAGATCATATAGGTCACCATGGTGGCCTC 7252  
Db 7195 GAAATCTATTTTGACTCTAATATTGACTTTCAACTGGTAATTGGATTTCATGGTGGCCTG 7254  
QY 7253 TATGATCCACTCACCAAGCTTGTCCACATGGGCGGCGAGATTATGATGTGCTGGCCGA 7312  
Db 7255 TATGACCCACTCACCAAAATTAATCCACTTTGGAGAAAGAGATTATGACATTTTGGCAGGA 7314  
QY 7313 CGTGGACTAGCCCAGACCAAGCTGTGGAAAGCACCTTTAGTAGCAGCAACGTCATGCCCT 7372  
Db 7315 CGGTGGACAAACCTGACATAGAAATCTGGA--AAAGAAATGGGAAGGACCCAGCTCCT 7371  
QY 7373 TTTAATCTCTATATGTTCAAAAAACAACACCCCATCAGCAACTCCAGGACATCAAGTGC 7432  
Db 7372 TTTAACTTGTACATGTTTAGGAATAACAACCCCTGCAAGCAAAATCCATGACGTGAAAGAT 7431  
QY 7433 TTTATGACAGATGTTAAACAGCTGGCTGCTCACCTTTGGATTCCAGCTPACACAACGTTGATC 7492  
Db 7432 TACATCAGAGATGTTAAACAGCTGGCTGGTGACATTTGGTTTCCATTCGACAAATGCTATT 7491  
QY 7493 CCTGGTTATCCCAAAACAGACATGGATGCCATGGAACCCCTCCTACGAGCTCATCCACACA 7552  
Db 7492 CCTGGATTCCCTGTTCCCAAAATTTGATTTAACAGAACCTTCTTTACGA-----A 7539  
QY 7553 CAGATGAAAAACGACAGGAGTGGGACAAACAGCAAGTCTATCCTCGGGGTACAGTGTGAAGTA 7612  
Db 7540 CTTGTGAAGAGTCAGCAGTGGGATGATATACCGCCCATCTTCGGAGTCCAGCAGCAAGTG 7599  
QY 7613 CAGAAGCAGCTCAAGGCCCTTTGTACCTTAGAACGGTTTGACCGCTCTATGGCTCCACA 7672  
Db 7600 GCGCGGACAGGCCAAAGGCCCTTCCCTGTCGCTGGGGAAGATGGCCGAGGTGACGGCGG 7659  
QY 7673 ATCACCAGCTGCCAGAGGCTCCAAAGACTCAAGAAAGTTTGCATCCAGCGGCTCAGTCTTT 7732  
Db 7660 CGCCGGGCCCGGC--GGCGCGCAGTCCCTGGCTGTGGTTTCGCCACGGTCAAAGTCGCTGATC 7716  
QY 7733 GGCAAGGGGGTCAAGTTTTCCTTTGAAGGATGGCCGAGTGACCAACAGACATCATCAGTGTG 7792  
Db 7717 GGCAAGGGCGTCATGTGGCCGTCAGCCAGGGCCGCGTGCAGACCAACGTCGCTCAACATC 7776  
QY 7793 GCCAATGAGGATGGGCGGAAGGGTTGCTGCCCATCTTGAACCATGCCCACTACCTAGAGAAC 7852  
Db 7777 GCCAACGAGGACTGCAACAAGGTGGCGGCGCTGCTCAACAACCGCCTTCTACCTGGAGAAC 7836  
QY 7853 CTGCACTTCACCATTTGATGGGGTGGATAACCATTAATCTTTGTGAACACGAGACCTTCAGAA 7912  
Db 7837 CTGCACTTCACCATCGAGGGCAAGGACACGCACTACTTTCATCAAGACCAACCGCCCGAG 7896



QY	7913	GGTGACCTGCCCATCTCTGGCCCTCAGTGGGGGGCGGGAACCTCTGGAGAATGGGTCAAC	7972
Db	7897	AGCGACCTGGGCACGCTGCGGTTGACCAAGCGGCCGCAAGCGCTGGAGAACGGCATCAAC	7956
QY	7973	GTCACCTGTGCCAGATCAACACACAGTACTTAATGGCAGGACTAGACGCTACACAGACATC	8032
Db	7957	GTGACGGTGTGCGAGTCCACCACCGTGTGTAACGGCAGGACGGCAGGTTCCGGGACGTG	8016
QY	8033	CAGCTCCAGTACGGGGCACTGTGCTTGAACACACAGCTACGGGACACACGTTTGGATGAGGAG	8092
Db	8017	GAGATGCAGTTCGGCGCGCTGGCGCTGCACGTGCGCTACGGCATGACCCCTGGACGAGGAG	8076
QY	8093	AAGGCACGGGTCTCTGGAGCTGGCCCGGCAGAGAGCCGTGCGCCAAAGCTGGGCCCGCGAG	8152
Db	8077	AAGGCGCGCATCTCTGGAGCAGGCGCGGCAGCGCGCTCGCCGGGCTGGGCGCGCGAG	8136
QY	8153	CAGCAGAGACTGCGGGAAGGGAGGAAGGCCTGCGGGCCTGGACAGAGGGGGAGAAGCAG	8212
Db	8137	CAGCAGCGCTGCGGACGCGGAGGAGGGCGCGCCTCTGGACGGAGGGCGGAGAGCGG	8196
QY	8213	CAGGTGCTGAGCAGAGCGGGGTGCAAGGCTACGACGGCTTTTTCGTGATCTCTGTGCGAG	8272
Db	8197	CAGCTGCTGAGCGCGGCAAGGTGCAAGGCTACGACGGGTACTACGTACTCTCGGTGGAG	8256
QY	8273	CAGTACCCAGAACTGTCTAGACAGCGGCCAACACATCCACTTTCATGAGACAGACGAGATG	8332
Db	8257	CAGTACCCCGAGCTGGCCGACAGCGCCAAACATCCAGTTCTCTCGGCGAGCGGAGATC	8316
QY	8333	GGCCGGAGGTGAC	8345
Db	8317	GGCAGGAGGTAAC	8329
RESULT 14			
ID	ABQ82343	standard; cDNA; 8675 BP.	
XX	ABQ82343;		
AC			
XX			
DT	17-DEC-2002	(first entry)	
DE	Human NOV15a	encoding cDNA SEQ ID NO:35.	
XX			
KW	Human; NOVX; cytostatic; neuroprotective; anticonvulsant; cardiovascular; cerebroprotective; nootropic; antidiabetic; antiinflammatory; fungicide; antirheumatic; antiarthritic; immunosuppressive; antiallergic; virucide; antianaemic; antibacterial; protozoacide; antihelminthic; gene therapy; cancer; leukaemia; lymphoma; melanoma; neurological disorder; epilepsy; stroke; ischaemic cerebrovascular disease; Alzheimer's disease; allergy; pick's disease; vesicular transport disease; cystic fibrosis; goitre; diabetes mellitus; Grave's disease; gastrointestinal disorder; vaccine; ulcerative colitis; gastric disorder; duodenal disorder; infection; autoimmune disease; allergic reaction; autoimmune haemolytic anaemia; rheumatoid arthritis; gene; chromosome 4; ss.		
OS	Homo sapiens.		
XX			
FH	Key	Location/Qualifiers	
FT	CDS	151..8328	
FT		/*tag= a	
FT		/product= "NOV15a"	
FT		/transl_except= (pos:1249..1251,aa:Ser)	
XX			
PN	WO200262999-A2.		
XX			
PD	15-AUG-2002.		
XX			
PF	31-DEC-2001; 2001WO-US049976.		
XX			
PR	29-DEC-2000; 2000US-0258928P.		
PR	02-JAN-2001; 2001US-0259415P.		
PR	04-JAN-2001; 2001US-0259785P.		

PR	20-FEB-2001; 2001US-0269814P.		
PR	09-MAR-2001; 2001US-0279863P.		
PR	29-MAR-2001; 2001US-0279832P.		
PR	29-MAR-2001; 2001US-0279833P.		
PR	13-APR-2001; 2001US-0283889P.		
PR	18-APR-2001; 2001US-0284447P.		
PR	25-APR-2001; 2001US-0286683P.		
PR	29-MAY-2001; 2001US-0294080P.		
PR	16-AUG-2001; 2001US-0312915P.		
PR	17-AUG-2001; 2001US-0313325P.		
PR	17-SEP-2001; 2001US-0322699P.		
PR	26-NOV-2001; 2001US-0333350P.		
XX			
PA	(CURA-) CURAGEN CORP.		
XX			
PI	Spytek KA, Li L, Wolenc AR, Vernet CAM, Eisen A, Liu X;		
PI	Malyankar U, Shimkets RA, Tchernev VT, Spaderna SK, Gorman L;		
PI	Kekuda R, Patturajan M, Gusev V, Gangolli EA, Guo X, Shenoy S;		
PI	Rastelli L, Casman SJ, Boldog F, Burgess CE, Edinger S, Ellerman K;		
PI	Gunther E, Smithson G, Millet I, Macdougall JR;		
XX			
DR	WPI; 2002-732706/79.		
DR	P-PSDB; ABP53586.		
XX			
PT	New NOVX polypeptides and polynucleotides useful for treating NOVX-		
PT	associated disorders, such as cancers, neurological disorders, disorders		
PT	of vesicular transport, gastrointestinal disorders, and autoimmune		
PT	diseases.		
XX			
PS	Claim 8; Page 110-112; 444pp; English.		
XX			
CC	The present invention describes novel human proteins designated NOVX,		
CC	where X is 1 to 20 e.g. NOV1. NOVX sequences can have neuroprotective,		
CC	cytostatic, anticonvulsant, cerebroprotective, nootropic, cardiovascular,		
CC	antidiabetic, antiinflammatory, antirheumatic, antiarthritic, virucide,		
CC	immunosuppressive, antiallergic, antianaemic, antibacterial, fungicide,		
CC	protozoacide and antihelminthic activities, and can be used in gene		
CC	therapy. The NOVX proteins, nucleotides or antibodies can be used in the		
CC	manufacture of a medicament for treating a syndrome associated with a		
CC	human disease selected from NOVX-associated disorder, such as cancers		
CC	(e.g. leukaemia, lymphoma, melanoma or cancer of the liver, lung, muscle,		
CC	ovary, testis and uterus), neurological disorders (e.g. epilepsy, stroke,		
CC	ischaemic cerebrovascular disease, Alzheimer's disease or Pick's		
CC	disease), disorders of vesicular transport (e.g. cystic fibrosis,		
CC	diabetes mellitus, Grave's disease, or goitre), gastrointestinal		
CC	disorders (e.g. ulcerative colitis, or gastric and duodenal disorders),		
CC	autoimmune diseases (e.g. allergic reactions, autoimmune haemolytic		
CC	anaemia, or rheumatoid arthritis), viral, bacterial, fungal, helminthic		
CC	and protozoal infections. The NOVX proteins can be used as immunogens to		
CC	produce antibodies and as vaccines. The NOVX nucleotide sequences may be		
CC	used in chromosome mapping, identifying individuals from minute		
CC	biological samples (tissue typing), and in forensic identification of a		
CC	biological sample. The present sequence encodes human NOV15a, which is		
CC	located on chromosome 4		
XX			
SQ	Sequence 8675 BP; 2362 A; 2067 C; 2201 G; 2041 T; 0 U; 4 Other;		
	Query Match 41.6%; Score 3472.6; DB 6; Length 8675;		
	Best Local Similarity 65.2%; Pred. No. 0;		
	Matches 5442; Conservative 2; Mismatches 2693; Indels 216; Gaps 14;		
QY	35 ATGGACGTGAAGGAGAGGAAGCCTTACCGCTCGCTGACCCGGCGC---CGCGACCCGAG	91	
Db			
	151 ATGGATGTGAAAGAACGCGAGGCCTTACTGCTCCTGACCAAGAGCAGACGAGAAGGAA	210	
QY	92 CGCCGCTACACCAGCTCGTCCGGGACAGCGAGGAGGGCAAAG---CCCCGAGAAATCG	148	
Db			
	211 CGCGCTACACAATTCCTCCGAGACAATGAGGAGTGCCGGGTACCCACACAGAAGTCC	270	
QY	149 TACAGCTCCAGCGAGACCCCTGAAGGCCTACGACACAGGA---CGCCCGCCTAGCCTATGGC	205	
Db			
	271 TACAGTCCAGCGAGACATTGAAAGCTTTTGATCATGATTCCTCGCGGCTGCTTACGGC	330	

QY 206 AGCCGGTCAAGGACATTGTGCCGACGAGGCGGAGGAAATTCTGCCGCACAGGTGCCAAC 265  
Db 331 AACAGAGTGAAGGATTTGGTTACAGAGAAGCAGAGGTTCACTAGACAAGGACAGAAAT 390  
QY 266 TTCAACCTGCGGAGCTGGGGCTGGAAGAAGTAACGCCCCCTCAACGGGACCCCTGTACCGG 325  
Db 391 TTTACCTTAAGGCAGTTAGGAGTTTGTGAACACGACAACTCGAAGAGGACTTGGCATTTTGT 450  
QY 326 ACAGACATTGGCCTGCCCAATGCGGCTACTCCATGGGGCTGGCTCTGATGCCGACATG 385  
Db 451 GCGAAATGGGGCTCCCTCACAGAGGTTACTCTATCAGTGCAGGTCAGATGCTGATACT 510  
QY 386 GAGGCTGACACGGTGTGTCCCCTGAGCACCCCGTGCCTGTGTGGGCGGAGCACACGG 445  
Db 511 GAAATGAAGCAGTGATGTCCCCAGAGCATGCCATGAGACTTTGGGGCAGGGGGTCAAA 570  
QY 446 TCAGGGCGCAGCTCCTGCCTGTCCAGCGGGGCCAAATTCCAATCTCACACTCACCGACAC 505  
Db 571 TCAGGGCGCAGCTCCTGCCTGTCAAGTCGGTCCAACTCAGCCCTCACCCCTGACAGATACG 630  
QY 506 GAGCATGAAACACTGAGACTGATCATCCGGGCGGCTGCAGAACCAACGCGCGGCTCCGG 565  
Db 631 GAGCACGAAACAAATGTCGACAGTGAGAAATGAGCAACCTGCAAGCAATCAAGGCCAGTCT 690  
QY 566 ACGCCGCGCGCTCTCGCACGCCACACCCCCAACCCAGCACCCACGCGGCTCCATT 625  
Db 691 ACCCTGCAGCCCTTGCCGCTTCCCATAGCAGCACTCTGCACAGCATCATCCATCCATC 750  
QY 626 AACTCCCTGAACCGGGGCAACTTTCACGCCGAGGAGCAACCCAGACCCCGCCCCCACGGAC 685  
Db 751 ACTTCTCTCAACAGAAACTCCCTGTACCAATAGAAGGAACAGAGTCCGGCCCCCGCGCT 810  
QY 686 CACTCGCTCTCCGAGAGCCCCCTGCGCGGCGGCCCCAGGAGCCTGCCACAGCCCCAGGAG 745  
Db 811 GCTTTGCCCGCGAGCTGCAAC-----CACACCCGAGTCCGTCCAGCTGCAGGAC 861  
QY 746 AACTGGCTGTCAAACAGCAACATCCCCCTGGAGACCAGGAACCTAGGCAAGCAGCCATT 805  
Db 862 AGCTGGGTCTTGCGAGTAATGTACCACCTGGAAAGCAGGCATTT----- 905  
QY 806 CTAGGGACATTGCAAGSACAACCTCATTTGAGATGAGACATTCTCGGCGCCTCCCGCCATGAT 865  
Db 906 ----- 905  
QY 866 GGGCTTACAGTGACGGGCACCTTCTCTTCAAGCCTGGAGGCACCTCCCGCTCTTCTGC 925  
Db 906 -----CCTATTCAAAACAGGAACAGGTACAAACGCCACTGTTCAGT 945  
QY 926 ACCACATCACAGGGTACCCACTGACGTCAGCACAGTGTACTCTCCTCGGCCCGACCC 985  
Db 946 ACTGCAACCCCAAGGATACACAATGGCATCTGGCTCTGTTTATTACCACTACTCGGCCA 1005  
QY 986 CTGCCCCGACACCTTGCGCCGGCCGCTTTAACTCAAGAACCCCTCCAAGTACTGT 1045  
Db 1006 CTACCTAGAAACACCCCTATCAAGAAAGTGTCTTTAAATTCAGAAAGTCTTCAAAAGTACTGT 1065  
QY 1046 AACTGGAAGTGGCAGCCCTGAGCGCCATCGTCATCTCAGCCACTCTGGTTCATCCTGCTG 1105  
Db 1066 AGCTGGAATGCACTGCACTGTGTGCCGTAGGGTCTCGGTGCTCCTGGCAATACTCCTG 1125  
QY 1106 GCATACITTTGTGGCCATGCACCTGTTTGGCCATAAACTGGCACCTGCAGCCGATGGAGGG 1165  
Db 1126 TCTTATTTTATAGCAATGCATCTCTTTGGCCCTCAACTGGCAGCTACAGCAGACTGAAAT 1185  
QY 1166 CAGATGTATGATACCGGAGGACACAGCCAGAGTTGGCCTGTGCCAACCGACGTCTCC 1225  
Db 1186 GACACATTTGAGA-----ATGGAAGAGTGAAATCTTGATACCATGCCAACAAACACTGTG 1239  
QY 1226 CTATACCCCTCAGGGGCACTGGCTTAGAGACCCCTGACAGGAAAGGCAAGGAACCA 1285  
Db 1240 TCATTACCTNNTGGAGACA----- 1258  
QY 1286 GAAGGAAAGCCCACTAGTCTTTCTTCCAGAGGACAGTTTTCATAGATTTCTGGAGAAATTGAT 1345

Db 1259 -ATGGAATAATTAGTGGATTTTACGCAAGAAAAATAACACCATAGATTCGCGAGAACTTGAT 1317  
QY 1346 GTGGGAAGCGAGCCTCCCAGAAGATTCTCTCTGGCACTTTTCTGGAGATCTCAAGTGTTC 1405  
Db 1318 ATTGGCCGAAGAGCAATTCAAGAGATTCTCCCGGATCTTCTCTGGAGATCACAGCTCTTC 1377  
QY 1406 ATAGACCATCTGTGCATCTGAAATTCAAATTTCAATGTGTCTCTGGGAAAGGCAGCCCTGGTGGC 1465  
Db 1378 ATTGATCAGCCACAGTTTCTTAAATTCAAATATCTCTTTCAGAAAGATGATGATTGGA 1437  
QY 1466 ATTTATGGCAGAAAAAGCCCTCCCTCTCTTCACATA-----CACAGTTTGACTTT 1513  
Db 1438 GTATATGGCCGGAAGAAAGTTTACCGCCTTCCCATACTCAGTCCTCCCCCAGTATGACTTC 1497  
QY 1514 GTGAGCTGCTGGATGGCAGGAGGCTCTTAAACCAGGAGCGCGGAGCCTAGAGGGGACC 1573  
Db 1498 GTGAGCTCCTGGATGGCAGCAGGCTGATTGTCAGAGAGCAGCGGAGCCTGTGAGACG 1557  
QY 1574 CCGCGCCAGTCTCGGGAACTGTGCCCCCTCCAGCCATGAGACAGGCTTCATCCAGTAT 1633  
Db 1558 GAGAGAGCCGGCGGCAGGCGAGATCCGTCAGCCTTCATGAGCGCGCTTATCCAGTAC 1617  
QY 1634 TTGGATTACGAATCTGGCACTTGGCTTTTACAAATGACCGAAAGGAGTCAGAAAGTGT 1693  
Db 1618 TTGGATTCTGGAATCTGGCATCTGGCTTTTATAATGATGGGAAAAATGCAGACAGGTG 1677  
QY 1694 TCCTTTCTACCACTGCCATTGAGTCGGTGGATAACTGCCCCAGCAACTGCTATGGCAAT 1753  
Db 1678 TCTTTTAATACCAATTGTTATAGAGTCTGGTGGAAATGTCCCCGAAATTGCCATGGAAAT 1737  
QY 1754 GGTGACTGCATCTCTGGACCTGCCACTGCTTCTTCTGGGTTTCTGGGCCCGACTGTGGC 1813  
Db 1738 GGAGAAATGCGTTTCTGGAACCTTGCCATTGTTTCCAGGATTTCTGGTCCGAGTTGTCA 1797  
QY 1814 AGAGCCTCCTGCCCGCTGCTCTGTAGCGGAAATGGCCAATACATGAAAGGCAGATGCTG 1873  
Db 1798 AGAGCCGCTGTCCAGTGTTATGTAGTGSAAACGGGCAGTACTCCAAGSGCGCTGCCTG 1857  
QY 1874 TGCCACAGTGGCTGGAAAGGCGCTGAGTGCATGTGCCCCAACCAACCACTGATCGATGTG 1933  
Db 1858 TGTTTCAGCGGCTGGAAGGGCACCGAGTGTGATGTGCCGACTACCCAGTGTATTGACCCA 1917  
QY 1934 GCCTGCAGCAACCATGGCACCTGCATCACGGGCACCTGCATCTGCAACCTGGCTACAAG 1993  
Db 1918 CAGTGTGGGGTCTGGGATTTGTATCATGCGGCTCCTGTGCTTGAGCTCAGGATACAA 1977  
QY 1994 GCGAGAGCTGTGAGGAAGTGGACTGCATGGACCCCAACATGTTTACGGCGGGGTGTCTGC 2053  
Db 1978 GGAGAAAGTTGTGAAGAAGCTGACTGTATAGACCCCTGGGTGTTCTTAATCATGGTGTGT 2037  
QY 2054 GTGAGAGSGGAATGCCATTGCTTTGTGGATGGGAGGCACCAACTCGGAGACCCCCAGG 2113  
Db 2038 ATCCACGGGGAATGTCACTGCAGTCCAGGATGGGAGGTAGCAATTGTGAAATACTGAAG 2097  
QY 2114 GCCACATGCTTAGACCCAGTGTTCAGGCCACGGAACCTTCTCCCGGACACCGGGCTTTGC 2173  
Db 2098 ACCATGTGTCCAGACCAAGTGTCTCCGGCCACGGAACGTATCTTCAAGAAAGTGGCTCCTGC 2157  
QY 2174 AGCTGTGACCAAGCTGGACTGGACACGACTGTTCTATCGAGATCTGTGCTGCCGACTGT 2233  
Db 2158 ACGTGTGACCCCTAACTGGACTGGCCAGACTGCTCAACGAAATATGTTCTGTGGACTGT 2217  
QY 2234 GGTGGCCATGGCGTGTGCGTAGGGGCACTGCCGCTGCGAGGATGGCTGGATGGGGCA 2293  
Db 2218 GGCTCACACGCGTGTGCAATGGGGGAGCGTGTGCTGTGAAGAAAGCTGGACGGGCCA 2277  
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Db 2278 GCCTGTAATCAGAGAGCCTGCCACCCCGCTGTGCCGAGCACCGGACCTGCAAGGATGGC 2337  
QY 2354 AAGTCGAGTGCAGCCCTGGCTGGAAATGGCGGAACACTGCACCATCGCTCACTATCTGGAT 2413

Db 2338 AAGTGTGAATGCAGCCAGGGCTGGAATGGAGAGCACTGCACATATCGCTCACTATTTTGGAT 2397

Qy 2414 AGGGTAGT-----TAAAGAGGGTTGCCCTGGGTTGTGCAATGGCAAC 2455

Db 2398 AAGATAGTTAAAGACAAGATAGGATATAAGAGGGTTGTCTCTGGTCTGTGCAACAGCAAT 2457

Qy 2456 GGCAGATGTACTTAGACCTGAATGGTTGGCACTGCGTCTGCCAGCTGGGCTGGAGAGGA 2515

Db 2458 GGAAGATGTACCTGGACCAAAATGGCGGACATTTGTGTGCCAGCCCTGGATGGAGAGGA 2517

Qy 2516 GCTGGCTGTGACACTTCCATGGAGACTGCCCTGGCGGTGACAGCAAAAGACAATGATGGAGAT 2575

Db 2518 GCAGGCTGTGACGTAGCCATGGAGACTCTTTGACAGATAGCAAGGACAATGAAGGGGAT 2577

Qy 2576 GGCCTGGTGGACTGCATGGACCCCTGACTGCTGSCCTCAGCCCCCTGTGCCATATCAACCCG 2635

Db 2578 GGACTCATTTGACTGCATGGATCCCGATTTGCTGCTACAGAGTTCTCTGCCAGAATCAGCCC 2637

Qy 2636 CTGTGCCCTTGGCTCCCTTAACCTCTCGGACATCATCCAGGAGACACAGCTCCCTGTGTCA 2695

Db 2638 TATTGTCGGGGACTGCCGGATCCTCAGGACATCATTAGCCAAAGCCTTCAATCGCCTTCT 2697

Qy 2696 CAGCAGAACTTACACTCTTCTATGACCGCATCAAGTTCTCTCGTGGGCAGGGACAGCAGC 2755

Db 2698 CAGCAAGCTGCCAAATCCTTTTATGATCGAATCAGTTTCTTTATAGGATCTGATAGCACC 2757

Qy 2756 CACATAATCCCCGGGAGAAACCCCTTTGATGGAGGGCATGCTTGTGTTATTTCGTGGCCAA 2815

Db 2758 CATGTTATACCTGGAGAAAGTCCTTTCAATAAGAGCCCTTGCACTGTGTATCAGAGGCCAA 2817

Qy 2816 GTGATGACATCAGATGGAAACCCCTCGTTTGGTGTGAACATCAGTTTTTGTCAATAACCCCT 2875

Db 2818 GTACTGACTGCTGATGGAACTCCACTTATTGGAGTAAATGTCTCGTTTTTCCATTAACCCA 2877

Qy 2876 CTCCTTTGGATATACAAATCAGCAGGCAAGATGGCAGCTTTGACTTGGTGACAATGGCGGC 2935

Db 2878 GAAATATGGATATACTATTACCCGCCAGGACGGATGTTTGACTTGGTGGCAAAATGGTGG 2937

Qy 2936 ATCTCCATCATCCTCGGTTTCGAGCGGGCACCTTTTCATCACACAGGAGCACACCCTGTGG 2995

Db 2938 GCCTCTCTAACTTTGGTATTGAACGATCCCCATTCCTCACTCAGTATCATACTGTGTGG 2997

Qy 2996 CTGCCATGGGATCGCTTCTTTGTCTATGGAAACCATCATCATGAGACATGAGGAGAATGAG 3055

Db 2998 ATTCCATGGAAATGTCTTTTATGTATGGATACCCCTAGTATCCCTAGTCATGGAGAAAGAGAATGAC 3057

Qy 3056 ATTCCCAGCTGTGACCTGAGCAATTTTGGCCGCCCCCAACCCAGTCGTCTCTCCATCCCCA 3115

Db 3058 ATTCCCAGCTGTGATCTGAGTGGATTCGTGAGGCCAAATCCCATCATTTGTGTCACTACCT 3117

Qy 3116 CTGACGTCTTCGCCAGCTCCTGTGCAGAGAAAGGCCCATTTGTCCGGGAAATTCAGGCT 3175

Db 3118 TTATCCACCTTTTTCAGATCTTCTCCTGAAGACAGTCCCATCATTTCCGAAACACAGGTA 3177

Qy 3176 TTGCAGGAGGAAATCTCTATCTCTGGCTGCAAGATGAGGCTGAGCTACCTGAGCAGCCGG 3235

Db 3178 CTCACGAGGAAACTACAATTCAGGAACAGATTTTGAAACTCTCCTACTTGAGTTCAGAG 3237

Qy 3236 ACCCCTGGCTACAAATCTGTCTCTGAGGATCAGCCTCACCCACCCGACCATCCCCTTCAAC 3295

Db 3238 GCTGCAGGGTATAAGTCAGTTCTCAAGATCACCATGACCCAGTCTATTATTCCATTTAAT 3297

Qy 3296 CTCAATGAAGGTGCACCTCATGGTAGCGGTGGAGGGCCGCTCTTCAGGAAGTGGTTGCGCT 3355

Db 3298 TTAATGAAGGTTTCATCTTTATGGTAGCTGTAGTAGGAAGACTCTTCCAAAAGTGGTTTCCT 3357

Qy 3356 GCAGCCCCAGACCTGTCTTATTTTCATTTGGGACAAGACAGACGCTCTACAAACCAAGAG 3415

Db 3358 GCCTCACCAAACTTGGCCCTATACTTTTCATATGGGATAAAACAGATGCATATAATCAGAAA 3417

Qy 3416 GTGTTTGGGCTTTCAGAAAGCCTTTGTTTCCGTGGGTTATGAATATGAATCCTGCCCAGAT 3475

Db 3418 GTCTATGGTCTATCTGAAGCTGTGTGTCAAGTGGATATGAGTATGAGTCGTGTGTTGGAC 3477

Qy 3476 CTAATCCTGTGGGAAAAAAGRAACAACAGTGTCTGAGGGCTATGAAATTGACGCGTCCAAG 3535

Db 3478 CTGACTCTGTGGGAAAAAGAGGACTGCCATTCTGCAGGGCTATGAATTGGATGCGTCCAAC 3537

Qy 3536 CTTGAGGATGGAGCCCTAGACAAACATCATGCCCTCAACATTTCAAAGTGGTATCCTGCAC 3595

Db 3538 ATGGTGGCTGGACATTAGATAAACATCACGTGCTGGATGTACAGAACGGTATACTGTAC 3597

Qy 3596 AAAGGAATGGGGAGAACCAAGTTTGTGTCTCAGCAGCCCTCCTGTCTATTTGGGAGCATATG 3655

Db 3598 AAGGAAACGGGGAAAAACCAGTTTCATCTCCAGCAGCCTCCAGTCTGTAGTAGCATATG 3657

Qy 3656 GGCAATGGGCGCCGGAGAAAGCATCTCTCTGCCCCCAGCTGCAACGGCCTTGCTGACGGCAAC 3715

Db 3658 GGCAATGGGCGAAAGGCGCAGCATTTCTCTGCCCCAGTTGCAATGGTCAAGCTGATGGTAAC 3717

Qy 3716 AAGCTCCTGGCCCCCAGTGGCCCTCACCTGTGGCTCTGACGGGAGCCTCTATGTGGGTGAT 3775

Db 3718 AAGTTACTGGCCCCCAGTGGCGCTAGCTTGTGGGATCGATGGCAGTCTGTACGTAGGCGAT 3777

Qy 3776 TTCAACTACATTAGAAGGATCTTCCCCTCTGGAAATGTCAACCAACATCCTTAGAGCTGAGG 3835

Db 3778 TTCAACTACGTGCGGCGGATATTCCCCTTCTGGAAATGTAAACAAGTGTCTTAGAACTAAGA 3837

Qy 3836 AATAAGATTTCAGACATAGTCACAGTCCAGCACACAAATACTACCTGSCCAGACACCC 3895

Db 3838 AATAAGATTTTAGACATAGCAGCAACCCAGCTCATAGATACTACCTTGCAACGGATCCA 3897

Qy 3896 ATGAGTGGGCGCTCTTCCCTTCTGACAGCAACAGCCGGGGTCTTTAAAAATCAAGTCC 3955

Db 3898 GTCACGGGAGATCTGTACGTTTCTGACACAAACACCCGCAGAAATTTTATCGCCCCAAGTCA 3957

Qy 3956 ACTGTGGTGAAGGACCTTGTCAAGAACTCTGAGGTGGTTGCGGGGACAGGTGACCAG 4015

Db 3958 CTTACGGGGCAAAAAGACTTGACTTAAAAATGCAGAAATCGTCGACGGGACAGGGAGCAA 4017

Qy 4016 TGCCCTCCCCTTTGATGACACTCGCTGCGGGGATGGTGGGAAGGCCACAGAACCCACACTC 4075

Db 4018 TGCCCTTCGGTTTGACGAGGCGAGATGTGGGGATGGAGGAAGGCCGTGGAAGCCACACTC 4077

Qy 4076 ACCAATCCCAGGGGTATTACAGTGGACAAAGTTTGGGCTGATCTACTTCTGTGGATGGCAC 4135

Db 4078 ATGAGTCCCAAAGGAATGGCAGTTGATAAGAAATGGATTAATCTACTTTTGTGTGATGGAACC 4137

Qy 4136 ATGATCAGACGCATCGATCAGAAATGGGATCATCTCCACCCTGCTCGGCTCTAATGATCTC 4195

Db 4138 ATGATTAGGAAAGTTGACCAAAATGGAATCATATCAACTCTTCTGGGCTCTAACGATTTG 4197

Qy 4196 ACATCAGCCCCGGCACTCAGCTGTGATTTCTGTATGGATATTTCCCAGGTAAGACTGGAG 4255

Db 4198 ACTTCAGCCAGACCTTTAACTTGTGACACCAGCATGCACATCAGCCAGGTACGTCTGGAA 4257

Qy 4256 TGGCCCAACAGACTTAGCCATCAACCCAAATGGACAACTCATCTTTATGTCTCTCGACAACAAT 4315

Db 4258 TGGCCCACTGACCTAGCCATTAAACCCCTATGGATAAATCCATTTATGTCTCTGGATAATAAT 4317

Qy 4316 GTGGTCTCTGCAAAATCTCTGAAAAACCAACAGGTGGCATTTGTCCGGGAGGCCCATGCAC 4375

Db 4318 GTAGTTTTCAGATCACTGAAAAATCGTCAAGTTGCGATTGCTGTGGAACGGCCCATGCAC 4377

Qy 4376 TGCCAGGTCCCTGGCATTGACCACTTCCCTGCTAAAGCAAGGTGGCCATCCACGCAACCCCTG 4435

Db 4378 TGTGAGGTTCCCGGAGTGG--AAATATCCTGTGGGGAAGCACGCGGTGCAGACAACACTG 4434

Qy 4436 GAGTCAGCCAACCGCTTTGGCTGTTTCACACAATGGGCTCCTGTATATTGTCTGAGACTGAT 4495

Db 4435 GAATCAGCCACTGCCATTGCTGTCTCTACAGTGGGCTCCTGTACATTACTGAAACTGAT 4494

Qy 4496 GAGAAAAAGATCAACCGCATCAGGCAGGTCAACCACTAGTGGAGAGATCTCACTCGTTGCT 4555

Db 4495 GAGAAAGAAATTAAACCGGATAAGGCAGGTCAACAACAGATGGAGAAATCTCCTTAGTGSCC 4554



QY 4556 GGGGCCCCAGTGGCTGTGACTGTAAAAATGATGCCAACTGTGAATGTTTTTCTGGAGAC 4615  
Db 4555 GGAATACCTTCAGAGTGTGACTGCAAAAATGATGCCAACTGTGACTGTTACCAGAGTGA 4614  
QY 4616 GATGGTTATGCCAAGGATGCAAAAGTTAAATACCCCATCTTCCCTGGCTGTGTGCTGAT 4675  
Db 4615 GATGGCTACGCCAAGGATGCCAAACTCAGTGCCCCATCCTCCCTGGCTGCTTCTCCAGAT 4674  
QY 4676 GGGGAGCTCTACGTGGCCGACCTTGGGAAACATCCGAAATTCGGTTTATCCGGAAGAACAG 4735  
Db 4675 GGTACACTGTATATTGCAGATCTAGGGAATATCCGGATCCGGGCTGTGTCAAAGAATAAG 4734  
QY 4736 CCTTTCCTCAACACCCAGAACATGTATGAGCTGTCTTCCACCAATTGACCAGGAGCTCTAT 4795  
Db 4735 CCTTTACTTAACCTCTATGAACCTTCTATGAAGTTGCGTCTCCAACTGATCAAGAACTCTAC 4794  
QY 4796 CTGTTTGTATACCACCGGAAGCACCTGTGTACCCCAAGCCTGCCACAGGAGACTACCTG 4855  
Db 4795 ATCTTTGACATCAATGGTACTCACCAATATACTGTAAGTTTAGTCACGTGGTATTAACCTT 4854  
QY 4856 TACAACCTTACCTTACACTGGGACGGGACATCACACTCATCACAGACAACAATGGCAAC 4915  
Db 4855 TACAAATTTAGCTACAGCAATGACAAATGATATTACTGCTGTGACAGACAGCAATGGCAAC 4914  
QY 4916 ATGGTAATGTCCGCCGAGACTCTACTGGGATGCCCCCTCTGSGCTGGTGGTCCCAGATGGC 4975  
Db 4915 ACCCTTAGAATTAGACGGGACCCCAATCGCATGCCAGTTCGAGTGGTGTCTCCTGATAAC 4974  
QY 4976 CAGGTGTACTGGGTGACCATGGGCACCAACAGTGCACTCAAGAGTGTGACCACACAAGGA 5035  
Db 4975 CAAGTGATATGGTTGACAAATAGGAACAAATGGATGTTTGAAGGCATGACTGCTCAAGGA 5034  
QY 5036 CACGAGTTGGCCATGATGACATACATGGCAATTCGGCCCTTCTGGCAACCAAAAGCAAT 5095  
Db 5035 CTGGAATTAGTTTGTTTACTTACCATGGCAATAGTGGCCTTTTAGCCACTAAAAAGTGAT 5094  
QY 5096 GAAACGGATGGACAACATTTTATGAGTACGACAGCTTTGGCCGCTGACAAAATGTGACC 5155  
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QY 5156 TTCCCTACTGGCCAGGTGAGCAGTTTTCCGAAGTGATACAGACAGTTTCAAGTGATGCCAG 5215  
Db 5155 TTTCCAACTGGAGTGGTCACAAACCTGCATGGGACATGGACAAGGCTATCACAGTGGAC 5214  
QY 5216 GTAGAGACCTCCAGC--AAGGATGATGTCACCATAAACCAACCACTGTCTGCCTCAGGC 5272  
Db 5215 ATTGAGTCATCTAGCCGAGAAGAGATGTACGATCACCTTCAAACTGTCTCCTCGATCGAT 5274  
QY 5273 GCCTTCTACACTGCTGCAAGACCAAGTCCGGAACAGCTACTACATCGGGCCGATGGC 5332  
Db 5275 TCTTTCTACACCATGGTTTCAAGATCAGTTAAGAAAACAGCTACCAGATTGGTTATGACGGC 5334  
QY 5333 TCCTTGGCGGTGCTGTGGCCAAACGGCATGGAGGTGGCGCTGCAGACTGAGCCCCACTTG 5392  
Db 5335 TCCCTCAGAATTATCTACGCCAGTGGCCTGGACTCACACTACCAAAACAGAGCCGCACGTT 5394  
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QY 5513 TTTGGGCGCGGCTGCGGGTGCAACAACCGAAATCTCCTATCTCTGGACTTTGATCGCGTA 5572  
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QY 5573 ACACGCACAGAGAAGATCTATGATGACCAACCGCAAGTTTCACCCCTTCGGATTTCTGTACGAC 5632  
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Db 5635 ACCTGTGGGCACCCGACTCTCTGGCTGCCAAGCAGCAAGCTGATGGCCGTCAATGTCAACC 5694  
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QY 5753 TACGACAGGCGGGCCGCATCACATCCAGGATCTTCGCTGATGGGAAGACATGGAGCTAC 5812  
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Db 5875 TACGATATGTGGACCGCCTGTCTGCCATCACCATGCCCAGTGTGGCTCGCCACACCATG 5934  
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QY 6353 CTCATCGCTATGATGATGTGTCAGGCAAGACAGAGCAGTTTGGGAAGTTTGGTGTCAATT 6412  
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Qy 8333 GGCCGGAGGTGAC 8345

Db 8317 GGCAGGAGGTAAC 8329

RESULT 15

ADH41998

ID ADH41998 standard; DNA; 8636 BP.

XX

AC ADH41998;

XX

DT 25-MAR-2004 (first entry)

XX

DE Novel human nucleic acid NOV40h #2.

XX

KW ds; gene; cardiovascular; antiarteriosclerotic; hypotensive; cytostatic; anorectic; antidiabetic; immunosuppressive; anti-HIV; neuroprotective; nootropic; antiparkinsonian; antiasthmatic; antiinfertility; cardiomyopathy; atherosclerosis; hypertension; cancer; obesity; diabetes; AIDS; multiple sclerosis; graft-versus-host disease; Alzheimer's disease; Parkinson's disease; asthma; fertility disorder; chromosome mapping; tissue typing; preventive medicine; pharmacogenomic; vaccine.

OS Homo sapiens.

XX

PN WO2003102159-A2.

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PD 11-DEC-2003.

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PF 04-JUN-2003; 2003WO-US017573.

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PR 04-JUN-2002; 2002US-0385490P.

PR 04-JUN-2002; 2002US-0385615P.

PR 04-JUN-2002; 2002US-0385755P.

PR 05-JUN-2002; 2002US-0386041P.

PR 06-JUN-2002; 2002US-0386355P.

PR 06-JUN-2002; 2002US-0386357P.

PR 06-JUN-2002; 2002US-0386447P.

PR 06-JUN-2002; 2002US-0386459P.

PR 06-JUN-2002; 2002US-0386465P.





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Db 2338 AAGTGTGAATGCAGCCAGGCTGGAATGGAGAGCACTGCACATTCGCTCACTATTTGGAT 2397  
Qy 2414 AGGGTAGT-----TAAAGAGGGTTGCCCTGGGTTGTCAATGGCAAC 2455  
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Qy 2456 GGCAGATGTPACCTTAGACCTGAATGTTGGCACTGCGTCTGCCAGTGGGCTGGAGAGGA 2515  
Db 2458 GGAAGATGTACCTTGGACCAAAATGGCGGACATTGTGTGTGCCAGCTGGATGGAGAGGA 2517  
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Qy 2696 CAGCAGAACCTTACACTCCTTCTATGACCGCATCAAGTTCCCTCGTGGGAGGACAGCACG 2755  
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Qy 2816 GTGATGACATCAGATGGAACCCCTTGTGTTGGTGTGAACATCAGTTTGTCAATAACCCCT 2875  
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Qy	5216	GTAGAG	ACCTCCAGC	--	-AAGG	ATGATGT	CACCATAA	CCACCA	ACCTG	TGCTGC	CTCAGGC	5272				
Db	5215	ATTGAG	TCATAG	CCGAGA	AGATGT	CAGCAT	CACTTCA	AAATCT	GTCTC	CTCGAT	CGAT	5274				
Qy	5273	GCCTT	CTACAC	ACTGCT	GCAAGAC	CAAGTCC	GGAAAC	AGCTACT	ACATCG	GGGCCG	GATGGC	5332				
Db	5275	TCCTT	CTACAC	CACTGG	TTCAAGAT	CAGTTA	AGAAAC	AGCTACC	AGATTG	GTATTAG	GACGGC	5334				
Qy	5333	TCCTT	GCGGCT	GTGCT	GGCCAA	CGGCAT	GAGGTGG	CGCTGC	AGACTG	AGCCCC	ACTTG	5392				
Db	5335	TCCCT	CAGAA	TTATCT	ACGCC	AGTGG	CCCTGGA	CTCAC	ACTAC	CAAA	CAGAGCCG	CACTT	5394			
Qy	5393	CTGG	CTGG	CACCGT	CAACCC	CAACCGT	GGCAAG	AGGAAT	GTAC	CGCTG	CCCCAT	CGACAAC	5452			
Db	5395	CTGG	CTGG	CACCGT	TAATCC	GACGTT	CCCAAG	AAACAT	GTACTT	GGCTG	GGCGAG	AAAC	5454			
Qy	5453	GGCT	CTAA	CCCTGG	TGGAGT	GGCGCAG	CGCAAG	AGAGC	AGGCTCG	GGGGCC	AGGTC	ACTGTC	5512			
Db	5455	GGT	CAAA	AACTGG	TGGAAT	TCGAA	AAAGAG	CAAGCC	AAAGG	AAAGT	CAATGTC	5514				
Qy	5513	TTTGG	GCGCGG	CTCGG	GTGCAC	AAACCG	AAATCT	CTAT	CTCTG	GACTTT	GATCG	CGTA	5572			
Db	5515	TTTGG	CGCGA	AGCTC	AGGGT	TAATGG	CAGAA	AACTCT	TTTCA	GTGACT	TTGAT	CGA	CA	5574		
Qy	5573	ACACG	CACAG	AAATCT	ATGATG	ACCA	CCGCAAGT	TTCA	CCCTT	CGGAT	TCTGT	ACGAC	5632			
Db	5575	ACAA	AGAC	AGAAA	AGATCT	ATGACG	ACCA	CCGTAA	ATTTCT	ACTG	AGGAT	CGCTAC	GAC	5634		
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Db	5635	ACGT	CTGG	CAC	CCGACT	CTCTGG	CTGCC	AAAGC	AGCTG	ATGG	CCGTCA	ATGT	CACC	5694		
Qy	5693	TACT	CCCT	TGGG	GTACAT	TGCTG	GCA	TCCAG	AGGG	CATCAT	GTCTG	AAAGAA	TGGAA	5752		
Db	5695	TATT	CATCC	ACAG	GTCA	AAATGG	CCAG	CATCC	AGG	CA	CCACTAG	CGG	AGAA	AGTAGAT	5754	
Qy	5753	TACG	AC	CAGG	CGCG	CGCAT	CACATCC	AGGATCT	TTCG	TGATGG	GAAG	ACATG	SAGCT	AC	5812	
Db	5755	TATG	ACGGA	CAGG	GAGGAT	CGTGTCT	CGGTCT	TTTCTG	TGATGG	TAA	ACATG	SAGTTAC	5814			
Qy	5813	ACAT	ACTTAG	AGA	AGTCC	ATGGTCT	GCTACT	ACAG	CCAG	AGGCA	GCTATAT	CTTTGAG	5872			
Db	5815	ACAT	ATTTAG	AAA	AGTCC	ATGGTCT	TCTG	CTTCT	ATAG	CCAG	CGGCA	GATAC	ATCTTC	GAA	5874	
Qy	5873	TTCG	ACA	AGAA	ATGAC	CGCCTCT	CTTCTGT	GACG	ATGCC	CAAC	GTGG	CGCG	CAG	ACACTA	5932	
Db	5875	TACG	ATAT	GTGG	ACCG	CTGTCT	GCCATC	ACCATG	CCCATG	GTGG	CTCG	CCAC	CA	CAATG	5934	
Qy	5933	GAG	ACCAT	CCGCTC	AGTGG	CTACTAC	AGAAA	CACTAT	CA	AGCCCC	CTGAG	GGGCA	ATGCC	5992		
Db	5935	CAG	ACCAT	CCGATCC	ATTGG	CTACTAC	CGCA	ACATATA	CA	ACCCCC	CTCG	GAA	AGCA	AGCC	5994	
Qy	5993	TCAG	TCATAC	AGGACTT	CACTG	AGGATGG	GCACCT	CTTCA	CAC	ACCTTCT	TAC	CTGG	CACT	6052		
Db	5995	TCCAT	CATC	ACG	GA	CTACA	AGGAGG	CTGCT	CTACA	AA	CAGCTT	CTTGG	GATACA	6054		
Qy	6053	GGCC	GCAG	GGTGAT	ATACA	AGTATG	GCAAA	CTGTCA	AAAG	CTGG	CAGAG	CGCTCT	ATGAC	6112		
Db	6055	AGT	CGGAG	GGTCTT	ATTC	AAATAC	AGAG	GCAGACT	AGG	CTCTC	AGAA	ATTTT	ATATGAT	6114		
Qy	6113	ACC	AC	AGGT	CAGTTT	CACTAT	GACG	AGCGG	CATGCT	GAA	AGAC	CATCA	ACCTA	6172		
Db	6115	AGC	ACA	AGAG	TCAG	TTTAC	TGATGA	AA	CAGC	AGGAGT	CTTA	AGAC	AGTAA	ACCTC	6174	
Qy	6173	CAGA	ATGAG	GGCTTCA	CTG	CA	CCATCC	GCTAC	CGT	CAG	ATTGG	GCCCTG	ATTGAC	CGA	6232	
Db	6175	CAG	AGT	GATGG	TTTATTT	TGC	ACCAT	TATAG	ATA	CAGG	CAAT	TGGT	CTCCCT	GATTGAC	AGG	6234
Qy	6233	CAG	ATCTT	CCGCTTCA	CTG	AGG	AA	GGCATGG	T	CA	CGCC	CGTTT	TGACT	CA	CAACTATGAC	6292
Db	6235	CAG	ATTTT	CCGCTT	TAGT	GA	AGATGG	GATGG	TAA	TGCA	AGATTT	TG	ACT	ATAG	CTATGAC	6294





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OM nucleic - nucleic search, using sw model

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(without alignments)  
11853.974 Million cell updates/sec

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**Perfect score:** 8354  
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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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		Match					
1	8354	100.0	8354	6	AX556500	AX556500	Sequence
2	8225	98.5	8645	6	AX600210	AX600210	Sequence
3	7779.2	93.1	8438	6	AX675551	AX675551	Sequence
4	6975.4	83.5	8585	9	AB025413	Mus muscu	AB025413
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6	6601.2	79.0	9722	9	AF059485	Mus muscu	AF059485
7	6048.2	72.4	10826	8	AB037723	Homo sapi	AB037723
8	4422.8	52.9	9264	5	AB026980	Danio rer	AB026980
9	4197.2	50.2	8993	8	HSM806812	Homo sapi	BX640737
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13	3473.8	41.6	8675	6	AX662353	Sequence	AX662353
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23	3352.8	40.1	7698	8	AB040888	AB040888	Homo sapi
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## ALIGNMENTS

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 DEFINITION  
 SEQUENCE 13 from Patent WO02057453.  
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 VERSION  
 AX556500.1 GI:25899736  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Homo sapiens (human)  
 Homo sapiens  
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 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Hominiidae; Homo.  
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 REFERENCE  
 AUTHORS  
 Gangolli, E.A., Patturajan, M., Vernet, C.A., Malyankar, U.M.,  
 Kekuda, R., Stone, D.J., Anderson, D., Shimkets, R.A., Burgess, C.E.,  
 Zerhusen, B.D., Liu, X., Spytek, K.A., Casman, S.J., Boldog, F.L.,  
 Smithson, G., Li, L. and Ji, W.  
 Polypeptides and nucleic acids encoding same  
 Patent: WO 02057453-A 13 25-JUL-2002;  
 Curagen Corporation (US)  
 TITLE  
 JOURNAL  
 FEATURES  
 source  
 Location/Qualifiers  
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ORIGIN							
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QY	61	CCGCTCGTGTAACCCCGCGCGCCGCGACGCCGAGCGCCGCTACACCAGCTCGTCGCGGCACAG	120				
Dd	61	CCGCTCGCTGACCCGCGCGCCGCGACGCCGAGCGCCCGCTACACCAGCTCGTCGCGGCACAG	120				
QY	121	CGAGGAGGGCAAAAGCCCCCGCAGAAATCGGTACAGCTCCAGCGAGACCCCTGAAGGCCTACGA	180				



Db	121	CGAGGAGGCAAAAGCCCCGACGAAATCGTACAGCTCCAGCGAGACCCCTGAAGGCGCTACGA	180
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Qy	301	GCCCCCTCAGCGGACCCCTGTACCGGACAGACATTGGCTGCCCCCAATGCGGCTACTCCAT	360
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Qy	361	GGGGCTGGCTCTGATGCCGACATGGAGGCTGACACGGTGCTGTCCCTGAGCACCCCGT	420
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Qy	421	GCCTGTGTGGGCGGAGCACACGGTCAAGGCGCAGCTCCTGCTGTCCAGCGCGGCCAA	480
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Qy	481	TTCCAATCTCACACTCACCGACACCGAGCATGAAAACACTGAGACTGATCATCCGGCGG	540
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Qy	661	CAACCCAGCCCGGCCCCACGGACCACTCGCTCTCCGGAGAGCCCCCTGCCGCGCGC	720
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Qy	721	CCAGGAGCTGCCACGCCCCAGGAGAACTGGTGCTCAACAGCAACATCCCCCTGGAGAC	780
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Qy	841	CATTCTCGGCGCCTCCGCGCATGATGGGCTTACAGTGACGGGCACCTTCTTCAAGCC	900
Db	841	CATTCTCGGCGCCTCCGCGCATGATGGGCTTACAGTGACGGGCACCTTCTTCAAGCC	900
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Db	901	TGGAGGACCTCCCCGCTCTTCTGCACCAATCAACAGGGTACCCACTGACGTCCAGCAC	960
Qy	961	AGTGTACTCTCCTCCGCCCCGACCCCTGCCAGCACCTTCGCCCCGGCCCTTTAA	1020
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Qy	1021	CCTCAAGAAAGCCCTCCAAGTACTGTAACTGGAAGTGGCAGCCCTGAGCGCCATCGTCAAT	1080
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Db	1141	CTGGCACCTGAGCCCGATGGAGGGGAGATGTATGAGATCACGGAGGACACAGCCAGCAG	1200
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Db	1261	TGACAGGAAAGCAAAAGAACCCACAGAAAGAACCCAGTAGTTTCTTTCCAGAGGACAG	1320
Qy	1321	TTTCATAGATTCTGGAGAAATTGATGTGGAAAGCGGAGCCTCCCAGAAAGATTCTCTCTGG	1380
Db	1321	TTTCATAGATTCTGGAGAAATTGATGTGGAAAGCGGAGCCTCCCAGAAAGATTCTCTCTGG	1380
Qy	1381	CACCTTCTGGAGATCTCAAGTGTTCATAGACCATCTGTGCATCTGAAATTCATGTGTC	1440
Db	1381	CACCTTCTGGAGATCTCAAGTGTTCATAGACCATCTGTGCATCTGAAATTCATGTGTC	1440
Qy	1441	TCTGGGAAAGCAGACCCCTGGTTGGCAATTTATGGCAGAAAAGGCCCTCCCTCTCACATAC	1500
Db	1441	TCTGGGAAAGCAGACCCCTGGTTGGCAATTTATGGCAGAAAAGGCCCTCCCTCTCACATAC	1500
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Qy	1561	CCTAGAGGGGACCCCGCGCCAGTCTCGGGGAACTGTGCCCCCTCCAGCCATGAGACAGG	1620
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Db	1621	CTTCATCCAGTATTGGATTTCAGGAATCTGGCACCTTGCTTTTACAATGACGGAAGGA	1680
Qy	1681	GTCAGAAAGTGGTTTCTCTTCTCACCACTGCCATGAGTCGGTGGATAACTGCCCCAGCAA	1740
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Qy	1741	CTGCTATGGCAATGGTGACTGCATCTCTGGGACCTGCCACTGCTTCTGGGTTTCTTGGG	1800
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Qy	1801	CCCCGACTGTGGCAGAGCCTCTGCCCCGTCTGTAGCGGAAATGGCCAAATACATGAA	1860
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Qy	1861	AGGCAGATGCTTGTGCCACAGTGGCTGGAAAGGCGCTGAGTCGATGTGCCACCAACCA	1920
Db	1861	AGGCAGATGCTTGTGCCACAGTGGCTGGAAAGGCGCTGAGTCGATGTGCCACCAACCA	1920
Qy	1921	GTGTATCGATGTGGCCTGCAGCAACCATGGCACCTGCATCAGGGGCACCTGCATCTGCAA	1980
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Qy	1981	CCCTGGCTACAAGGGCGAGAGCTGTGAGGAAAGTGGACTGCATGGACCCACATGTCAGG	2040
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Qy	2041	CCGGGGTGTCTGCGTGAGAGGCGAATGCCATTGCTTTGTGGGATGGGGAGGCACCACTG	2100
Db	2041	CCGGGGTGTCTGCGTGAGAGGCGAATGCCATTGCTTTGTGGGATGGGGAGGCACCACTG	2100
Qy	2101	CGAGACCCCGAGGCGCACATGCTTAGACCAGTGTTCAGGCCACGGAACTTCTCTCCCGGA	2160
Db	2101	CGAGACCCCGAGGCGCACATGCTTAGACCAGTGTTCAGGCCACGGAACTTCTCTCCCGGA	2160
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Db	2161	CACCGGGCTTTGCAGCTGTGACCCCAAGCTGGACTGGACACGACTGTTCTATCGAGATCTG	2220
Qy	2221	TGCTGCCGACTGTGGTGGCCATGGCGTGTCCGTAGGGGGCACCTGCCGCTGCGAGGATGG	2280
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Qy	2281	CTGGATGGGGGACGCTTGCACCCAGCGGGCCTGCCACCCCGCTGTGCCGAGCATGGGAC	2340
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QY	2461	ATGTACCTTAGACCTGAATGGTTGGCACTGCGTCTGCGCAGCTGGCTGGAGAGGAGCTGG	2520
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Db	3061	CAGCTGTGACCTGAGCAATTTGCCCCGCCCAACCCAGTCGTCTCTCCATCCCCACTGAC	3120
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QY	3181	GGAGGAAATCTCTATCTCTGGCTGCAAGATGAGGCTGAGCTACCTGAGCAGCGGACCC	3240
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QY	4081	TCCCAGGGGTATTACAGTGGACAAAGTTTGGGCTGATCTACTTCGTGGATGSCACCATGAT	4140
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Db 5161 TACTGGCCAGGTGAGCAGTTTCCGAAGTGATACAGACAGTTTCAGTGCATGTCCAGGTAGA 5220

Qy 5221 GACCTCCAGCAAGGATGATGTCACCATAACCAACCAACCTGTCTGCCCTCAGGCGCCTTCTA 5280

Db 5221 GACCTCCAGCAAGGATGATGTCACCATAACCAACCAACCTGTCTGCCCTCAGGCGCCTTCTA 5280

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Db 5281 CACACTGTGTCAAGACCAAGTCCGGAAACAGCTACTACATCGGGGCGGATGGCTCCTTGGC 5340

Qy 5341 GCTGTGCTGGCCAAACGGCATGGAGTGGCGCTGCAGACTGAGCCCCACTTGTGGCTGG 5400

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Db 6241 CCGCTTCACTGAGGAAGGCATGGTCAACGCCCGTTTGACTACAACTATGACAAACAGCTT 6300

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Db 6301 CCGGTGACCAGCATGCAGGCTGTGATCAACGAGACCCCACTGCCCATTTGATCTCTATCG 6360

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Db	6721		
QY	6781	TGACGTGCAATACAAGATGGATGAGGATGGCTTCCTGAGGCAGCGGGCGGTGATATCTT	6840
Db	6781		
QY	6841	TGAGTACAACCTCAGCTGGCCCTGCTCATCAAGSCTACAACCGGGCTGGCAGCTGGAGTGT	6900
Db	6841		
QY	6901	CAGGTACCGCTACGATGGCCCTGGGGCGCGGTGTCCAGCAAGACGACCCACGCCACCA	6960
Db	6901		
QY	6961	CCTGCAGTTCTTATGCAGACCTTGACCAACCCCAACCAAGGTCA CCACTGTACAACCA	7020
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QY	7021	CTCCAGCTCTGAGATCACCTCCCTCTACTACGACTTGCAAGGACACCTCTTTGCCATGGA	7080
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Db	7081		
QY	7141	CTTTAGTGGAACAGGTTTGATGATCAAGCAAACTCCTGTACACAGCCCTATGGGAGATCTA	7200
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QY	7201	CATGGATACCAACCCCAACTTTTCAGATCATATAGGCTACCATGGTGGCCTCTATGATCC	7260
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QY	7261	ACTCACCAAGCTTGTCCACATGGGCGCGGAGATTATGATGTCTGGCCGACGCTGGAC	7320
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QY	7321	TAGCCAGACCAACGAGCTGTGGAAGCACCTTAGTAGCAGCAACGTCATGCTTTTAATCT	7380
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QY	7381	CTATATGTTCAAAAACAACACCCCATCAGCAACTCCAGGACATCAAGTGTTCATGAC	7440
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QY	7501	TCCCAAACCAAGATGGATGCCATGGAAACCTCCTACGAGCTCATCCACACAGATGAA	7560
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QY	7561	AACGCAGGAGTGGGACAAACAGCAAGTCTATCCTCGGGGTACAGTGTGAAGTACAGAAGCA	7620
Db	7561		
QY	7621	GCTCAAGGCCCTTTGTCACTTAGAACGGTTTGACCAAGCTCTATGGCTCCACAATCACCAG	7680
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QY	7681	CTGCCAGCAGGCTCCAAAGACCAAGAAAGTTTGATCCAGCGGCTCAGTCTTTGGCAAGGG	7740
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QY	7741	GGTCAAGTTTGCCCTTGAAGGATGGCCGAGTGACCAAGAGATCATCAGTGTGGCCAATGA	7800
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Db	7801	GGATGGCGAAGGGTTGCTGCCATCTTGAACCATGCCACTACCTAGAGAACCTGCACCT	7860
QY	7861	CACCATTTGATGGGTGGATACCCATTACTTTGTGAACCAGGACCTTCAGAAAGGTGACCT	7920
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QY	7921	GGCCATCCTTGGGCCTCAGTGGGGGGCGGCAACCCCTGGAGAATGGSGTCAACGTCACTGT	7980
Db	7921		
QY	7981	GTCCAGATCAACACACAGTACTTAATGGCAGGACTAGACGCTACACAGACATCCAGCTCCA	8040
Db	7981		
QY	8041	GTACGGGCACTGTCTTGAACACACGCTACGGGACAAACGTTGGATGAGGAAAGGCACG	8100
Db	8041		
QY	8101	GGTCCTGAGCTGGCCCGCAGAGAGCCGTGCGCCAAAGCGTGGCCCGCAGCAGAG	8160
Db	8101		
QY	8161	ACTCGGGAAAGGGAGGAAGGCCTGCGGCCTGGACAGAGGGGGAGAACGACAGGTGCT	8220
Db	8161		
QY	8221	GAGCACAGGCGGGTGCAAGGCTACGACGGCTTTTTCGTGATCTCTGTGAGCAGTACCC	8280
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QY	8281	AGAACTGTGAGACAGCGCCCAACAACATCCACTTCATGAGACAGAGCGGCGGAG	8340
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AX600210			
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ACCESSION	AX600210		
VERSION	AX600210.1	GI:28400252	
KEYWORDS	.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	1		
AUTHORS	Yue,H., Yao,M.G., Ison,C.H., Lu,Y., Warren,B.A., Elliott,V.S., Baughn,M.R., Ding,L., Xu,Y., Gietzen,K.J., Tang,T.Y., Lal,P.G., Duggan,B.M., Burford,N., Lu,D.A., Richardson,T.W., Tran,U.K., Khare,R. and Wallia,N.K.		
TITLE	Proteins associated with cell growth, differentiation, and death		
JOURNAL	Patent: WO 02072830-A 22 19-SEP-2002;		
FEATURES	Incyte Genomics, Inc. (US)		
source	Location/Qualifiers		
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	/db_xref="taxon:9606"		
ORIGIN	/note="Incyte ID No: 7488573CB1"		
Query Match	98.5%;	Score 8225;	DB 6; Length 8645;
Best Local Similarity	99.4%;	Pred. No. 0;	
Matches 8300;	Conservative	0; Mismatches	21; Indels 33; Gaps 3;
QY	1	GTTTGTGGATGTGGAGGAGCGCGGGCGGAGCCATGGACGTGAAGGAGAGGAGCCCTTA	60

D <sub>b</sub>	83	GTTTGTGGATNTGGAGGAGCGCGGCCGAGGCCATTGGACGTGAAGAGAGAAAGCCTTA	142
Q <sub>y</sub>	61	CCGCTCGTGACCCGGGCGCGGACGCCGAGCGCCGCTACACCAGTCGTCCGCGGACAG	120
D <sub>b</sub>	143	CCGCTCGTGACCCGGGCGCGGACGCCGAGCGCCGCTACACCAGTCGTCCGCGGACAG	202
Q <sub>y</sub>	121	CGAGGAGGCAAAAGCCCCGCAGAAATCGTACAGCTCCAGCGAGACCTGAAGGCCTACGA	180
D <sub>b</sub>	203	CGAGGAGGCAAAAGCCCCGCAGAAATCGTACAGCTCCAGCGAGACCTGAAGGCCTACGA	262
Q <sub>y</sub>	181	CCAGGACGCCCGCCTAGCCTATGGCAGCGCGCTCAAGGACATTGTGCGCAGGAGGCCGA	240
D <sub>b</sub>	263	CCAGGACGCCCGCCTAGCCTATGGCAGCGCGCTCAAGGACATTGTGCGCAGGAGGCCGA	322
Q <sub>y</sub>	241	GGAAATTCGCCGCACAGGTGCCAATTCACCCCTGCGGGAGCTGGGGCTGGAAGAATAAC	300
D <sub>b</sub>	323	GGAAATTCGCCGCACAGGTGCCAATTCACCCCTGCGGGAGCTGGGGCTGGAAGAATAAC	382
Q <sub>y</sub>	301	GCCCCCTCACGGGACCTGTACCGGACAGACATTGGCCCTGCCCAATGCGGGCTACTCCAT	360
D <sub>b</sub>	383	GCCCCCTCACGGGACCTGTACCGGACAGACATTGGCCCTGCCCAATGCGGGCTACTCCAT	442
Q <sub>y</sub>	361	GGGGGTGGTCTGATGCCGACATGGAGGTGACACGGTGCTGTCCCCTGAGCAACCCCGT	420
D <sub>b</sub>	443	GGGGGTGGTCTGATGCCGACATGGAGGTGACACGGTGCTGTCCCCTGAGCAACCCCGT	502
Q <sub>y</sub>	421	GCCTCTGTGGGCGCGGAGCACACGGTCAAGSGCGCAGCTCCTGCCTGTCCAGCCGGCCAA	480
D <sub>b</sub>	503	GCCTCTGTGGGCGCGGAGCACACGGTCAAGSGCGCAGCTCCTGCCTGTCCAGCCGGCCAA	562
Q <sub>y</sub>	481	TTCCAATCTCACACTCACCGACACCGGAGCATGAAACACATGAGACTGATCATCCGGGCGG	540
D <sub>b</sub>	563	TTCCAATCTCACACTCACCGACACCGGAGCATGAAACACATGAGACTGATCATCCGGGCGG	616
Q <sub>y</sub>	541	CCTGCAGAACCAACCGCGGGCTCCGGACGCGCGCGCGCGCTCTCGACGCCCAACACCCC	600
D <sub>b</sub>	617	CCTGCAGAACCAACCGCGGGCTCCGGACGCGCGCGCGCGCTCTCGACGCCCAACACCCC	676
Q <sub>y</sub>	601	CAACCAGAACCAACCGCGGGCTCCATTACTCCTGAAACCGGGGCAAATTCAAGCCGAGGAG	660
D <sub>b</sub>	677	CAACCAGAACCAACCGCGGGCTCCATTACTCCTGAAACCGGGGCAAATTCAAGCCGAGGAG	736
Q <sub>y</sub>	661	CAACCCAGCCCGGCCCCCAGCGACCACTCGCTCTCCGAGAGCCCCCTGCGCGCGCGCGC	720
D <sub>b</sub>	737	CAACCCAGCCCGGCCCCCAGCGACCACTCGCTCTCCGAGAGCCCCCTGCGCGCGCGCGC	796
Q <sub>y</sub>	721	CCAGGAGCCTGCCACCGCCAGGAGAACTGGTGCTCAACAGCAACAATCCCCCTGGAGAC	780
D <sub>b</sub>	797	CCAGGAGCCTGCCACCGCCAGGAGAACTGGTGCTCAACAGCAACAATCCCCCTGGAGAC	856
Q <sub>y</sub>	781	CAGGAACCTAGSCAAGCAGCCATTCCCTAGGACATTCAGGACAAACCTCATTTGAGATGGA	840
D <sub>b</sub>	857	CAGAAACCTAGSCAAGCAGCCATTCCCTAGGACATTCAGGACAAACCTCATTTGAGATGGA	916
Q <sub>y</sub>	841	CATTCTCGGCGCCTCCCGCCATGATGGGGCTTACAGTGACGGGCACCTTCCTCTTCAAGCC	900
D <sub>b</sub>	917	CATTCTCGGCGCCTCCCGCCATGATGGGGCTTACAGTGACGGGCACCTTCCTCTTCAAGCC	976
Q <sub>y</sub>	901	TGGAGGCACCTCCCGCTCTTCTGCAACCAATCACAGGGTACCCACTGACGTCCAGCAC	960
D <sub>b</sub>	977	TGGAGGCACCTCCCGCTCTTCTGCAACCAATCACAGGGTACCCACTGACGTCCAGCAC	1036
Q <sub>y</sub>	961	AGTGTAATCTCTCCGCCCCCGACCCCTGCCCGCAGCACTTCGCCCGCGCGCCTTTAA	1020
D <sub>b</sub>	1037	AGTGTAATCTCTCCGCCCCCGACCCCTGCCCGCAGCACTTCGCCCGCGCGCCTTTAA	1096
Q <sub>y</sub>	1021	CCTCAAGAAAGCCCTCCAAGTACTGTAACTGGAAGTGCAGCCCTGAGCGGCATCGTCAT	1080
D <sub>b</sub>	1097	CCTCAAGAAAGCCCTCCAAGTACTGTAACTGGAAGTGCAGCCCTGAGCGGCATCGTCAT	1156
Q <sub>y</sub>	1081	CTCAGCCACTCTGGTCACTCCTGCTGGCATACTTTGTGGCCATGCACCTGTTGGCCTAAA	1140

1157	CTCAGCCACTCTGGTCATCCTGCTGGCATACTTTGTGGTAAGCACCT-----CTTCAA	1211
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1571	ACAGTTTGACTTTGTGGAGCTGCTGGATGGCAGGAGCTCCTAAACCCAGGAGCGCGGAG	1630
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1751	GTCAGAAAGTGGTTTCCTTTCTCAACCATGCCATTGAGTCGGTGGATAACTGCCCCAGCAA	1810
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1931	AGGCAGATGCTTGTGCCACAGTGGCTGGAAGGCGCTGAGTCGATGTGCCCAACCA	1990
1921	GTGTATCGATGTGGCCTGCAGCAACCATGGCACCTGCATCACGGGACCTGCATCTGCAA	1980
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2101	CGAGACCCCGAGGCCACATGCTTAGACCAAGTGGAATGCATGGACCCCACTTCTCCCGGA	2160
2171	CGAGACCCCGAGGCCACATGCTTAGACCAAGTGGAATGCATGGACCCCACTTCTCCCGGA	2230
2161	CACCGGCTTTGCAGCTGTGACCCCAAGCTGGACTGGACACGACTGTTCTATCGAGATCTG	2220
2231	CACCGGCTTTGCAGCTGTGACCCCAAGCTGGACTGGACACGACTGTTCTATCGAGATCTG	2290



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Db	2291	TGCTGCCGACTGTGCTGGCCATGGCGTGTGCGTAGGGGGCACCTGCCGCTGCGAGGATGG	2350
QY	2281	CTGGATGGGGGACGCTTGCAGACCGCGGGCCCTGCCACCCGCGCTGTGCGGAGCATGGGAC	2340
Db	2351	CTGGATGGGGGACGCTTGCAGACCGCGGGCCCTGCCACCCGCGCTGTGCGGAGCATGGGAC	2410
QY	2341	CTGCCGCGACGGCAAGTCGAGTGCAGCCCTGGCTGGAATGGCGAACTGCACCATCGC	2400
Db	2411	CTGCCGCGACGGCAAGTCGAGTGCAGCCCTGGCTGGAATGGCGAACTGCACCATCGC	2470
QY	2401	TCACATATCTGGATAGGGTAGTTAAAGAGGGTTGGCCCTGGGTTGTGCAATGGCAACGGCAG	2460
Db	2471	TCACATATCTGGATAGGGTAGTTAAAGAGGGTTGGCCCTGGGTTGTGCAATGGCAACGGCAG	2530
QY	2461	ATGTACCTTAGACCTGAATGGTTGGCACTGCCCTGCCAGCTGGGCTGGAGAGGAGCTGG	2520
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QY	2941	CATCATCCTGCGGTTGAGCGGGCACCTTTTCATCACACAGGAGCACACCCCTGTGGCTGCC	3000
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Db	3071	ATGGGATCGCTTCTTGTTCATGGAAACCATCATCATGAGACATGAGGAGATGAGATTCC	3130
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Db	3131	CAGCTGTGACCTGAGCAATTTTGGCCGCCCAACCCAGTCTCTCTCCATCCCCACTGAC	3190
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QY	3181	GGAGGAAATCTCTATCTCTGGCTGCAAGATGAGGCTGAGCTACCTGAGCAGCGGGACCCC	3240
Db	3251	GGAGGAAATCTCTATCTCTGGCTGCAAGATGAGGCTGAGCTACCTGAGCAGCGGGACCCC	3310
QY	3241	TGGCTACAAATCTGTCTGAGGATCAGCCTCACCCACCCGACCATCCCTTCAACCTCAT	3300
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AX675551

LOCUS AX675551 8438 bp DNA linear PAT 27-MAR-2003  
DEFINITION Sequence 1 from Patent WO2055704.

ACCESSION AX675551

VERSION AX675551.1 GI:293333552

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.

REFERENCE

AUTHORS

1  
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Spytek,K.A., Zhong,M., Gangolli,E.A., Burgess,C.E., Patturajan,M.,  
Vernet,C.A., Taylor,S., Tchernev,V.T., Miller,C.E., Guo,X.,  
Boldog,F.L., Grosse,W.M., Alsobrook,J.P., Gerlach,V.,  
Edingermark,S., Rothernberg,M.E., Ellerman,K., Macdougall,J.,  
Malyankar,U., Millet,I., Peyman,J., Smithson,G., Gunther,E. and  
Stone,D.J.

TITLE

Proteins, polynucleotides encoding them and methods of using the  
same

JOURNAL

Patent: WO 02055704-A 1 18-JUL-2002;

Curagen Corporation (US)



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QY	1285	AGAAGGAAAGCCAGTAGTTTCTTTCCAGAGGACAGTTTCTGGAGATCTCAAGTGTT	1344
Db	1261	AGAAGGAAAGCCAGTAGTTTCTTTCCAGAGGACAGTTTCTGGAGATCTCAAGTGTT	1320
QY	1345	TGTGGAAAGCGAGCCTCCAGAAGATTCTCTCTGGCACCTTTCTGGAGATCTCAAGTGTT	1404
Db	1321	TGTGGAAAGCGAGCTTCCAGAAGATTCTCTCTGGCACCTTTCTGGAGATCTCAAGTGTT	1380
QY	1405	CATAGACCATCCTGTGCATCTGAAATTCATATGTCTCTGGAAAGGCAGCCCTGGTTGG	1464
Db	1381	CATAGACCATCCTGTGCATCTGAAATTCATATGTCTCTGGAAAGGCAGCCCTGGTTGG	1440
QY	1465	CATTTATGGCAGAAAGGCCTCCCTCCTTCACATACACAGTTTGACTTTGTGGAGTGTCT	1524
Db	1441	CATTTATGGCAGAAAGGCCTCCCTCCTTCACATACACAGTTTGACTTTGTGGAGTGTCT	1500
QY	1525	GGATGGCAGGAGGCTCTAAACCCAGGAGCGCGGAGCCTAGAGGGGACCCCGCGCCAGTC	1584
Db	1501	GGATGGCAGGAGGCTCTAAACCCAGGAGCGCGGAGCCTAGAGGGGACCCCGCGCCAGTC	1560
QY	1585	TCGGGGAACGTGTGCCCCCTCCAGCCATGAGACAGGTTTCAAGTATTTGGATTTCAGG	1644
Db	1561	TCGGGGAACGTGTGCCCCCTCCAGCCATGAGACAGGTTTCAAGTATTTGGATTTCAGG	1620
QY	1645	AATCTGGCACCTTGGCTTTTACAATGACGGAAGGAGTCAAGAGTGGTTTCTTTCTCAC	1704
Db	1621	AATCTGGCACCTTGGCTTTTACAATGACGGAAGGAGTCAAGAGTGGTTTCTTTCTCAC	1680
QY	1705	CATGCCATTGAGTCGGTGGATAAATGCCCCCAGCAACTGCTATGGCAATGGTGAAGTGCAT	1764
Db	1681	CACTGCCATT-----CTTGATTCTGGGCTCTCTGTTGGGTGATGGAGAAATGCGT	1731
QY	1765	CTCTGGGACCTGCCACTGCTTCTGGGTTTCTTGGGCCCCGACTGTGGCAGAGCCTCCTG	1824
Db	1732	TTCTGGAACTTGCCATTGTTTCCAGGATTTCTGGGTCCGATTTGTTCAAGAGCCGCTG	1791
QY	1825	CCCCGTGCTCTGTAGCGGAAATGGCCAATACATGAAGGACAGATGCTTGTGCCACAGTGG	1884
Db	1792	TCCAGTGTATGTAGTGGCAACGGGCAGTACTCCAAGGCGGCTGCCTGTGTTTCAGCGG	1851
QY	1885	CTGGAAGGCGCTGAGTGGATGTGCCCAACCAACCAAGTGTATCGATGTGGCCTGCAGCAA	1944
Db	1852	CTGGAAGGCGCACCGAGTGTGATGTGCCGACTACCCAGTGTATTGACCCACAGTGTGGGG	1911
QY	1945	CCATGGCACCTGCATCACGGGCACCTGCATCTGCAAACCCCTGGCTACAAGGGCGAGAGCTG	2004
Db	1912	TCGTGGGATTGTATCATGGGCTCCTGTGCTTGCAACTCAGGATACAAAGGAGAAAGTTG	1971
QY	2005	TGAGGAAGTGGACTGCATGGACCCCACTGTTTCAGGGCCGGGGTGTCTCGTGTAGAGGGCA	2064
Db	1972	TGAAGAAGCTGACTGTATAGACCCCTGGGTGTTCTAATCATGCTGTGTATCCACGGGGA	2031



QY 2065 ATGCCATTGCTTTGTGGGATGGGAGGACCAACTGGAGAGCCCCAGGGCCACATGCTT 2124  
Db |||||  
QY 2032 ATGTCACTGCAGTCCAGGATGGGAGGTAGCAATTGTGAAATACTGAAGACCATGTGTCC 2091  
Db |||||  
QY 2125 AGACCAAGTGTTCAGGCCACGGAACCTTCCCTCCCGGACACCGGGCTTTGCAGCTGTGACCC 2184  
Db |||||  
QY 2092 AGACCAAGTGTCCGGCCACGGAACGTATCTTCAAGAAAGTGGCTCCTGCACGTGTGACCC 2151  
QY 2185 AAGCTGGACTGGACACGACTGTTCTATCGAGATCTGTGCTGCCGACTGTGGTGGCCATGG 2244  
Db |||||  
QY 2152 TAACTGGACTGGCCCAAGCTGCTCAAAACGAAATATGTTCTGTGGA CTGTGGCTCACACGG 2211  
QY 2245 CGTGTGCGTAGGGGGACCTGCCCGCTGCGAGGATGGTGGATGGGGCAGCCTGCGCACCA 2304  
Db |||||  
QY 2212 CGTTTGCATGGGGGGACGTGTGCTGTGAAGAAAGGCTGGACGGGCCCCAGCCTGTAAATCA 2271  
QY 2305 GCGGGCCTGCCACCCGCGTGTGCCGAGCATGGGACCTGCCGACCGCAAGTGGGAGTG 2364  
Db |||||  
QY 2272 GAGAGCCTGCCACCCCGCTGTGCCGAGCACGGGACCTGCCGACGGCAAGTGGGAGTG 2331  
QY 2365 CAGCCCTGGCTGGAATGSGGAACACTGCACCATC-----GCTCACTATCTGGATAGGGT 2418  
Db |||||  
QY 2332 CAGCCCTGGCTGGAATGSGGAACACTGCACCATCTCCCTAGCTCACTATCTGGATAGGGT 2391  
QY 2419 AGTTAA-----AGAGGTTGCCCTGGGTTGTGCAATGGCAACGGCAGATGTACTTAGA 2472  
Db |||||  
QY 2392 AGTTAAACTTTTCAAGGGTTGCCCTGGGTTGTGCAATGGCAACGGCAGATGTACTTAGA 2451  
QY 2473 CCTGAATGGTTGGCACTGGCTGTGCCAGCTGGGCTGGAGAGGAGCTGGCTGTGACACTTC 2532  
Db |||||  
QY 2452 CTTGAATGGTTGGCACTGGCTGTGCCAGCTGGGCTGGAGAGGAGCTGGCTGTGACACTTC 2511  
QY 2533 CATGGAGACTGCCCTGCGGTGACAGCAAAAGACAATGATGGAGATGGCCTGGTGGACTGCAT 2592  
Db |||||  
QY 2512 CATGGAGACTGCCCTGCGGTGACAGCAAAAGACAATGATGGAGATGGCCTGGTGGACTGCAT 2571  
QY 2593 GGACCCCTGACTGCTGCCCTCCAGCCCCCTGTGCCATATCAACCCGCTGTGCCCTCCCC 2652  
Db |||||  
QY 2572 GGACCCCTGACTGCTGCCCTCCAGCCCCCTGTGCCATATCAACCCGCTGTGCCCTCCCC 2631  
QY 2653 TAAACCCCTCTGGACATCATCCAGGAGACACAGGTCCTGTGTCAAGCAGCAACCTACACTC 2712  
Db |||||  
QY 2632 TAAACCCCTCTGGACATCATCCAGGAGACACAGGTCCTGTGTCAAGCAGCAACCTACACTC 2691  
QY 2713 CTTCTATGACCGCATCAAGTTCCTCGTGGCAGGACAGCACGCACATAATCCCCGGGGA 2772  
Db |||||  
QY 2692 CTTCTATGACCGCATCAAGTTCCTCGTGGCAGGACAGCACGCACATAATCCCCGGGGA 2751  
QY 2773 GAAACCCCTTTGATGGAGGGATGCTTGTGTTATTCTGTGGCCAAAGTGATGACATCAGATGG 2832  
Db |||||  
QY 2752 GAAACCCCTTTGATGGAGGGATGCTTGTGTTATTCTGTGGCCAAAGTGATGACATCAGATGG 2811  
QY 2833 AACCCTCCCTGGTGTGNAACATCAGTTTGTCAATAACCCCTCTCTTTTGGATATACAAT 2892  
Db |||||  
QY 2812 AACCCTCCCTGGTGTGNAACATCAGTTTGTCAATAACCCCTCTCTTTTGGATATACAAT 2871  
QY 2893 CAGCAGGCAAGATGGCAGCTTTGACTTGGTGACAAATGGCGGCATCTCCATCATCTCGG 2952  
Db |||||  
QY 2872 CAGCAGGCAAGATGGCAGCTTTGACTTGGTGACAAATGGCGGCATCTCCATCATCTCGG 2931  
QY 2953 GTTCGAGCGGGCACCTTTTCATCACACAGGAGCACACCTGTGGCTGCCATGGGATCGCTT 3012  
Db |||||  
QY 2932 GTTCGAGCGGGCACCTTTTCATCACACAGGAGCACACCTGTGGCTGCCATGGGATCGCTT 2991  
QY 3013 CTTTGTCAATGGAACCATCATCATGAGACATGAGGAGAATGAGATTTCCCAGCTGTGACCT 3072  
Db |||||  
QY 2992 CTTTGTCAATGGAACCATCATCATGAGACATGAGGAGAATGAGATTTCCCAGCTGTGACCT 3051  
QY 3073 GAGCAATTTTGGCCCGCCCAACCCAGTCGTCTCTCCATCCCCCACTGACGTCCTTTCGCCAG 3132  
Db |||||  
QY 3052 GAGCAATTTTGGCCCGCCCAACCCAGTCGTCTCTCCATCCCCCACTGACGTCCTTTCGCCAG 3111

QY 3133 CTCCTGTGCAGAGAAAGGCCCCCATTTGTGCCGGAATTCAGGCTTTGCAGGAGGAAATCTC 3192  
Db |||||  
QY 3112 CTCCTGTGCAGAGAAAGGCCCCCATTTGTGCCGGAATTCAGGCTTTGCAGGAGGAAATCTC 3171  
QY 3193 TATCTCTGGCTGCAAGATGAGGCTGAGCTA CTTGAGCAGCCGGACCCCTGGCTACAAATC 3252  
Db |||||  
QY 3172 TATCTCTGGCTGCAAGATGAGGCTGAGCTA CTTGAGCAGCCGGACCCCTGGCTACAAATC 3231  
QY 3253 TGTCTGAGGATCAGCCTCACCCACCCGACCAATCCCTTCAACCTCATGAAGTGCACCT 3312  
Db |||||  
QY 3232 TGTCTGAGGATCAGCCTCACCCACCCGACCAATCCCTTCAACCTCATGAAGTGCACCT 3291  
QY 3313 CATGGTAGCGGTGAGGGCCGCTCTTTCAGGAAGTGGTTCGCTGCAGCCCCAGACCTGTC 3372  
Db |||||  
QY 3292 CATGGTAGCGGTGAGGGCCGCTCTTTCAGGAAGTGGTTCGCTGCAGCCCCAGACCTGTC 3351  
QY 3373 CTATTATTTTCAATTTGGGACAAGACAGACGCTCTACAAACCAAGAGGTGTTTGGGCTTTTCA 3432  
Db |||||  
QY 3352 CTATTATTTTCAATTTGGGACAAGACAGACGCTCTACAAACCAAGAGGTGTTTGGGCTTTCA 3411  
QY 3433 AGCCTTTGTTTCCGTGGGTTATGAATATGAATCTCTGCCCCAGATCTAATCCTGTGGGAAAA 3492  
Db |||||  
QY 3412 AGCCTTTGTTTCCGTGGGTTATGAATATGAATCTCTGCCCCAGATCTAATCCTGTGGGAAAA 3471  
QY 3493 AAGAAACAACAGTGTGCAGGGCTATGAAATTGACGCGTCCAAGCTTGGAGGATGGAGCCT 3552  
Db |||||  
QY 3472 AAGAAACAACAGTGTGCAGGGCTATGAAATTGACGCGTCCAAGCTTGGAGGATGGAGCCT 3531  
QY 3553 AGACAAACATCATGCCCTCAACATTTCAAAGTGT -- ATCCTGCACAAAGGAATGGGA 3609  
Db |||||  
QY 3532 AGACAAACATCATGCCCTCAACATTTCAAAGTGTGGCATCTCTGCACAAAGGGAATGGGA 3591  
QY 3610 GAAACCAAGTTTGTGTCTCAGCAGCCCTCCTGTCTATTGGGAGCATCATTGGGCAATGGGCGCG 3669  
Db |||||  
QY 3592 GAAACCAAGTTTGTGTCTCAGCAGCCCTCCTGTCTATTGGGAGCATCATTGGGCAATGGGCGCG 3651  
QY 3670 GAGAAAGCATCTCTGCCCCCAGCTGCAACGGCCCTTGTGACGGCAACAAGCTCTTGGCCCCC 3729  
Db |||||  
QY 3652 GAGAAAGCATCTCTGCCCCCAGCTGCAACGGCCCTTGTGACGGCAACAAGCTCTTGGCCCCC 3711  
QY 3730 AGTGGCCCTCACCTGTGGCTCTGACGGGAGCCTCTATGTGGGTGATTTCAACTACATTAG 3789  
Db |||||  
QY 3712 AGTGGCCCTCACCTGTGGCTCTGACGGGAGCCTCTATGTGGGTGATTTCAACTACATTAG 3771  
QY 3790 AAGGATCTTCCCCTCTGGAAATGTCAACCAACATCTTAGAGCTGAGG-----AATAAAGA 3843  
Db |||||  
QY 3772 AAGGATCTTCCCCTCTGGAAATGTCAACCAACATCTTAGAGCTGAGGGTCAGAAATAAAGA 3831  
QY 3844 TTTTCAGACATAGTACAGTCCAGCACACAAATACTACTCTGGCCACAGACCCCATGAGTGG 3903  
Db |||||  
QY 3832 TTTTCAGACATAGTACAGTCCAGCACACAAATACTACTCTGGCCACAGACCCCATGAGTGG 3891  
QY 3904 GGCCGTCTTCTTCTGACAGCAACAGCCGGGGTCTTTAAATCAAGTCCACTGTGGT 3963  
Db |||||  
QY 3892 GGCCGTCTTCTTCTGACAGCAACAGCCGGGGTCTTTAAATCAAGTCCACTGTGGT 3951  
QY 3964 GGTGAAGGACCTTGTCAAGAACTCTGAGGTGGTTCGGGGGACAGGTGACCAAGTGCCTCCC 4023  
Db |||||  
QY 3952 GGTGAAGGACCTTGTCAAGAACTCTGAGGTGGTTCGGGGGACAGGTGACCAAGTGCCTCCC 4011  
QY 4024 CTTTGTATGACACTCGCTCGGGGATGGTGGGAAGGCCACAGAACCCACACTCAACAATCC 4083  
Db |||||  
QY 4012 CTTTGTATGACACTCGCTCGGGGATGGTGGGAAGGCCACAGAAAGCCACACTCACCAATCC 4071  
QY 4084 CAGGGGT-----ATTACAGTGGACAAGTTTGGGCTGATCTACTTCGTGGATGGCAC 4134  
Db |||||  
QY 4072 CAGGGGTCCCCCAGGCATTA CAGTGGACAAGTTTGGGCTGATCTACTTCGTGGATGGCAC 4131  
QY 4135 CATGATCAGACGCAATCGATCAGAAATGGGATCATCTCCACCCTGCTCGGCTCTAATGATCT 4194  
Db |||||  
QY 4132 CATGATCAGACGCAATCGATCAGAAATGGGATCATCTCCACCCTGCTCGGCTCTAATGATCT 4191  
QY 4195 CACATCAGCCCCGGCCACTCAGCTGTGATTCTGTGATGATTTTCCAGGTAATA----- 4249

Db	4192	CACATCAGCCCGCCACTCAGCTGTGATTTCTGTCTATGGATATTTCCACGGTAAGACAGGT	4251	Db	5272	CTCAGGCGCCTTCTACACACTGCTGCAAGACCAAGTCCGGAACAGTACTACATCGGGGC	5331
QY	4250	-----CTGGAGTGGCCCAAGACTTAGCCCATCAACCAATGGACAACCTACTTTATGTCTCT	4305	QY	5326	CGATGGCTCCTTTGCGGCTGCTGCTGGCCAAACGGCATGGAGGTGGCGTGCAGACTGAGCC	5385
Db	4252	TCACCTGGAGTGGCCCAAGACTTAGCCCATCAACCAATGGACAACCTACTTTATGTCTCT	4311	Db	5332	CGATGGCTCCTTTGCGGCTGCTGCTGGCCAAACGGCATGGAGGTGGCGTGCAGACTGAGCC	5391
QY	4306	CGACAACAATGTGGTCCCTGCAAAATCTCTGAAAAACCAACAGGTGCGCATTTGTGCGCCGGAG	4365	QY	5386	CCACTTGTCTGGCTGGCACCCGTCAACCCCAACCGTGGGCAAGAGGAATGTACCGTGCCTCAT	5445
Db	4312	CGACAACAATGTGGTCCCTGCAAAATCTCTGAAAAACCAACAGGTGCGCATTTGTGCGCCGGAG	4371	Db	5392	CCACTTGTCTGGCTGGCACCCGTCAACCCCAACCGTGGGCAAGAGGAATGTACCGTGCCTCAT	5451
QY	4366	GCCCATGCATGCCAGGTCCCTGGCATTTGACCACTTCTCTGCTAAGCAAGGTGGCCATCCA	4425	QY	5446	CGACAACGGCCTCAACCTGGTGGAGTGGCGCCAGCGCAAAAGAGCAGGCTCGGGGCCAGGT	5505
Db	4372	GCCCATGCATGCCAGGTCCCTGGCATTTGACCACTTCTCTGCTAAGCAAGGTGGCCATCCA	4431	Db	5452	CGACAACGGCCTCAACCTGGTGGAGTGGCGCCAGCGCAAAAGAGCAGGCTCGGGGCCAGGT	5511
QY	4426	CGCAACCTTGAGTCAAGCATCCGCTTTGGCTGTTTACACAATGGGGTCCCTGTATATTGC	4485	QY	5506	CACCTGTCTTTGGCGCCCGCTGCGGGTG-----CACAAACCGAAATCTCCTATCTCT	5556
Db	4432	CGCAACCTTGAGTCAAGCATCCGCTTTGGCTGTTTACACAATGGGGTCCCTGTATATTGC	4491	Db	5512	CACCTGTCTTTGGCGCCCGCTGCGGGTGCTCCAGGTTCAAAACCGAAATCTCCTATCTCT	5571
QY	4486	TGAGACTGATGAGAAAAAGATCAACCGCATCAGGCAAGTCAACACTAGTGGAGAGATCTC	4545	QY	5557	GGACTTTGATCGGTAAACACGCACAGAGAAGATCTATGATGACCAACCGCAAGTTACCCCT	5616
Db	4492	TGAGACTGATGAGAAAAAGATCAACCGCATCAGGCAAGTCAACACTAGTGGAGAGATCTC	4551	Db	5572	GGACTTTGATCGGTAAACACGCACAGAGAAGATCTATGATGACCAACCGCAAGTTACCCCT	5631
QY	4546	ACTCGTTGCTGGGGCCCCACTGGCTGTGACTGTAAAAATGATGCCAACTGTGATTGTTT	4605	QY	5617	TCGGATTCTGTACGACCAGGCGGGCGGCCAGGCTCTGGTCACCCAGCAGCAGGCTGAA	5676
Db	4552	ACTCGTTGCTGGGGCCCCACTGGCTGTGACTGTAAAAATGATGCCAACTGTGATTGTTT	4611	Db	5632	TCGGATTCTGTACGACCAGGCGGGCGGCCAGGCTCTGGTCACCCAGCAGCAGGCTGAA	5691
QY	4606	TTCTGGAGACGATGGTTATGCCAAGGATGCAAAGTTAAATACCCCATCTTCCTTGGCTGT	4665	QY	5677	TGGTGTCAACGTGACATATCTCCCTGGSGGTTACATTTGGCATCCAGAGGGGCATCAT	5736
Db	4612	TTCTGGAGACGATGGTTATGCCAAGGATGCAAAGTTAAATACCCCATCTTCCTTGGCTGT	4671	Db	5692	TGGTGTCAACGTGACATATCTCCCTGGSGGTTACATTTGGCATCCAGAGGGGCATCAT	5751
QY	4666	GTGTGCTGATGGGAGCTCTACCTGGCCGACCTTGGGAAACATCCGAATTCGGTTTATCCG	4725	QY	5737	GTCTGAAAGAATGGAATACGACCAGGCGGGCCGCATCACATCCAGGATCTTCGCTGATGG	5796
Db	4672	GTGTGCTGATGGGAGCTCTACCTGGCCGACCTTGGGAAACATCCGAATTCGGTTTATCCG	4731	Db	5752	GTCTGAAAGAATGGAATACGACCAGGCGGGCCGCATCACATCCAGGATCTTCGCTGATGG	5811
QY	4726	GAAAGCAAGCCTTTCTCAACACCCAGAAACATGTATGAGCTGTCTTCAACCAATTGACCA	4785	QY	5797	GAAAGCATGGAGCTACACATACCTTAGAGAAGGAGGTGTCCAGTCCATGGTGTCTACT	5844
Db	4732	GAAAGCAAGCCTTTCTCAACACCCAGAAACATGTATGAGCTGTCTTCAACCAATTGACCA	4791	Db	5812	GAAAGCATGGAGCTACACATACCTTAGAGAAGGAGGTGTCCAGTCCATGGTGTCTACT	5871
QY	4786	GGAGCTCTATCTGTTTGATACCAACCGGCAAGCACCTGTACACCCAAAGCCTGCCACAGG	4845	QY	5845	ACACAGCCAGAGGCAATGATCTTTGAGTTTCGACAAGAAATGACCGCCTCTCTTCTGTGAC	5904
Db	4792	GGAGCTCTATCTGTTTGATACCAACCGGCAAGCACCTGTACACCCAAAGCCTGCCACAGG	4851	Db	5872	ACACAGCCAGAGGCAATGATCTTTGAGTTTCGACAAGAAATGACCGCCTCTCTTCTGTGAC	5931
QY	4846	AGACTACCTGTACAACCTTACCTTACCTGGGACGGCGACATCACACTCATCACAGACAA	4905	QY	5905	GATGCCCAACGTGGCGCGGCAGACACTAGAGACCACTCCGCTCAGTGGGCTACTACAGAAA	5964
Db	4852	AGACTACCTGTACAACCTTACCTTACCTGGGACGGCGACATCACACTCATCACAGACAA	4911	Db	5932	GATGCCCAACGTGGCGCGGCAGACACTAGAGACCACTCCGCTCAGTGGGCTACTACAGAAA	5991
QY	4906	CAATGGCAACATGGTAAATGTCCGCGGAGACTCTACTGGGATGCCCTCTGGCTGGTGGT	4965	QY	5965	CATCTATCAGCCCCCTGAGGGCAATGCCCTCAGTTCATACAGGACTTCACTGAGGATGGCA	6024
Db	4912	CAATGGCAACATGGTAAATGTCCGCGGAGACTCTACTGGGATGCCCTCTGGCTGGTGGT	4971	Db	5992	CATCTATCAGCCCCCTGAGGGCAATGCCCTCAGTTCATACAGGACTTCACTGAGGATGGCA	6051
QY	4966	CCAGATGGCCAGGTGTACTGGGTGACCATGGGCACCAACAGTGCACCTCAAGAGTGTGAC	5025	QY	6025	CCTCCTTACACACCTTCTACCTGGGCACCTGGCCGCAAGSGTGATATACAAGTATGGCAAACT	6084
Db	4972	CCAGATGGCCAGGTGTACTGGGTGACCATGGGCACCAACAGTGCACCTCAAGAGTGTGAC	5031	Db	6052	CCTCCTTACACACCTTCTACCTGGGCACCTGGCCGCAAGSGTGATATACAAGTATGGCAAACT	6111
QY	5026	CACACAAGGACACGAGTTGGCCATGATGACATACCATGGCAATTCGGGCCTTCTGGCAAC	5085	QY	6085	GTCAAAAGCTGGCAGAGACCGTCTATGACACCACCAAGGTCAGTTTCACCTATGACGAGAC	6144
Db	5032	CACACAAGGACACGAGTTGGCCATGATGACATACCATGGCAATTCGGGCCTTCTGGCAAC	5091	Db	6112	GTCAAAAGCTGGCAGAGACCGTCTATGACACCACCAAGGTCAGTTTCACCTATGACGAGAC	6171
QY	5086	CAAAAGCAATGAAAAACGGATGGACAACATTTATGAGTACGACAGCTTTGGCCCGCTGAC	5145	QY	6145	GGCAGGCATGCTGAAGACCATCAACCTACAGAAATGAGGCTTACCTGCACCATCCGCTA	6204
Db	5092	CAAAAGCAATGAAAAACGGATGGACAACATTTATGAGTACGACAGCTTTGGCCCGCTGAC	5151	Db	6172	GGCAGGCATGCTGAAGACCATCAACCTACAGAAATGAGGCTTCACTGCACCATCCGCTA	6231
QY	5146	AAATGTGACTTCCCTACTGGCCAGGTGAGCAGTTTCCGAAGTGATACAGACAGTTTCAGT	5205	QY	6205	CCGTGAGATTGGGCCCTCTGATTGACCGACAGATCTTCGCTTCACTGAGGAAGGCATGGT	6264
Db	5152	AAATGTGACTTCCCTACTGGCCAGGTGAGCAGTTTCCGAAGTGATACAGACAGTTTCAGT	5211	Db	6232	CCGTGAGATTGGGCCCTCTGATTGACCGACAGATCTTCCGCTTCACTGAGGAAGGCATGGT	6291
QY	5206	GCATGTCCAGGTAGAGACCTCCAGCAGGATGATGTCAACCATTAACCAACCTGTCTGC	5265	QY	6265	CAACGCCCGTTTTTGACTACAACTATGACAAACAGCTTCCGSGTGACCAGCATGCAGGCTGT	6324
Db	5212	GCATGTCCAGGTAGAGACCTCCAGCAGGATGATGTCAACCATTAACCAACCTGTCTGC	5271	Db	6292	CAACGCCCGTTTTTGACTACAACTATGACAAACAGCTTCCGSGTGACCAGCATGCAGGCTGT	6351
QY	5266	CTCAGGCGCCTTCTACACACTGCTGCAAGACCAAGTCCGGAAACAGCTACTACATCGGGGC	5325	QY	6325	GATCAACGAGACCCCACTGCCCCATTGATCTCTATCGCTATGATGTGTGAGGCAAGAC	6384
				Db	6352	GATCAACGAGACCCCACTGCCCCATTGATCTCTATCGCTATGATGTGTGAGGCAAGAC	6411



Qy	6385	AGAGCAGTTTGGGAAGTTTGGTGTCA	TTTACTATGACATTAACCAGATCATCACCACAGC	6444	
Db	6412	AGAGCAGTTTGGGAAGTTTGGTGTCA	TTTACTATGACATTAACCAGATCATCACCACAGC	6471	
Qy	6445	TGTCATGACCCACACCAAGCATTTT	TGATGCATATGGCAGGATGAAGGAAGTGCAGTATGA	6504	
Db	6472	TGTCATGACCCACACCAAGCATTTT	TGATGCATATGGCAGGATGAAGGAAGTGCAGTATGA	6531	
Qy	6505	GATCTTCCGCTCGTCA	TGATGTACTGGATGACCGTCCAGTATGATAACATGGGGCGAGTAGT	6564	
Db	6532	GATCTTCCGCTCGTCA	TGATGTACTGGATGACCGTCCAGTATGATAACATGGGGCGAGTAGT	6591	
Qy	6565	GAAGAAGGAGCTGAAGGTAGGACCC	CTACGCCAATACCACCTCGTACTCTCTATGAGTATGA	6624	
Db	6592	GAAGAAGGAGCTGAAGGTAGGACCC	CTACGCCAATACCACCTCGTACTCTCTATGAGTATGA	6651	
Qy	6625	TGCTGACGGCCAGCTGCAGACAGT	CTCCATCAATGACAAGCCACTCTGGCGCTACAGCTA	6684	
Db	6652	TGCTGACGGCCAGCTGCAGACAGT	CTCCATCAATGACAAGCCACTCTGGCGCTACAGCTA	6711	
Qy	6685	CGACCTCAATGGGAACCTGCAC	TTACTGAGCCCTGGGAACAGTGCAACGGCTCACACCACT	6744	
Db	6712	CGACCTCAATGGGAACCTGCAC	TTACTGAGCCCTGGGAACAGTGCAACGGCTCACACCACT	6771	
Qy	6745	ACGGTATGACATCCGGACCGCAT	CACCTCGGCTGGGTGACGTGCAATACAGATGGATGA	6804	
Db	6772	ACGGTATGACATCCGGACCGCAT	CACCTCGGCTGGGTGACGTGCAATACAGATGGATGA	6831	
Qy	6805	GGATGGCTTCTTGAGGACGGGG	CGGTGATATCTTTGAGTACAACCTCAGCTGGCCTTGCT	6864	
Db	6832	GGATGGCTTCTTGAGGACGGGG	CGGTGATATCTTTGAGTACAACCTCAGCTGGCCTTGCT	6891	
Qy	6865	CATCAAGGCCTACAACCGGGCT	GGCAGCTGGAGTGCAGGTACCGCTACGATGGCCTGGG	6924	
Db	6892	CATCAAGGCCTACAACCGGGCT	GGCAGCTGGAGTGCAGGTACCGCTACGATGGCCTGGG	6951	
Qy	6925	GCGGCGCGTGTCCAGCAAGAG	CAGCAGCCACCGCTGCAGTTCTTCTATGCAGACCT	6984	
Db	6952	GCGGCGCGTGTCCAGCAAGAG	CAGCAGCCACCGCTGCAGTTCTTCTATGCAGACCT	7011	
Qy	6985	GACCAACCCACCAAGGTCA	CCCCACCTGTACAACCACTCCAGCTCTGAGATCACCTCCCT	7044	
Db	7012	GACCAACCCACCAAGGTCA	CCCCACCTGTACAACCACTCCAGCTCTGAGATCACCTCCCT	7071	
Qy	7045	CTACTACGACTTGCAAGGAC	ACCCTCTTTGCCATGGAGCTGAGCAGTGGTGATCAGTTT	7104	
Db	7072	CTACTACGACTTGCAAGGAC	ACCCTCTTTGCCATGGAGCTGAGCAGTGGTGATCAGTTT	7131	
Qy	7105	CATAGCTTGTGACAAACAT	CGGACCCCTCTTGCTGTCTTTAGTGGAACAGGTTTGATGAT	7164	
Db	7132	CATAGCTTGTGACAAACAT	CGGACCCCTCTTGCTGTCTTTAGTGGAACAGGTTTGATGAT	7191	
Qy	7165	CAAGCAAAATCCTGTAC	ACAGCCTATGGGGAGATCTACATGGATACCAACCCCACTTTCA	7224	
Db	7192	CAAGCAAAATCCTGTAC	ACAGCCTATGGGGAGATCTACATGGATACCAACCCCACTTTCA	7251	
Qy	7225	GATCATCATAGGCTACCAT	TGGTGGCCTCTATGATCCACTCACC	AAAGCTTGTCCACATGGG	7284
Db	7252	GATCATCATAGGCTACCAT	TGGTGGCCTCTATGATCCACTCACC	AAAGCTTGTCCACATGGG	7311
Qy	7285	CCGGCGAGATTATGAT	TGCTGGCCGGACCGCTGGACTAGCCAGACCGAGCTGTGGAA	7344	
Db	7312	CCGGCGAGATTATGAT	TGCTGGCCGGACCGCTGGACTAGCCAGACCGAGCTGTGGAA	7371	
Qy	7345	GCACCTTAGTAGCAGCA	ACGTCATGCCCTTTTAATCTCTATATGTTCAAAAACAACAACCC	7404	
Db	7372	GCACCTTAGTAGCAGCA	ACGTCATGCCCTTTTAATCTCTATATGTTCAAAAACAACAACCC	7431	
Qy	7405	CATCAGCAACTCCCAGG	ACATCAAGTGCTTCATGACAGATGTTAACAGCTGGCTGCTCAC	7464	
Db	7432	CATCAGCAACTCCCAGG	ACATCAAGTGCTTCATGACAGATGTTAACAGCTGGCTGCTCAC	7491	

Qy	7465	CTTTGGATTCCAGCTACACAAC	CGTGATCCCTGGTTATCCCAAACCCAGACATGGATGCCAT	7524
Db	7492	CTTTGGATTCCAGCTACACAAC	CGTGATCCCTGGTTATCCCAAACCCAGACATGGATGCCAT	7551
Qy	7525	GGAACCCCTCTACGAGCTCAT	CCACACACAGATGAAAAACGAGGAGTGGGACAAACAGCA-	7583
Db	7552	GGAACCCCTCTACGAGCTCAT	CCACACACAGATGAAAAACGAGGAGTGGGACAAACAGCAA	7611
Qy	7584	-----	-----AGTCTATCTCTCGGGGTACAGTGTGAAGTACAGAAGCA	7620
Db	7612	GGTAATTCTCTGCACAAGGCT	GCCAGTCTATCTCTCGGGGTACAGTGTGAAGTACAGAAGCA	7671
Qy	7621	GCTCAAGGCCCTTTGTACCT	TTAGAACGGTTTGACCAGCTCTATGGGTCCACAATCACCCAG	7680
Db	7672	GCTCAAGGCCCTTTGTACCT	TTAGAACGGTTTGACCAGCTCTATGGGTCCACAATCACCCAG	7731
Qy	7681	CTGCCAGCAGGCTCCAAAG	ACCAAGATTTGCATCCAGCGGCTCAGTCTTTGGCAAGGG	7740
Db	7732	CTGCCAGCAGGCTCCAAAG	ACCAAGATTTGCATCCAGCGGCTCAGTCTTTGGCAAGGG	7791
Qy	7741	GGTCAAGTTTGCCTTGAAG	GATGGCCGAGTGACCAACAGACATCATCAGTGTGGCCCAATGA	7800
Db	7792	GGTCAAGTTTGCCTTGAAG	GATGGCCGAGTGACCAACAGACATCATCAGTGTGGCCCAATGA	7851
Qy	7801	GGATGGCGAAGGTTGCTG	CCATCTTGAACCATGCCACTACCTAGAGAACCTGCACCT	7860
Db	7852	GGATGGCGAAGGTTGCTG	CCATCTTGAACCATGCCACTACCTAGAGAACCTGCACCT	7911
Qy	7861	CACCATTTGATGGGTGATA	CCCCATTACTTTGTGAAAAACAGGACCTTCAGAAAGGTGACCT	7920
Db	7912	CACCATTTGATGGGTGATA	CCCCATTACTTTGTGAAAAACAGGACCTTCAGAAAGGTGACCT	7971
Qy	7921	GGCCATCCTGGGCTCAGT	GGGGGGCGGGAACCTTGAGAAATGGGGTCAACGTCACTGT	7980
Db	7972	GGCCATCCTGGGCTCAGT	GGGGGGCGGGAACCTTGAGAAATGGGGTCAACGTCACTGT	8031
Qy	7981	GTCCAGATCAACACAGTA	CTTAATGGCAGGACTAGACGCTACACAGACATCCAGCTCCA	8040
Db	8032	GTCCAGATCAACACAGTA	CTTAATGGCAGGACTAGACGCTACACAGACATCCAGCTCCA	8091
Qy	8041	GTACGGGGCACTGTGCTT	TGAACACACGCTACGGGACAAACGTTGGATGAGGAGAGGCACG	8100
Db	8092	GTACGGGGCACTGTGCTT	TGAACACACGCTACGGGACAAACGTTGGATGAGGAGAGGCACG	8151
Qy	8101	GGTCTGGAGCTGCCCGG	CAGAGAGCCGTGCGCCAAAGCGTGGGCCCGGAGCAGAGAG	8160
Db	8152	GGTCTGGAGCTGCCCGG	CAGAGAGCCGTGCGCCAAAGCGTGGGCCCGGAGCAGAGAG	8211
Qy	8161	ACTCGGGAAGGGAGGAAG	CGCCTGCGGGCTTGACAGAGGGGGGAGAACGACAGGTGCT	8220
Db	8212	ACTCGGGAAGGGAGGAAG	CGCCTGCGGGCTTGACAGAGGGGGGAGAACGACAGGTGCT	8271
Qy	8221	GAGCACAGGGCGGTC	CAAGGCTACGACGGCTTTTCTGTGATCTCTGTCTGAGCAGTACCC	8280
Db	8272	GAGCACAGGGCGGTC	CAAGGCTACGACGGCTTTTCTGTGATCTCTGTCTGAGCAGTACCC	8331
Qy	8281	AGAACTGTCAGACAGCG	CCAAACAATCCACTTCATGAGACAGAGCGAGATGGGCCGGAG	8340
Db	8332	AGAACTGTCAGACAGCG	CCAAACAATCCACTTCATGAGACAGAGCGAGATGGGCCGGAG	8391
Qy	8341	GTGACAGAGAGGAC	8354	
Db	8392	GTGACAGAGAGGAC	8405	

RESULT 4	
AB025413	
LOCUS	AB025413
DEFINITION	Mus musculus mRNA for Ten-m4, complete cds.
ACCESSION	AB025413
VERSION	AB025413.1
KEYWORDS	Ten-m4.
SOURCE	Mus musculus (house mouse)

8585 bp mRNA linear ROD 08-MAY-1999





Db 995 ATTCTCAGCGCCTCCCGCCATGATGGGGCTTACAGTACGGGCACCTTCCTCTTCAAGCCC 1054

QY 902 GGAGGCACCTCCCCGGCTCTTCTGCACCACATCACAGGGTACCCACTGACGTCCAGCAC 961

Db 1055 GGAGGCACCTCCCCGGCTCTTCTGCACCACATCCCCAGGGTACCCCTTAACGTCTAGCACC 1114

QY 962 GTGTACTCTCCCTCCGCCCCGACCCCTGCCCCCGCAGCACCTTCGCCCGGCCCGCCTTTAAC 1021

Db 1115 GTGTACTCGCCCCCAACCCCGGCCCTGCCCCCGCAGCACCTTCTCCGACCAGCCTTTAAC 1174

QY 1022 CTCAAGAAAGCCCTCAAAGTACTGTAACCTGGAAGTGGCGAGCCCTGAGCGCCATCGTCATC 1081

Db 1175 CTCAAGAAAGCCTTCCAAGTACTGCAACTGGAAGTGTGACGCGCTGAGCGCCATCCTCATC 1234

QY 1082 TCAGCCACTCTGGTCACTCCTGCTGGCATACTTTGTGGCCATGCACCTGTTTGGCCTAAAC 1141

Db 1235 TCAGCTACGCTCGTCACTCCTGCTCGCATACTTTGTGGCCATGCACCTGTTTGGCCTAAAC 1294

QY 1142 TGGCACCTGCAGCCGATGGAGGG- - - - GCAGATGTATGAGATCACGGAGGACACAGCC 1195

Db 1295 TGGCACCTGCAGCCGATGGAGGGCAGATGCAGATGTATGAGATCACGGAGGACACAGCC 1354

QY 1196 AGCAGTTGGCCTGTGCCAACCGACGCTCTCCCTATACCCCTCAGGGGGCACTGCTTAGAG 1255

Db 1355 AGCAGCTGGCCTGTGCCAACCGACGCTCTCCCTGTATCCCTCAGGGGGCACCTGGCTTAGAG 1414

QY 1256 ACCCTTGACAGGAAAGCAAAGGAACACAGAAAGGAAGCCAGTAGTTTCTTCCAGAG 1315

Db 1415 ACCCTTGACAGGAAAGCAAAGGAGCCGCAGAAAGGAAGCCAAAGTAGTTTATTTCCAGAG 1474

QY 1316 GACAGTTTCATAGATTCTGGAGAAATTGATGTGGGAAGCGAGCCTCCCAGAAGATTCCCT 1375

Db 1475 GACAGTTTATAGATTCTGGAGAAATCGATGTGGGAGACGGGCTTCCCAGAAGATTCCG 1534

QY 1376 CCTGGCACTTCTGGAGATCTCAAGTGTTTCATAGACCATCCTGTGCATCTGAAATTCAAT 1435

Db 1535 CCTGGAACGTTCTGGAGATCTCAGGTGTTTCATAGACCACCCCTGTACACCTGAAGTTCAAT 1594

QY 1436 GTGTCTCTGGGAAAGGCACCCCTGGTTGGCATTTATGGCAGAAAAGGCCCTCCCTCTCA 1495

Db 1595 GTGTCTCTGGGAAAGCAGCTCTGGTTGGCATTTATGGCAGAAAAGGCCCTTCTCCTTCC 1654

QY 1496 CATAACAGTTTGACTTTGTGGAGCTGTGGATGGCAGGAGGCTCCTAACCCAGGAGCG 1555

Db 1655 CATACTCAGTTTGACTTTGTGGAGCTCCTGGATGGAAAGAGGCTCCTAACCCAGAGGCA 1714

QY 1556 CGGAGCCTAGAGGGGACCCCGCCAGTCTCGGGAACTGTGCCCCCTCCAGCCATGAG 1615

Db 1715 AGGAGCCTGGAGGTCCTCAGCGCCAATCACGGGGCCCTGTTCGCCCATCCAGCCATGAG 1774

QY 1616 ACAGGCTTCATCCAGTATTTGGATTCAGGAATCTGGCAATCTGGCACTTGGCTTTTACAATGACGGA 1675

Db 1775 ACCGGTTTCATCCAGTATCTGGATTCAGGAATCTGGCACTTGGCCTTTTACAATGATGGA 1834

QY 1676 AAGGAGTCAGAAAGTGGTTTCCTTCTCACCACTGCCAATTGAGTCGGTGGATACTGCCCC 1735

Db 1835 AAAGAAATCTGAAGTGGTTTCATTTCTCACCCACCGCCATGAAATCAGTGGATACTGCCCC 1894

QY 1736 AGCAACTGCTATGGCAATGGTGAATGCTCTGGGAGCTGCCACTGCTTCTCGGGTTTC 1795

Db 1895 AGCAACTGCTATGGTAACGCTGACTGCAATTTCCGGGAGCTGCCACTGCTTCTCGGGTTT 1954

QY 1796 CTGGGCCCCGACTGTGGCAGAGCCTCTGCCCCGCTGCTCTGTAGCGGAAATGGCCAATAC 1855

Db 1955 CTGGGCCCCTGACTGTGGCCGAGCATCCTGTCCCGTGTGTGAGTGGGACGGCCAGTAC 2014

QY 1856 ATGAAAGGCAGATGCTTGTGCCACAGTGGCTGGAAGSGCGCTGAGTCGATGTGCCACCC 1915

Db 2015 ATGAAAGGCAGGTGCCTGTGCCACAGTGGCTGGAAGSGGTGCCGAATGTGACGTGCCACC 2074

QY 1916 AACCAGTGTATCGATGTGGCCTGCAGCAACCATGGCACTGCATCACGGGCACCTGCATC 1975

Db 2075 AACCAAGTGTATCGACGTGGCCTGCAGCAGTTCATGGCACCTGCATCATGGGCACCTGCATC 2134

QY 1976 TGCAACCCCTGGCTACAAGGGCGAGAGCTGTGAGGAAGTGGAATGCATGGACCCACATGT 2035

Db 2135 TGCAACCCCGGCTACAAGGGCGAGAGCTGCGAGGAAGTGGAATGCATGGACCCACATGT 2194

QY 2036 TCAGGCCGGGTGTCTGCGTGAGAGAGGCGGAATGCCATTGCTTTGTGGGATGGGAGGCACC 2095

Db 2195 TCCAGCAGGGGTGTCTGTGTCTAGAGGCGAGTGCACACTGCTCTGTGGGATGGGAGGCACC 2254

QY 2096 AACTGCGAGACCCCCAGGGCCACATGCTTAGACCAGTGTTCAGGCCACGGAACTTCCTC 2155

Db 2255 AACTGCGAGACACCCAGGGCCACATGCTTGGACCAGTGTCTAGGCCACGGAACTTTCCTC 2314

QY 2156 CCGGACACCCGGCTTTTGACGCTGTGACCCCAAGCTGGACTGGACACGACTGTTCTATCGAG 2215

Db 2315 CCAGACACAGGACTTTTGCAACTGTGACCCCAAGCTGGACTGGACACGACTGTTCCATTGAG 2374

QY 2216 ATCTGTCTGCCGACTGTGGTGGCCATGGCGTGTGCGTAGGGGGCACCTGCCGCTGCGAG 2275

Db 2375 ATCTGTCCGCTGACTGTGGTGGCCATGGCGTCTGCGTAGGAGGCACCTGCCGCTGTGAG 2434

QY 2276 GATGGCTGGAATGGGGCAGCCTGCGACCGAGCGGGCCTGCCACCCGCGCTGTGCCGAGCAT 2335

Db 2435 GATGGTTGGATGGGGCCCGCATGCGACCAACCGGCCCTGCCACCCACGCTGTGCAGAACAC 2494

QY 2336 GGGACCTGCCGACGGCAAGTGCAGTGCAGCCCTGGCTGGAATGGCGAACTGCACCC 2395

Db 2495 GGGACCTGCCGGGACGGCAAGTGCGAATGCAGCCCGGCTGGAATGGAGAGCACTGCACC 2554

QY 2396 ATCGCTCACTATCTGGATAGGGTAGTTAAAGAGGGTTGCCCTGGGTGTGCAATGGCAAC 2455

Db 2555 ATCGCTCACTATCTGGATAGGGTAGTTAAAGAGGGCTGTCTGGCTGTGCAATGGAAAT 2614

QY 2456 GGCAGATGTACCTTAGACCTGAATGGTTGGCACTGCGTCTGCCAGCTGGGCTGGAGAGGA 2515

Db 2615 GGCAGATGTACCCCTGGACCTGAATGGGTGGCACTGTGTCTGCCAGCTGGGCTGSCGAGGG 2674

QY 2516 GCTGGCTGTGACACTTCCATGGAGACTGCCCTGCGGTGACAGCAAGACAATGATGGAGAT 2575

Db 2675 ACTGGCTGCGACACATCCATGGAAACGGGCTGTGAGACGGCAAGGACAACGACGGAGAT 2734

QY 2576 GGCCTGGTGGACTGCATGGACCCCTGACTGTCTGCCCTCAGCCCTGTGCCATATCAACCCG 2635

Db 2735 GGCCTGGTGGACTGCATGGACCCCTGACTGTCTGCCCTCAGCCTCTCTGTATGTCAACCCG 2794

QY 2636 CTGTGCCCTTGGCTCCCTTAACCCCTCTGGACATCATCCAGGAGACACAGGTCCCTGTGTCA 2695

Db 2795 CTGTGCCCTAGGCTCCCTTGACCCCTCTGGACATCATCCAAGAGACACAGGCCCTGTATCC 2854

QY 2696 CAGCAGAACCTTACACTCCTTCTATGACCCGCATCAAGTTCTCGTGGGCAAGGACACGACG 2755

Db 2855 CAGCAGAACCTGAAACCCCTTCTACGATCGAATCAAGTTCTCGTGGGCAAGGACAGCACA 2914

QY 2756 CACATAATCCCCGGGAGAAACCCCTTTGATGGAGGGCATGCTTGTGTTATTCTGTGGCCAA 2815

Db 2915 CACAGCATCCCCGGGAGAAACCCCTTTGACGGAGGGCATGCTTGTGTCTATCCGTGGACAA 2974

QY 2816 GTGATGACATCAGATGGAACCCCTGGTTGGTGGTGAACATCAGTTTTGTCAATAACCT 2875

Db 2975 GTGATGACGTGAGATGGGACCCCATTTGGTTGGCGTGAACATCAGTTTTCATCAATAACCT 3034

QY 2876 CTCTTTGGATATACAATCAGCAGGCAAGATGGCAGCTTTGACTTGGTGACAAAATGGCGGC 2935

Db 3035 CTCTTTGGATACACAAATCAGCAGGCAAGATGGCAGCTTTGACCTGGTCACAAAATGGCGGC 3094

QY 2936 ATCTCCATCATCCTCGGCTTCGAGCGGGCACCTTTTCATCACACAGGAGCACACCTCTTGG 2995

Db 3095 ATCTCCATCATCTTGAGATTGAAAGGGCACCCCTTCATCACACAGGAGCATACCTCTTGG 3154

QY 2996 CTGCCATGGGATCGCTTCTTTGTGATGGAAACCATCATCATGAGACATGAGGAGAAATGAG 3055

Db 3155 CTACCCCTGGGATCGCTTCTTTGTGATGGAAACCATCGTTCATGAGACACGAGGAGAAATGAG 3214



QY	3056	AT	TCCAGCTGTGACCTGAGCAAA	TTTGCCCGCCCAACCCAGT	CGTCTCTCCATCCCCA	3115
Db	3215	AT	CCCCAGCTGTGACCTGAGCAAC	TTTGCCCGTCCCAACCCGTGTGGT	CTCTCCATCCCCA	3274
QY	3116	CT	GACGTCTTCGCCAGCTCCTGTG	CAGAGAAAGSCCCCATTTGTG	CCGGAATTCAGGCT	3175
Db	3275	CT	GACATCATTCGCCAGCTCCTGTG	CTGAGAAAGSCCCCATTTGTCC	CAGAAATCCAGGCC	3334
QY	3176	TT	GAGGAGGAATCTCTATCTCTGG	CTGCAAGATGAGGCTGAGCTAC	CTGAGCAGCCGG	3235
Db	3335	CT	GCAAGGGAATCGTCATCGCTGG	CTGCAAGATGAGGTTGAGCTAC	CTGAGCAGCCGC	3394
QY	3236	AC	CCCTGGCTACAAATCTGTCCTG	AGGATCAGCCTCACCCACCGAC	CCATCCCCCTTCAAC	3295
Db	3395	AC	TCTGGCTATAAGTCTGTCTGAG	GATCAGTCTACACACCCCAAC	CCATCCCCCTTCAAC	3454
QY	3296	CT	CATGAAGGTGCACCTCATGGT	AGCGGTGAGGCGCGCTCTTTC	CAGGAAGTGGTTCGCT	3355
Db	3455	CT	CATGAAGGTCCACCTCATGGT	GGCAGTCGAGGTCGGCTCTTC	CAGGAAGTGGTTGCC	3514
QY	3356	GC	AGCCCCAGACCTGTCTTATTT	TCATTTGGGACAAGACAGACG	TCTACAAACAGAAG	3415
Db	3515	GC	AGCTCTGACCTGTCTTATCTTC	ATCTGGGACAAGACAGATGTCT	ACAAACAGAAG	3574
QY	3416	GT	GTTTGGCTTTCAGAAAGCCTTT	TGTTTCCGTGGTTATGAATAT	GAATCCTGCCAGAT	3475
Db	3575	GT	GTTTGGATTCTCAGAAAGCCT	TTGTTTCCGTGGTTATGAGTAT	GAATCCTGCCAGAT	3634
QY	3476	CT	AAATCCTGTGGGAAAAAAGAA	ACAGTGCTGCAGGGCTATGAA	ATTGACCGCTCAAG	3535
Db	3635	CT	GATCCTGTGGGAGAAAGGAC	AGCGGTGCTGCAGGGCTATGAA	ATTGATGCCTCAAG	3694
QY	3536	CT	TGAGGATGGAGCCTAGACAA	ACATCATGCCCTCAACATTCAA	AGTGGTATCCTGCAC	3595
Db	3695	CT	TGGGGCTGGAGTCTGGATA	AGACCATGCCCTGAACAATCC	AGAGTGGCATCCTGCAC	3754
QY	3596	AA	AGGAATGGGAGAACCAAGTTT	TGTGTCTCAGCAGCCTCTGTCT	CATTGGGAGCATATG	3655
Db	3755	AA	AGGAATGGAGAGAACCAAGTT	TGTGTCTCCAGCAGCCACCGG	TCTATCGGAGCATATG	3814
QY	3656	GG	CAATGGCGCGGAGAAAGCAT	CTCCTGCCCCAGCTGCAACGG	CCTTGTGACGGCAAC	3715
Db	3815	GG	CAATGGCGCAGGAGAAAGTAT	CTCCTGCCCCAGCTGCAATGG	TCTTGTATGGCAAC	3874
QY	3716	AA	GCTCCTGGCCCCAGTGGCCCT	CACCTGTGGCTCTGACGGAG	CCCTCTATGTGGGTGAT	3775
Db	3875	AA	GCTCCTGGCCCCCGTGGCCCT	CACCTGCGGCTCTGATGGG	AGTCTCTACGTGGGAGAC	3934
QY	3776	TT	CACTACATTAGAAGGATCTTC	CCCTCTGGAAATGTCAACCA	ATCCTAGAGCTGAGG	3835
Db	3935	TT	CACTACATCCGCAGAAATCT	TCCCTCTGGAAATGTCAACA	ATCCTGGAGATGAGA	3994
QY	3836	AA	TAAAGATTTCAGACATAGTCA	AGTCCAGCACACAAATACTAC	CTGGCCACAGACCCC	3895
Db	3995	AA	TAAAGATTTCAGACATAGTCA	AGTCCAGCACACAAATACTAC	CTGGCTACAGACCCC	4054
QY	3896	AT	GAGTGGGCGCGTCTTCCTTT	CTGACAGCAACAGCCGGG	GTCTTTAAATCAAGTCC	3955
Db	4055	AT	GAGTGGGCGCGTCTTCCTGT	CTGACACCAACAGCCGGCGG	GTCTTCAAGGTCAAGTCC	4114
QY	3956	AC	TGTGGTGAAGGACCTTGTCTA	AGAACTCTGAGGTGGTTTGG	GGGACAGGTGACCAG	4015
Db	4115	ACC	ACAGTGTGAAGGACCTGGTGA	AGAACTCCGAGGTGGTAGC	AGGACTGGTGACCAG	4174
QY	4016	TG	CTCCCCCTTTGATGACACTCG	CTGCGGGATGGTGGGAAGSC	CAACAGAACCCACACTC	4075
Db	4175	TG	CTCCCCCTTTGATGATACCC	GTGCGGAGATGGTGGGAAG	SCCAAGCCACAGACGCTC	4234
QY	4076	AC	CAATCCAGGGGTATTACAGT	GGACAAAGTTTGGGCTGAT	CTACTCTCGTGGATGGCACC	4135
Db	4235	ACT	AACCCAGGGGAATTACAGT	GGACAAAGTTTGGGCTCAT	TTTATTTCTGTGGACGGCACC	4294
QY	4136	AT	GATCAGACGCATCGATCAGAA	ATGGGATCATCTCCACCCTG	CTCGGCTCTAATGATCTC	4195
Db	4295	AT	GATCAGACGTGTTGATCAAAA	ATGGAATCATCTCCACTTTG	CTGGCTCCAATGACCTC	4354
QY	4196	AC	ATCAGCCCGCCCACTCAGCT	GTGATTTCTCATGATATTTCC	CAGGTAAGACTGGAG	4255
Db	4355	AC	CTCGGCCAGGCCCTCAGCT	GTGACTCGTCAATGGAGATT	TCTCAGGTTGCGCTGGAG	4414
QY	4256	TG	CCCCACAGACTTAGCCATCA	ACCCCAATGGACAACTCAC	TTTATGTCTCGACAACAAT	4315
Db	4415	TG	CCCCACAGACTTAGCCATCA	ACCCCAATGGATAATTCTCT	CTATGTCTCGACAACAAT	4474
QY	4316	GT	GTCTCTGTCAAAATCTCTGA	AAAAACCAAGGTGCGCATTT	GCGGAGGCCCATGCAC	4375
Db	4475	GT	GTCTCTGTCAAAATCTCCGA	AAACCAAGGTAGCATTTG	CTGGAGGCCCATGCAC	4534
QY	4376	TG	CCAGGTCCCTGGCATTTGAC	CACTTCTCTGCTAAGCAAG	TGGCCATCCACGCAACCTG	4435
Db	4535	TG	CCAGGTCCCTGGCATCGACC	CACTTCTGCTGAGCAAGTA	GCCATCCATGCGGACCCTG	4594
QY	4436	GAG	TCAGCCACCGCTTTGGCTGT	TTTCAACAATGGGGTCTCT	GTATATTGCTGAGACTGAT	4495
Db	4595	GAG	TCAGCCACTGCTCTGGCCG	TTTCAACAATGGAGTCTTG	TACATCGCTGAGACCGAC	4654
QY	4496	GAG	AAAAAGATCAACCGCATCAG	GCGGTACCACTAGTGGAGAT	CTCACTCGTTGCT	4555
Db	4655	GAG	AAAAAGATCAATCGCATCAG	GCGGTACTACAAGTGGTGA	GATCTCACTGGTTGCT	4714
QY	4556	GG	GGCCCCCAGTGGCTGTGACT	GTAAAAATGATGCCAACTGT	GATTGTTTCTGGAGAC	4615
Db	4715	GG	TGCCCCCAGTGGCTGTGACT	GTAAAAATGATGCCAACTGT	GACTGCTTCTCTGGAGAT	4774
QY	4616	GAT	GGTTATGCCAAGGATGCAAA	AGTTAAATACCCCATCTTCT	TGGCTGTGTGTGCTGAT	4675
Db	4775	GAT	GGTTACGCCAAGGATGCAAA	AGTGAATACCCCATCGTCT	TGGCTGTGTGTGCTGAC	4834
QY	4676	GG	GAGCTCTACGTGGCCGACCT	TGGGAACATCCGAATTCGG	TTTATCCGGAAGAACAAAG	4735
Db	4835	GG	GAGCTCTATGTGGCCGACCT	TGGGAACATCCGAATTCGA	TTTATCCGGAAGAACAAAG	4894
QY	4736	CT	TTCTCAACACCCAGAACATG	TATGAGCTGTTTACCCTTAC	CAAAATTGACCAGGAGCTCTAT	4795
Db	4895	CT	TTCTGAACACCTCAGAACAT	GTACGAGCTATCTCCCCCAT	CGACCAGGAGCTGTAC	4954
QY	4796	CT	TTTGATACCCGCAAGCACCT	GTACACCCAAAGCTGCCCA	CAGGAGACTACTCTG	4855
Db	4955	CT	TTTGATACCCAGTGSAAAGCA	TCTGTACACTCAGAGCCTAC	CCACAGGGGACTACCTG	5014
QY	4856	TACA	ACTTCACTACCTGCGGACG	GCGACATCACACTCATCAC	AGACAAATGGCAAC	4915
Db	5015	TACA	ACTTCACTACAGGGGACGGG	ACATCACACATATCACCGA	CAACAAATGGCAAC	5074
QY	4916	AT	GTAAATGTCCGCCGAGACT	CTACTGGGATGCCCTCTTG	GCTGGTCCCAGATGGC	4975
Db	5075	AT	GTGAACGTCCGCCGAGACTCT	ACCGGATGCCTCTCTGGT	GGTAGTCCCAGATGGC	5134
QY	4976	CAG	GTGTACTGGGTGACCAATGG	GCACCAACAGTGTGACCA	CACAAGGA	5035
Db	5135	CAG	GTATACTGGGTAACCATGGG	CAACCAACAGGCACTCAGA	AGTGTGACCAACAAGGA	5194
QY	5036	CAC	GAGTTGGCCATGATGACATA	CCATGGCAATTCGGCTTCT	TGGCAACCAAAAGCAAT	5095
Db	5195	CAC	GAGCTAGCCATGATGACATA	CCATGGCACTCTGGCTCT	TGGCAACCAAAAGCAAT	5254
QY	5096	GAAA	CCGATGGACAAATTTTATGA	TGACGAGCTTTGGCGCCT	TGACAAATGTGACC	5155
Db	5255	GAAA	CCGGTGGACAAACGTTTAT	GATGATGACAGTTTGTG	CTGCTGACAAACGTGACC	5314
QY	5156	TT	CCCTACTGGCCAGGTGAGCA	GTTCGGAAGTGATACAGAC	AGTTCAGTGCATGTCCAG	5215
Db	5315	TT	TCCAACTGGCCAGGTGAGCA	GTTCGGAAGCGATACAGAC	AGCTCAGTGCACGTGCAG	5374
QY	5216	GT	AGACCTCCAGCAAGGATGA	TGTCAACCAACCACTGTCT	GCTCTGCTCAGGCGCC	5275



Db 5375 GTAGAGACCTCAAGCAAAAGATGACGTCAACCATAACCAACCAACCTGTCTGCTTCGGGTGCC 5434  
QY 5276 TTCTACACACTGCTGCAAGACCAAGTCCGGAACAGCTACTACATCGGGGCGGATGGCTCC 5335  
Db 5435 TTCTACACCCCTGTTACAAGACCAAGTCCGGAACAGCTACTACATCGGGGCTGATGGCTCC 5494  
QY 5336 TTGCGGCTGCTGCGCCAAACGGCATGGAGGTGGCGCTGCAGACTGAGCCCCACTTGGTG 5395  
Db 5495 CTGAGGCTGCTACTAGCCAAATGGCATGGAAATGGCTCTGCAGACTGAGCCACACCTGCTG 5554  
QY 5396 GCTGGCACCGTCAACCCCAACCGTGGGCAAGAGGAATGTACGCTGCCATCGACAACGGC 5455  
Db 5555 GCTGGCACTGTCAACCCCACTGTAGGCAAGAGGAATGTACACTGCCCAATTGATAATGGC 5614  
QY 5456 CTCAACCTGGTGGAGTGGCGCCAGCGCAAGAGCAGGCTCGGGGCCAGGTCACTGTCTTT 5515  
Db 5615 CTCAACCTGGTGGAGTGGCGGCAGCGCAAGGAGCAGGCTCGTGGCCAGGTCAACCGTCTTT 5674  
QY 5516 GGGCGCCGGCTGCGGGTGCAAAACCGAAATCTCCTATCTCTGGACTTTGATCGCGTAACA 5575  
Db 5675 GGACGCCGTCTGCGGGTTCAAAACCGAAACCTTGTCTTTGGACTTTGACCGGTGCACA 5734  
QY 5576 CGCACAGAGAAGATCTATGATGACCACCGCAAGTTCACCCCTTCGGATTCTGTACGACCAG 5635  
Db 5735 CGCACAGAGAAGATCTACGATGACCATCGCAAGTTCACCCCTTCGGATCCTATATGACCAG 5794  
QY 5636 GCGGGGCGGCCAGCCTCTGGTCACCCAGCAGCAGGCTGAATGGTGTCAACGTGACATAC 5695  
Db 5795 GCAGGGAGGCCAGCCTCTGGTCACCTAGCAGCAGGCTGAATGGTGTAAATGTGACCTAC 5854  
QY 5696 TCCCTGGGGTTACATTGTGGCATCCAGAGGGGCATCATGTCTGAAAGAATGGAATAC 5755  
Db 5855 TCCCTGGAGGTCACATGTCTGGAATCCAAAGSGGCATCATGTCTGAGAGAATGGAATAT 5914  
QY 5756 GACCAGGCGGCGCATCATCCAGGATCTTCGTGATGGGAAGACATGAGACTACACA 5815  
Db 5915 GATCAGGCAGGGCGCATCATCCGGATCTTTGCAGACGGGAAATGTGAGACTACAG 5974  
QY 5816 TACTTAGAGAAGTCCATGGTGTGCTACTACAGCCAGAGGCAGTATATCTTTGAGTTC 5875  
Db 5975 TACTTAGAGAAGTCCATGGTGTCTCATCTCCACAGCCAGAGGCAGTACATCTTCGAGTTT 6034  
QY 5876 GACAAGAATGACCGCCTCTCTGTGACGATGCCAAACGTGGCGCGGCAGACACTAGAG 5935  
Db 6035 GACAAGAATGACCGCCTCTCTGTGACCATGCCAAACGTAGCCCGGCAGACGCTGGAG 6094  
QY 5936 ACCATCCGCTCAGTGGCTACTACAGAAACATCTATCAGCCCCCTGAGGGCAATGCCTCA 5995  
Db 6095 ACCATCCGCTCAGTGGCTACTACAGGAACATCTACAGCCCCCGGAAGSAAACGCCCTCA 6154  
QY 5996 GTCATACAGGACTTCACTGAGGATGGGCACCTCCTTCACACCTTCTACCTTGGGCACCTGGC 6055  
Db 6155 GTCATTCAGGACTTCACTGAGGATGGACACCTGTTACATACCTTCTACTTGGGCACCGGC 6214  
QY 6056 CGCAGGGTGATATACAAGTATGGCAAACTGTCAAAGCTGGCAGAGACGCTCTATGACACC 6115  
Db 6215 CGCCGGGTGATTTACAAGTATGGCAAGTTGTCAAAGCTGGCCGAGACTCTGTATGACACC 6274  
QY 6116 ACCAAGGTCAAGTTTCACTATGACGAGACGGCAGGATGCTGAAGACCATCAACCTTACAG 6175  
Db 6275 ACTAAGGTAAGCTTCACTACGACGAGACCGCAGGATGCTGAAGACTGTCAACCTTACAG 6334  
QY 6176 AATGAGGGCTTCACTGCAACCATCCGCTACCGTACAGATGGGCCCTGATTTGACCGACAG 6235  
Db 6335 AATGAGGGCTTCACTGCACTATCCGCTACCGTACAGATGGGCCCTGATTTGATCGGCAG 6394  
QY 6236 ATCTTCCGCTTCACTGAGGAAGGCATGGTCAACCGCCGTTTGTGACTACAACTATGACAAC 6295  
Db 6395 ATCTTCCGTTTACGGGAAGAGGCATGGTCAATGCCCGTTTGTGATTACAACTATGACAAC 6454  
QY 6296 AGCTTCCGGGTGACCAAGCATGCAGGCTGTGATCAACGAGACCCCACTGCCCATTTGATCTC 6355

Db 6455 AGTTTCCGTGTGACTAGCATGCAGGCTGTGATCAATGAGACCCCACTGCCCATTTGACCTC 6514  
QY 6356 TATCGCTATGATGATGTGTGAGGCAAGACAGAGCAGTTTGGGAAGTTTGGTGTCAATTTAC 6415  
Db 6515 TACCGCTATGATGATGTGTGAGGAAAGACAGAGCAGTTTGGGAAGTTTGGTGTCACTAC 6574  
QY 6416 TATGACATTAAACCAGATCATCACACAGTGTGTATGACCCACACCAAGCATTTTGTGATGCA 6475  
Db 6575 TACGACATCAACCAGATCATTACCACAGCGCTCATGACCCACACCAAGCACTTTGATGCT 6634  
QY 6476 TATGGCAGGATGAAGGAAGTGCAGTATGAGATCTTCCGCTCGCTCATGTACTGATGACC 6535  
Db 6635 TATGGCAGGATGAAGGAAGTACAGTATGAGATTTTCCGGTCACTCATGTACTGGATGACT 6694  
QY 6536 GTCCAGTATGATAACATGGGGCGAGTAGTGAAGAAAGGAGCTGAAGGTAGGACCCCTACGCC 6595  
Db 6695 GTTCAGTATGATAACATGGGACGGGTAGTGAAGAAAGGAGCTGAAGGTGGGACCCCTATGCC 6754  
QY 6596 AATACCACTCGCTACTCCTATGAGTATGATGCTGACGGCCAGCTGCAGACAGTCTCCATC 6655  
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QY 6716 CCTGGAAACAGTGCACGGCTCACACCCTACCGGTATGACATCCGCGACCGCATCACTCGG 6775  
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QY 6776 CTGGGTGACGTGCAATACAAGATGGATGGATGGCTTCTGAGGCAGCGGGCGGTGAT 6835  
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QY 6896 AGTGTACGGTACCGCTACGATGGCCTGGGGCGGCGCGTGTCCAGCAAGAGCAGCCACAGC 6955  
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QY 6956 CACCACCTGCAGTTCTTCTATGCAGACCTGACCAACCCCAAGGTCAACCACCTGTAC 7015  
Db 7115 CACCACCTGCAGTTCTTCTACGCAGACCTGACCAACCCCAAGGTCAACCACCTCTAC 7174  
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QY 7076 ATGGAGCTGAGCAGTGGTGTGATGAGTTTATACATAGCTTGTGACAACATCGGGACCCCTCTT 7135  
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QY 7136 GCTGTCTTTAGTGGAAACAGGTTTGTATGATCAAGCAAAATCCTGTACACAGCCTATGGGGAG 7195  
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QY 7196 ATCTACATGGATACCAACCCCAACTTTCAGATCATATAGGCTACCATGGTGGGCTCTAT 7255  
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QY 7376 AATCTCTATATGTTCAAAAAACAACACCCCATCAGCAAACTCCCAGGACATCAAGTGCTTC 7435  
Db 7535 CATCTCTACATGTTTAAAGAAACAACAACCCCATCAGCAAACTCTCAGGACATCAAGTGCTTC 7594

QY	7436	ATGACAGATGTTAA	CAGCTGGCTGCTC	ACCTTTGGATTCCAG	TACACAACGTGATCCCT	7495
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QY	7496	GGTTATCCCAAA	CCAGACATGGATG	CCATGGAAACCTCCT	TACGAGCTCATCACACACAG	7555
Db	7655	GGCTATCCCAAG	CCAGACACAGATG	CCATGGAAACCTCCT	TACGAGCTCGTACACACACAG	7714
QY	7556	ATGAAAACGCAG	GAGTGGGACAA	CAGCAAGTCTAT	CCTCGGGGTACAGTGTGAAGTACAG	7615
Db	7715	ATGAAAAC	TCAGGAATGGGAC	AAACAGCAAGTCT	ATCCTCGGGGTACAGTGTGAAGTTCAG	7774
QY	7616	AAGCAGCTCA	AGGCCTTTGTCA	CCCTTAGAAACGG	TTTGACCAGCTCTATGGCTCCACAATC	7675
Db	7775	AAGCAACTCA	AGGCTTTCGTTA	CTTACCTTAGAA	ACGCTTTGACCAGCTCTACGGCTCGACCATC	7834
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Db	7835	ACCAGCTGCC	ACACAGGCCCTG	AGACAAAGAGT	TTTGCTCCAGTGGTTCCATCTTTGGC	7894
QY	7736	AAGGGGTCAA	AGTTTGCCTTGA	AGGATGGCCGAG	TGACCAAGACATCATCAGTGTGGCC	7795
Db	7895	AAGGGGTCAA	AGTTTGCCTTGA	AAAGATGGTCG	AGTGAACCACTGACATCATCAGTGTGGCC	7954
QY	7796	AATGAGGATG	GGCGAAGGGTTG	CTGCCATCTTGA	ACCATGCCACTACCTAGAGAACCTG	7855
Db	7955	AATGAGGATG	GGCGAGGATCG	CAGCCATCTTGA	AACATGCTCACTATCTAGAGAACCTT	8014
QY	7856	CACCTCACCA	TGATGGGGTGG	ATACCCATTACT	TTTGTGAAACCAGGACCTTCAGAAGGT	7915
Db	8015	CACCTCACCA	TGATGGGGTGG	ACACCCACTA	CTTTTGTGAAACCAGGACCTTCGSAAGGT	8074
QY	7916	GACCTGGCC	ATCCTGGGCCT	CAGTGGGGGG	CGGGAACCTTGGAGAAATGGGGTCAACGTC	7975
Db	8075	GACCTGGCC	ATCCTGGGCCT	CAGTGGGGGG	CGGAGAACCTTGGAGAAATGGGGTCAACGTC	8134
QY	7976	ACTGTGTCC	AGATCAACACAG	TACTTAATGGC	AGGATAGACGCTACACAGACATCCAG	8035
Db	8135	ACTGTGTCC	AGATCAACAC	CGATGCTCAG	TGGCAGGACTAGACGCTACACTGACATCCAG	8194
QY	8036	CTCAGTACGG	GCAC	TGTGTGAACAC	ACGCTACGGGACAACTGTTGGATGAGGAGAAG	8095
Db	8195	CTGCAGTAC	AGGCGCTGTG	CCCTGAACAC	CCCGCTACGGGACAACTGTTGATGAGGAAAAG	8254
QY	8096	GCACGGTCT	TGAGCTGGCC	CGGCAGAGAG	CCGTGCGCAAGCGTGGGCCCGCAGAGCAG	8155
Db	8255	GTGCGGTGT	CGAGCTGGCC	AGCAGAGAG	CTGTGCGCAGGCTTGGGCCCGCAGAGCAG	8314
QY	8156	CAGAGACTG	CGGGAAGGGG	AGGAGGCTG	CGGGCCTGGACAGAGGGGAGAGCAGCAG	8215
Db	8315	CAGAGACTG	CGGGAAGGGG	AGAGGGCCTG	CGGGCCTGGACAGATGGGGAAAAGCAGCAG	8374
QY	8216	GTGCTGAG	CACAGGGCG	GGTGCAAGG	CTACGACGGCTTTTTCGTGATCTCTGTGAGCAG	8275
Db	8375	GTGCTGA	ACACAGGGCG	GGTGCAAGG	CTACGACGGCTTCTTTGTGACCTCGGTGAGCAG	8434
QY	8276	TACCCAGAA	CTGTGAGAC	AGCGGCCAA	CATCCACTTCAATGAGACAGAGCGAGATGGGC	8335
Db	8435	TACCCAGAA	CTGTGAGAC	AGCGGCCAA	CAATATCCACTTCAATGAGACAGAGCGAGATGGGC	8494
QY	8336	CGGAGGTG	ACAGAGAGG	AC	8354	
Db	8495	CGAAGGTG	ACAGAAAGGC		8513	

RESULT 5  
CQ722991  
LOCUS CQ722991 7514 bp DNA linear PAT 03-FEB-2004  
DEFINITION Sequence 8925 from Patent WO02068579.  
ACCESSION CQ722991  
VERSION CQ722991.1 GI:42283848  
KEYWORDS

SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	1
AUTHORS	Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W.
TITLE	Kits, such as nucleic acid arrays, comprising a majority of humanexons or transcripts, for detecting expression and other uses thereof
JOURNAL	Patent: WO 02068579-A 8925 06-SEP-2002; PE Corporation (NY) (US)
FEATURES	Location/Qualifiers source 1..7514 /organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606"
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Query Match	80.2%; Score 6701.6; DB 6; Length 7514;
Best Local Similarity	93.1%; Pred. No. 0;
Matches 7295; Conservative	0; Mismatches 14; Indels 525; Gaps 6;
QY	517 CACTGAGACTGATCATCCGGGGCGGCTGCAGAAACACCGCGGCTCCGGACGCGCGCC 576 
Db	200 CGGGCGAAACGATCATCCGGGGCGGCTGCAGAAACACCGCGGCTCCGGACGCGCGCC 259 
QY	577 GCCGCTCTCGACGCCCCACACCCCCAACCCAGACACCGCGGCTCCATTAACTCCCTGAA 636 
Db	260 GCCGCTCTCGACGCCCCACACCCCCAACCCAGACACCGCGGCTCCATTAACTCCCTGAA 319 
QY	637 CCGGGGCAACTTCACGCGCGGAGGAGCAACCCAGCGCGGCCCCACCGACCACTCGCTCTC 696 
Db	320 CCGGGGCAACTTCACGCGCGGAGGAGCAACCCAGCGCGGCCCCACCGACCACTCGCTCTC 379 
QY	697 CGGAGAGCCCCCTGCGCGCGCGCCAGGAGCCCTGCGCCACGCGCCAGGAGAACTGGCTGCT 756 
Db	380 CGGAGAGCCCCCTGCGCGCGCGCCAGGAGCCCTGCGCCACGCGCCAGGAGAACTGGCTGCT 439 
QY	757 CAACAGCAACATCCCCCTGGAGACCAGGAACCTTAGCAAGCAGCCATTTCCTAGGACATT 816 
Db	440 CAACAGCAACATCCCCCTGGAGACCA----- 465 
QY	817 GCAGGACAACTCATTTGAGATGGACATTCTCGGGCGCTCCCGCCATGATGGGGCTTACAG 876 
Db	466 ----- 465 
QY	877 TGACGGGCACCTTCTCTTAAGCCTGGAGGCACCTCCCGCTCTTCTGCACCACATCACC 936 
Db	466 -----GGCACCTTCTCTTAAGCCTGGAGGCACCTCCCGCTCTTCTGCACCACATCACC 520 
QY	937 AGGGTACCCACTGACGTCAGCACAGTGTACTCTCTCCGCCCGCCGACCCCTGCCCGCAG 996 
Db	521 AGGGTACCCACTGACGTCAGCACAGTGTACTCTCTCCGCCCGCCGACCCCTGCCCGCAG 580 
QY	997 CACCTTCGCCCGCGCCCTTTAACTCAAGAAAGCCCTCCAAGTACTGTAACTGGAAGTG 1056 
Db	581 CACCTTCGCCCGCGCCCTTTAACTCAAGAAAGCCCTCCAAGTACTGTAACTGGAAGTG 640 
QY	1057 CGCAGCCCTGAGCGCCCATCGTCATCTCAGCCACTCTGTCATCTCTGTCATCTTTGT 1116 
Db	641 CGCAGCCCTGAGCGCCCATCGTCATCTCAGCCACTCTGTCATCTCTGTCATCTTTGT 700 
QY	1117 GGCCATGCACCTGTTTGGCCCTAAACTGGCACCTTGCGAGCCGATGGAGGGGCAGATGTATGA 1176 
Db	701 G----- 701 
QY	1177 GATCAGGAGGACACAGCCAGCAGTTGGCCTGTGCCAACCGACGTCTCCCTATACCCCTC 1236 
Db	702 ----- 701 
QY	1237 AGGGGGCACTGGCTTAGAGACCCCTGACAGGAAAGGCAAGAACCAAGAGGAAAGCC 1296 







QY	3457	ATATGAATCCTGCCAGATCTAATCCTGTGGGAAAAAGAAACAACAGTGTCTGCAGGGCTA	3516	Db	3701	AGAGATCTCACTCGTTGCTGGGGCCCCAGTGGCTGTGACTGTAAAAATGATGCCAACTG	3760
Db	2642	ATATGAATCCTGCCAGATCTAATCCTGTGGGAAAAAGAAACAACAGTGTGCAGGGCTA	2701	QY	4597	TGATTGTTTCTGGAGACGATGGTTATGCCAAGGATGCAAAAGTTAAATACCCCATCTTC	4656
QY	3517	TGAAATTGACGCGTCCAAGCTTGGAGGATGGAGCTAGACAAACATCATGCGCTCAACAT	3576	Db	3761	TGATTGTTTCTGGAGACGATGGTTATGCCAAGGATGCAAAAGTTAAATACCCCATCTTC	3820
Db	2702	TGAAATTGACGCGTCCAAGCTTGGAGGATGGAGCTAGACAAACATCATGCGCTCAACAT	2761	QY	4657	CTTGGCTGTGTGCTGATGGGAGCTCTACGTGGCCGACCTTGGGAACATCCGAATTCCG	4716
QY	3577	TCAAAGTGGTATCCTTGACACAAAGGAAATGGGGAGAACCAAGTTTGTGTCTCAGCAGCCTCC	3636	Db	3821	CTTGGCTGTGTGCTGATGGGAGCTCTACGTGGCCGACCTTGGGAACATCCGAATTCCG	3880
Db	2762	TCAAAGTGGCATCCTTGACACAAAGGAAATGGGGAGAACCAAGTTTGTGTCTCAGCAGCCTCC	2821	QY	4717	GTTTATCCGGAAGAAACAAGCCTTTCCTCAACACCCAGAACATGTATGAGCTGTCTTCACC	4776
QY	3637	TGTCATTGGGAGCATCATGGGCAATGGGCGCCGGAGAGCATCTCCTTGCCCCAGCTGCAA	3696	Db	3881	GTTTATCCGGAAGAAACAAGCCTTTCCTCAACACCCAGAACATGTATGAGCTGTCTTCACC	3940
Db	2822	TGTCAATTGGGAGCATCATGGGCAATGGGCGCCGGAGAGCATCTCCTTGCCCCAGCTGCAA	2881	QY	4777	AATTGACCAGGAGCTCTATCTGTTTGATACCACCCGGAAGCACCTGTACACCCAAAGCCT	4836
QY	3697	CGGCCCTTGCTGACGGGCAACAAGCTCCTGGCCCCAGTGGCCCTCACCTGTGGCTCTGACGG	3756	Db	3941	AATTGACCAGGAGCTCTATCTGTTTGATACCACCCGGAAGCACCTGTACACCCAAAGCCT	4000
Db	2882	CGGCCCTTGCTGACGGGCAACAAGCTCCTGGCCCCAGTGGCCCTCACCTGTGGCTCTGACGG	2941	QY	4837	GCCACAGGAGACTACCTGTACAACTTCACTACCTACACTGGGACCGGACATCACTCAT	4896
QY	3757	GAGCCTCTATGTGGTGATTTCAACTACATTAGAAAGATCTTCCCCTCTGGAAATGTCCAC	3816	Db	4001	GCCACAGGAGACTACCTGTACAACTTCACTACACTGGGACCGGACATCACTCAT	4060
Db	2942	GAGCCTCTATGTGGTGATTTCAACTACATTAGAAAGATCTTCCCCTCTGGAAATGTCCAC	3001	QY	4897	CACAGACAAATGGCAACATGGTAAATGTCGCGGAGACTCTACTGGGATGCCCTCTG	4956
QY	3817	CAACATCCTAGAGCTGAGGAATAAAGATTTTCAGACATAGTCCAGCACACAAATA	3876	Db	4061	CACAGACAAATGGCAACATGGTAAATGTCGCGGAGACTCTACTGGGATGCCCTCTG	4120
Db	3002	CAACATCCTAGAGCTG-----AGTCAAGTCCAGCACACAAATA	3040	QY	4957	GCTGGTGGTCCCAGATGGCCAGGTGTACTGGGTGACCATGGGCACCAACAGTGCACCTCAA	5016
QY	3877	CTACCTGGCCACAGACCCCATGAGTGGGCGCGTCTTCCCTTTCTGACAGCAACAGCCGGCG	3936	Db	4121	GCTGGTGGTCCCAGATGGCCAGGTGTACTGGGTGACCATGGGCACCAACAGTGCACCTCAA	4180
Db	3041	CTACCTGGCCACAGACCCCATGAGTGGGCGCGTCTTCCCTTTCTGACAGCAACAGCCGGCG	3100	QY	5017	GAGTGTGACCACACAAGGACACGAGTTGGCCATGTATGATGACATACCATGGCAATTCGGGCT	5076
QY	3937	GGTCTTTAAATCAAGTCCACTGTGGTGGTGAAGGACCTTGTCAAGAACTCTGAGTGGT	3996	Db	4181	GAGTGTGACCACACAAGGACACGAGTTGGCCATGTATGATGACATACCATGGCAATTCGGGCT	4240
Db	3101	GGTCTTTAAATCAAGTCCACTGTGGTGGTGAAGGACCTTGTCAAGAACTCTGAGTGGT	3160	QY	5077	TCTGGCAACCAAAAGCAATGAAAAACGATGGGCAACATTTTATGATACGACAGCTTTGG	5136
QY	3997	TGCGGGACAGGTGACCAAGTCCCTTTGATGACACTCGCTCGGGGATGGTGGAA	4056	Db	4241	TCTGGCAACCAAAAGCAATGAAAAACGATGGGCAACATTTTATGATACGACAGCTTTGG	4300
Db	3161	TGCGGGACAGGTGACCAAGTCCCTTTGATGACACTCGCTCGGGGATGGTGGAA	3220	QY	5137	CGCCTTGACAAATGTGACCTTCCCTACTGGCCAGGTGAGCAGTTTCCGAAAGTATACAGA	5196
QY	4057	GGCCACAGAAGCCACACTCAACCAATCCAGGGGTATTACAGTGGACAAAGTTTGGGCTGAT	4116	Db	4301	CGCCTTGACAAATGTGACCTTCCCTACTGGCCAGGTGAGCAGTTTCCGAAAGTATACAGA	4360
Db	3221	GGCCACAGAAGCCACACTCACCAATCCAGGGGCATTACAGTGGACAAAGTTTGGGCTGAT	3280	QY	5197	CAGTTCAGTGCAATGTCAGGTAGAGACCTCCAGCAAGGATGATGTACCATAAACCCACAA	5256
QY	4117	CTACTTCGTGGATGGCACCATGATCAGACGCATCGATCAGAAATGGGATCATCTCCACCCCT	4176	Db	4361	CAGTTCAGTGCAATGTCAGGTAGAGACCTCCAGCAAGGATGATGTACCATAAACCCACAA	4420
Db	3281	CTACTTCGTGGATGGCACCATGATCAGACGCATCGATCAGAAATGGGATCATCTCCACCCCT	3340	QY	5257	CCTGTCTGCCTCAGGGCCCTTCTACACACTGCTGCAAGACCAAGTCCGGAACAGCTACTA	5316
QY	4177	GCTCGGCTCTAATGATCTCACATCAGCCGGCCACTCAGCTGTGATTTCTGTATGGATAT	4236	Db	4421	CCTGTCTGCCTCAGGGCCCTTCTACACACTGCTGCAAGACCAAGTCCGGAACAGCTACTA	4480
Db	3341	GCTCGGCTCTAATGATCTCACATCAGCCGGCCACTCAGCTGTGATTTCTGTATGGATAT	3400	QY	5317	CATCGGGCCGATGGTCTCTTGGCGCTGCTGTGGCCAAACGGCATGGAGGTGGCGCTGCA	5376
QY	4237	TTCCCAGGTAAGACTGGAGTGGCCACAGACTTAGCCATCAACCCAATGGCAACTCACT	4296	Db	4481	CATCGGGCCGATGGTCTCTTGGCGCTGCTGTGGCCAAACGGCATGGAGGTGGCGCTGCA	4540
Db	3401	TTCCCAGGTTACCTGGAGTGGCCCCACAGACTTAGCCATCAACCCAATGGCAACTCACT	3460	QY	5377	GACTGAGCCCCACTTGTGGTGGCAACCGTCAACCCCAACCGTGGGCAAGAGGAATGTCA	5436
QY	4297	TTATGTCCTCGACAAACAATGTGGTCCTGCAAAATCTCTGAAAAACCAACAGGTGCGCATTTG	4356	Db	4541	GACTGAGCCCCACTTGTGGTGGCAACCGTCAACCCCAACCGTGGGCAAGAGGAATGTCA	4600
Db	3461	TTATGTCCTCGACAAACAATGTGGTCCTGCAAAATCTCTGAAAAACCAACAGGTGCGCATTTG	3520	QY	5437	GCTGCCCATCGACAAACGGCCTCAACCTGGTGGAGTGGCGCAGCCGCAAGAGCAGGCTCG	5496
QY	4357	CGCCGGGAGGCCATGCACCTGCCAGGTCCCTGGCATTTGACCACTTCTGCTAAGCAAGGT	4416	Db	4601	GCTGCCCATCGACAAACGGCCTCAACCTGGTGGAGTGGCGCAGCCGCAAGAGCAGGCTCG	4660
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QY	4417	GGCCATCCACGCAACCCCTGGAGTCAGCCACCGCTTTGGCTGTTTTCACAAATGGGTCCT	4476	Db	4661	GGGCCAGGTCACTGTCTTTGGCGCCGGCTGCGGGTTCACAAACCGAAATCTCCTATCTCT	4720
Db	3581	GGCCATCCACGCAACCCCTGGAGTCAGCCACCGCTTTGGCTGTTTTCACAAATGGGTCCT	3640	QY	5557	GGACTTTGATCGCGTAACACCGCACAGAGAAGATCTATGATGACCAACCGCAAGTTTCAACCCT	5616
QY	4477	GTATATTGCTGAGACTGAGAAAAAGATCAACCGCATCAGGCAGGTCAACCACTAGTGG	4536	Db	4721	GGACTTTGATCGCGTAACACCGCACAGAGAAGATCTATGATGACCAACCGCAAGTTTCAACCCT	4780
Db	3641	GTAATATTGCTGAGACTGATGAGAAAAAGATCAACCGCATCAGGCAGGTCAACCACTAGTGG	3700	QY	5617	TCGGATTCTGTACGACCAGGGGGGGCCCCAGCCTCTGGTCAACCACGACGAGGCTGAA	5676
QY	4537	AGAGATCTCACTCGTTGCTGGGGCCCCCAGTGGGCTGTGACTGTAAAAATGATGCCAACTG	4596				

Db 4781 TCGGATTCTGTACGACGAGCGGGGGCCAGCCTCTGGTCACCCAGCAGCAGGCTGAA 4840

Qy 5677 TGGTGTCAACGTTGACATACTCCCTGGGGGTTACATTGCTGGCATCCAGAGGGGCATCAT 5736

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Db 6101 CGTGTCCAGCAAGAGCAGCCACAGCCACCACTGCAGTTCTTCTATGACAGCCTGACCAA 6160

Qy 6991 CCCCACCAAGGTCACCCACCTGTACAACTCCAGCTCCAGCTCTGAGATCACTCCCTCTACTA 7050

Db 6161 CCCCACCAAGGTCACCCACCTGTACAACTCCAGCTCCAGCTCTGAGATCACTCCCTCTACTA 6220

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Qy 7231 CATAGGCTACCATGGTGGCCTCTATGATCCAATCACTCAAGCTTGTCCATGGGCCGGCG 7290

Db 6401 CATAGGCTACCATGGTGGCCTCTATGATCCAATCACTCAAGCTTGTCCATGGGCCGGCG 6460

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Db 6581 CAACTCCCAGGACATCAAGTGTCTCATGACAGATGTTAACAGCTGGCTGCTCACCTTTGG 6640

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Db	7421	CTTTTTCGTGATCTCTGTCGAGCAGTACCCAGAACTGTCTAGACAGCGCCCAACAATCCA	7480
QY	8311	CTTCATGACACAGAGCGGAGATGGGCGGGAGGTGA	8344
Db	7481	CTTCATGACACAGAGCGGAGATGGGCGGGAGGTGA	7514

RESULT 6	AF059485	AF059485	9722 bp	mRNA	linear	ROD 15-AUG-1998
AF059485	Mus musculus	DOC4 (Doc4)	mRNA, complete cds.			
LOCUS	AF059485	AF059485.1	GI:3170614			
DEFINITION	Mus musculus (house mouse)					
ACCESSION	Mus musculus					
VERSION	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.					
KEYWORDS	1 (bases 1 to 9722)					
SOURCE	Wang,X.Z., Kuroda,M., Sok,J., Batchvarova,N., Kimmel,R., Chung,P., Zinszner,H. and Ron,D.					
ORGANISM	Identification of novel stress-induced genes downstream of chop					
REFERENCE	EMBO J. 17 (13), 3619-3630 (1998)					
AUTHORS	9649432					
TITLE	2 (bases 1 to 9722)					
JOURNAL	Wang,X.-Z. and Ron,D.					
PUBMED	Direct Submission					
AUTHORS	Submitted (14-APR-1998) Skirball Institute, New York University					
TITLE	Medical Center, 550 First Ave., New York, NY 10016, USA					
JOURNAL	Location/Qualifiers					
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misc\_feature

ORIGIN

Query Match	79.0%;	Score	6601.2;	DB	9;	Length	9722;
Best Local Similarity	86.7%;	Pred. No.	0;				
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Gaps	4;						
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QY	62	CGCTCGCTGACCCGGCGCGGACGCCGAGCGCCGCTACACGAGCTCGTCCGCGGACAGC	121				
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Db 730 CAAGATGCTCGCCTAGCCTACGGCAGCGCGTCAAGGACATGGTACCACAGGAGCGCCGAG 789  
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Db	3070	CGGGCTGCCACCCACGCTGTGCAGAACACGGGACCCTGCGGGACGGCAAGTGCGAATGC	3129	Db	4123	TGGACAAGACAGATGTCTACAAACCAGAAAGGTGTTTGGACTCTCAGAAAGCCTTTGTTCC	4182
QY	2366	AGCCCTGGCTGGAATGGCGAACACTGCACCATCGCTCACTATCTGGATAGGGTAGTTAAA	2425	QY	3446	GTGGGTTATGAATATGAATCCTGCCCAGATCTAATCCTGTGGGAAAAAAGAACACAGTG	3505
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QY	2726	ATCAAGTTCCTCGTGGGACAGCAGCAGCACATAATCCCGGGGAGAACCCCTTTGAT	2785	QY	3806	GGAAATGTCAACCAATCCTTAGAGCTGAGGAAATAAGATTTCAGACATAGTCACAGTCCA	3865
Db	3463	ATCAAGTTCCTCGTGGGACAGGACAGCACACACAGCATCCCGGGGAGAACCCCTTTGAC	3522	Db	4543	GGAAATGTCAACCAATCCTGGAGATG-----AGTCACAGCCCA	4581
QY	2786	GGAGGGCATGCTGTGTTATTTCGTGGCAAGTGATGACATCAGATGGAACCCCTGGTT	2845	QY	3866	GCACACAAATACTACCTGGCCACAGACCCCATAGTGGGGCCGTCTTCCCTTTCTGACAGC	3925
Db	3523	GGAGGGCATGCTGTGTCTATCCGTGGACAAAGTGATGACGTGAGTGGGACCCCATTTGTT	3582	Db	4582	GCACACAAATACTACCTGGCTACAGACCCCATAGTGGGGCCGTCTTCTCTGTCTGACACC	4641
QY	2846	GGTGTGAACATCAGTTTGTCAATAACCTCTCTTTGGATATACAATCAGCAGGCAAGAT	2905	QY	3926	AACAGCCGGCGGTCTTTAAAAATCAAGTCCACTGTGTGGTGAAGGACCTTGTCAAGAAC	3985
Db	3583	GGCGTGAACATCAGTTTTCATCAATAACCTCTCTTTGGATATACAATCAGCAGGCAAGAT	3642	Db	4642	AACAGCCGGCGGTCTTCAAGGTCAAGTCCACCACACAGTGGTGAAGGACCTTGGTGAAGAAC	4701
QY	2906	GGCAGCTTTGACTTGGTGACAAATGGCGGCATCTCCATCATCCTGCGGTTTCGAGCGGGCA	2965	QY	3986	TCTGAGGTGGTTGCGGGGACAGGTGACCAAGTCCCTCCCTTTGATGACACTCGTGGGG	4045
Db	3643	GGCAGCTTTGACCTGGTCACAAATGGCGGCATCTCCATCATCTTGAGATTCGAAAGGGCA	3702	Db	4702	TCCGAGGTGGTAGCAGGGACTGGTGACCAAGTGCCTCCCTTTGATGATACCCGCTGCGGA	4761
QY	2966	CCTTTCATCACAGGAGCACACCTGTGGCTGCCATGGGATCGCTTCTTTGTCTATGGAA	3025	QY	4046	GATGTGGGAAGGCCACAGAAAGCCACACTCACCAATCCCAGGGGTATTACAGTGGACAAG	4105
Db	3703	CCCTTCATCACAGGAGCATACCCCTTGCGTACCCCTGGGATCGCTTCTTTGTCTATGGAA	3762	Db	4762	GATGTGGGAAGGCCACAGAAAGCCACAGAACCCAGCTCACTAACCCAGGGGAATTACAGTGGACAAG	4821
QY	3026	ACCATCATCATGAGACATGAGGAGAAATGAGATTCAGCTGTGACCTGAGCAATTTTGCC	3085	QY	4106	TTTGGGCTGATCTACTTCGTGGATGGCACCATGATCAGACGCATCGATCAGAATGGGATC	4165
Db	3763	ACCATCGTATGAGACACAGGAGAAATGAGATCCCAGCAGAGACCTGAGCAACTTTTGCC	3822	Db	4822	TTTGGGCTCATTTTATTTCTGTGGACGGCACCATGATCAGACGCTGTTGATCAAAATGGAATC	4881
QY	3086	CGCCCCAACCCAGTCGTCTCTCCATCCCCACTGACGTCTCTCGCCAGCTCCTGTGCAGAG	3145	QY	4166	ATCTCCACCTGTCTCGGCTCTPAATGATCTCACAATCAGCCCGCCACTCAGCTGTGATTCT	4225
Db	3823	CGTCCCAACCCCTGTGGTCTCTCCATCCTCCCACTGACATCCTTCGCCAGCTCCTGTGTGAG	3882	Db	4882	ATCTCCACTTTGCTGGGCTCCAATGACCTCACCTCGGCCAGGCCCTCAGCTGTGACTCC	4941
QY	3146	AAAGGCCCCCAATTGTGCCGGAAATTTCAGGCTTTGAGGAGGAAATCTCTATCTCTGGCTGC	3205	QY	4226	GTCTATGGATATTTCCAGGTAAGACTGGAGTGGCCACAGACTTAGCCATCAACCCCAATG	4285
Db	3883	AAAGGCCCCCAATTGTCCAGAAATCCAGGGCCCTGCAAGAGGAAATCGTCACTCGCTGGCTGC	3942	Db	4942	GTCTATGGAGATTTCTCAGGTTCCGCTGGAGTGGCCACAGACTTAGCCATCAACCCCAATG	5001
				QY	4286	GACAACTCACTTTATGTCTCTCGACAAACAATGTGGTCTCTGCAAAATCTCTGAAAAACCAACCAG	4345







QY	6506	ATCTTCCGCTCGCTCATGTACTGGATGACCGTCCAGTATGATAAATGSGCGAGTAGTG	6565	QY	7586	TCTATCCTCGGGGTACAGTGTGAAGTACAGAAGCAGCTCAAGGCCTTTGTACCTTAGAA	7645
Db	7222	ACTTTCGGTCACTCATGTACTGGATGACTGTTCAGTATGATAACATGGGACGGTAGTG	7281	Db	8302	TCTATCCTCGGGGTACAGTGTGAAGTTCAGAAGCAACTCAAGGCCTTCGTTACCTTAGAA	8361
QY	6566	AAGAAGGAGCTGAAGGTAGGACCCCTACGCCAATACCACTCGCTACTCCTATGAGTATGAT	6625	QY	7646	CGGTTTGACCAAGCTCTATGGCTCCACAATCACCAGTGCACAGAGCTCCTGAGACCAAG	7705
Db	7282	AAGAAGGAGCTGAAGGTGGGACCCCTATGCCAACACTACCCGCTACTCCTATGAGTATGAT	7341	Db	8362	CGCTTTGACCAAGCTCTACGGCTCGACCATCACCAGTGCCTGAGACCAAG	8421
QY	6626	GCTGACGGCCAGCTGCAGACAGTCTCCATCAATGACAAGCCACTCTGGCGCTACAGCTAT	6685	QY	7706	AAGTTTGCAATCCAGCGGCTCAGTCTTTGGCAAGGGGTCAGTTTGCTTGAAGGATGGC	7765
Db	7342	GCTGATGGCCAGCTGCAGACAGTCTCCATCAATGACAAGCCACTCTGGCGCTACAGCTAT	7401	Db	8422	AAGTTTGCTCCAGTGGTTCATCTTTGGCAAGGGGTCAGTTTGCTTGAAGATGGT	8481
QY	6686	GACCTCAATGGGAACCTGCACTTACTGAGCCCTGGGAACAGTGCACGGCTCACACCACTA	6745	QY	7766	CGAGTGACCAAGACATCATCAGTGTGGCCCAATGAGGATGGGCGAAGGGTTGCTGCCATC	7825
Db	7402	GACCTCAATGGGAACCTTACACTTGTCTGAGCCCTGGGAACAGCGCACGGCTCACACCACTA	7461	Db	8482	CGAGTGACCACTGACATCATCAGTGTGGCCCAATGAGGATGGGCGGAGGATCGCAGCCATC	8541
QY	6746	CGGTATGACATCCGCGACCGCATCACTCGGCTGGGTGAGCTGCAATACAAGATGGATGAG	6805	QY	7826	TTGAACCATGCCCCACTACCTAGAGAACCTGCACTTCAACCATTTGATGGGTTGATACCCAT	7885
Db	7462	CGGTATGACCTCCGTGACCGCATCACTAGGCTGGGTGATGTCTTCGAGTACAATTCAGCCGGCTGCTC	7521	Db	8542	TTGAACAATGTCTCACTATYTAGAGAACCTTCACTTCAACCATTTGATGGGTTGACACCCAC	8601
QY	6806	GATGGCTTCTTGAGGCAGCGGGCGGTGATATCTTTGAGTACAACACTCAGCTGGCCTGCTC	6865	QY	7886	TACTTTGTGAAACCAGGACCTTTCAGAAAGTGAACCTGGCCATCCTGGCCCTCAGTGGGGG	7945
Db	7522	GATGGCTTCTTGAGGCAGCGGGGTGGGATGTCTTCGAGTACAATTCAGCCGGCTGCTC	7581	Db	8602	TACTTTGTGAAACCAGGACCTTCGAAAGGTGACCTGGCCATCCTGGGCCTCAGTGGGGG	8661
QY	6866	ATCAAGGCCTACAACCGGGCTGGCAGCTGGAGTGTTCAGGTACCGCTACGATGGCCTGGGG	6925	QY	7946	CGCGGAACCCCTGGAGAAATGGGTCAACGTCACTGTGTCCCAGATCAACACAGTACTTAAT	8005
Db	7582	ATCAAAGCCTACAATCGGGCTAGTGGGTGGAGTGTTCAGGTACCGATCGATGGGCTGGGA	7641	Db	8662	CGGAGAACCCTGGAGAAATGGGTCAACGTCACTGTGTCCCAGATCAACACCATGCTCAGT	8721
QY	6926	CGGCGGTGTCCAGCAAGAGCAGCCACAGCCACCACCTGCACTCTGAGATCACTCCCTC	6985	QY	8006	GGCAGGACTAGACGCTACACAGACATCCAGTCCAGTACGGGGCACTGTGCTTGAACACA	8065
Db	7642	CGCCGAGTATCCAGCAAGAGCAGCCACCTTACAGCCACTCCAGCTCTGAGATTACATCCCTC	7701	Db	8722	GGCAGGACTAGACGCTACACTGACATCCAGTGCAGTACAGGGCGCTGTGCTGAACACC	8781
QY	7046	TACTACGACTTGCAAGGACACCTCTTTGCACTGGAGCTGAGCTGAGCACTGGTGTGATTTTAC	7105	QY	8066	CGCTACGGGACAAACGTGGATGAGGAAAGGTGCGGGTGTGGAGCTGGCCCGGCAGAGA	8125
Db	7762	TACTATGATCTCAAGGACACCTCTTTGCCATGGAGCTGAGCTGAGCACTGGCGATGAGTTTAC	7821	Db	8782	CGCTACGGGACAAACGTGGATGAGGAAAGGTGCGGGTGTGGAGCTGGCCAGGCAGAGA	8841
QY	7106	ATAGCTTGTGACAAACATCGGGACCCCTCTTGCTGTCTTTAGTGGAAACAGGTTTGTATGATC	7165	QY	8126	GCCGTGCGCCAAAGCTGGGCCCGCAGCAGCAGAGACTGCGGGAAGGGGAGGAAGGCCTG	8185
Db	7822	ATAGCTTGTGACAAACATCGGGACCCCGCTTGCTGTCTTCAGTGGAACTGGCTTGATGATT	7881	Db	8842	GCTGTGCGCCAGGCTTGGGCCCGAGAGCAGCAGAGACTGCGGGAAGGGGAGAGGGCCTG	8901
QY	7166	AAGCAAACTCTGTACACAGCCTATGSGGAGACTACATGGATACCAACCCCAACTTTTCAG	7225	QY	8186	CGGGCCTGGACAGAGGGGGAGAAAGCAGCAGGTGCTGAGCACAGGGCGGGTGCAAGGCTAC	8245
Db	7882	AAGCAGATCCTATACACGGCCTATGGGAGACTACATGGACACAAACCCCAACTTCCAG	7941	Db	8902	CGGGCCTGGACAGATGGGGAAGAACAGCAGAGGTGCTGAAACACGGGGCGGGTGCAAGGCTAC	8961
QY	7226	ATCATCATAGGCTACCATGGTGGCCTCTATGATCCACTCACCAAGCTTGTCCACATGGGC	7285	QY	8246	GACGGCTTTTTCGTGATCTCTGTGAGCAGTACCCAGAACTGTGAGACAGCGCCCAACAAC	8305
Db	7942	ATCATCATCGGCTACCACGGCGGCCTCTATGATCCACTCACCAAGCTTGTCCACATGGGC	8001	Db	8962	GACGGCTTCTTTGTGACCTCGGTGAGCAGTACCCAGAACTGTGAGACAGCGCCCAACAAT	9021
QY	7286	CGGCGAGATTATGATGTGCTGGCCGGACGCTGGACTAGCCAGACCCAGAGCTGTGGAAG	7345	QY	8306	ATCCACTTCATGAGACAGAGCGAGATGGCCGAGGTGAGAGGATGACAGAGAGGAC	8354
Db	8002	CGACGGGATTATGATGTGCTGGCTGGACGCTGGACAAAGCCAGACCATGAACTCTGGAAA	8061	Db	9022	ATCCACTTCATGAGACAGAGCGAGATGGCCGAGGTGAGAGGATGACAGAAAGGGC	9070
QY	7346	CACCTTAGTAGCAAGCAAGTCATGCGCTTTTAACTCTATATGTTCAAAACAAACACCC	7405	RESULT 7			
Db	8062	CGCCTGAGTAGCAACAGCATCGTGCCTTTTCACTCTACATGTTTAAAGAAACAAACACCC	8121	AB037723	Homo sapiens	mRNA	linear
QY	7406	ATCAGCAACTCCCAGGACATCAAGTGTCTTCATGACAGATGTTAACAGCTGGCTGCTCACC	7465	LOCUS	AB037723	10826 bp	PRI 06-AUG-2005
Db	8122	ATCAGCAACTCTCAGGACATCAAGTGTCTTCATGACAGATGTCAACAGCTGGCTGCTCACC	8181	DEFINITION	Homo sapiens mRNA for KIAA1302 protein, partial cds.		
QY	7466	TTTGGATTCCAGCTACACAACGTGATCCCTGGTTATCCCAAAACCAGACATGGATGCCATG	7525	ACCESSION	AB037723		
Db	8182	TTTGGATTCCAGCTGCACAACGTGATACCTGGCTATCCCAAGCCAGACACAGATGCCATG	8241	VERSION	AB037723.3	GI:71891744	
QY	7526	GAAACCTCCTACGAGCTCATCCACACAGATGAAAACGAGGAGTGGGACAAACAGCAAG	7585	KEYWORDS			
Db	8242	GAAACCTCCTACGAGCTCGTACACACACAGATGAAAACCTCAGGAATGGGACAAACAGCAAG	8301	SOURCE	Homo sapiens (human)		
				ORGANISM	Homo sapiens		
					Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
					Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;		
					Hominidae; Homo.		
				REFERENCE	1		
				AUTHORS	Nagase, T., Kikuno, R., Ishikawa, K.I., Hiroseawa, M. and Ohara, O.		
				TITLE	Prediction of the coding sequences of unidentified human genes.		
					XVI. The complete sequences of 150 new cDNA clones from brain which		
					code for large proteins in vitro		
				JOURNAL	DNA Res. 7 (1), 65-73 (2000)		
				PUBMED	10718198		
				REFERENCE	2	(bases 1 to 10826)	









Qy	5654	TGGTCA	6734	CTCACA
Db	3361	TGGTCA	4441	CTCACAC
Qy	5714	GCTGGC	6794	AAGATG
Db	3421	GCTGGC	4501	AAGATG
Qy	5774	ACATCC	6854	GCTGCT
Db	3481	ACATCC	4561	GCTGCT
Qy	5834	GTGCTG	6914	GATGSC
Db	3541	GTGCTG	4621	GATGSC
Qy	5894	TCTTCT	6974	TATGCA
Db	3601	TCTTCT	4681	TATGCA
Qy	5954	TACTAC	7034	ATCACCT
Db	3661	TACTAC	4741	ATCACCT
Qy	6014	GAGGAT	7094	GATGAG
Db	3721	GAGGAT	4801	GATGAG
Qy	6074	TATGCA	7154	GGTTGT
Db	3781	TATGCA	4861	GGTTGT
Qy	6134	TATGCA	7214	CCCACT
Db	3841	TATGCA	4921	CCCACT
Qy	6194	ACCATC	7274	GTCCAC
Db	3901	ACCATC	4981	GTCCAC
Qy	6254	GAAGGC	7334	GAGCTG
Db	3961	GAAGGC	5041	GAGCTG
Qy	6314	ATGCAG	7394	AACAAC
Db	4021	ATGCAG	5101	AACAAC
Qy	6374	TCAGGC	7454	TGGTGC
Db	4081	TCAGGC	5161	TGGTGC
Qy	6434	ATCACC	7514	ATGGAT
Db	4141	ATCACC	5221	ATGGAT
Qy	6494	GTGCAG	7574	GACAAC
Db	4201	GTGCAG	5281	GACNAC
Qy	6554	GGCGAG	7634	GTCACT
Db	4261	GGCGAG	5341	GTCACT
Qy	6614	TATGAT	7694	CCAAAG
Db	4321	TATGAT	5401	CCAAAG
Qy	6674	CGTACG	7754	TTGAAG
Db	4381	CGTACG	5461	TTGAAG
			7814	GTGTGC





QY	155	TCAGCGAGACCCCTGAAGGCCTACGACCCAGGACGCCCGCCTAGCCTATGGCAGCGCGTC	214
Db	443	TCGAGTGAGACCCCTCAAAGCCTTCGACCAGGACTCCAGACTGGCTTATGGCAGCGCGTC	502
QY	215	AAGGACATTGTGCCGAGGAGGCCGAGGAATTCTGCCGCACAGGTGCCAACTTCACCCCTG	274
Db	503	AAAGACCTGGTGACCATGAGGCCGACGAGTTCAGCAGACAAGGGCCGGACTTTCTCTCTC	562
QY	275	CGGGAGCTGGGGCTGGAAGAGTAACGCCCCCTCACGGGACCCCTGTACCGGACAGACATT	334
Db	563	AGAGACATGGCCTTCGAGATCCCGTCCGCCACATATGGGAGCGTACCCGGACAGAAATG	622
QY	335	GGCCTGCCCCAATGCGGCTACTCCATGGGGGTGGCTCTGATGCCGACATGGAGGCTGAC	394
Db	623	GGCCTTCCCCACCCGCACTACTCAGTGAGTGTGGCATCAGACGCTGACACAGAAACAGAC	682
QY	395	ACGGTGTCTCCCTTGAGCACCCCGTGCCTGTGSGGCCGGAG--CACACGGTTCAGGG	451
Db	683	GGCATAATGTCCCCCGAGCACGCCGTCCGCCCTCTGGGGCCGAGCAACACCAATCCGGC	742
QY	452	CGCAGCTCCTGCCTGTCAGCCGGGCCAATTCCAATCTCACACTCACCGACACCGAGCAT	511
Db	743	CGCAGTTCCTGCCTGTTACGACAGAGCCNACTCCAACCTTACGCTCACCGACACCGAGCAT	802
QY	512	GAAAACTGAGACTGATCATCC-----	534
Db	803	GAAAACTGAGAAATGCTCTCTGCAATTGCTCATGTGCTTCTCTTCCCTCTGCGAC	862
QY	535	-----	534
Db	863	TCCCCTTACCTCCCCCTTCCCACGCAGCCAAATCAGAGCCAGGGAAGTTGCTAGGTAAC	922
QY	535	-----	534
Db	923	AGCGGGCTCAGGCCGGCCGGGACTCTGAGTCGGAAGATGAGTTTGGCCCCCAATTCATTCT	982
QY	535	-----	538
Db	983	TTAGTTAAACCGGCTCAGGGAACGTCTGCACCTCCGGCCGCCGCTACTGCTAATGAGGGC	1042
QY	539	GGCCTGCAGAAACCACGCGGGCTCCGGACGCCGCCGCCGCTCTCGCACGCCCAACACC	598
Db	1043	TCGTTCCAGAAATCACTACGGTTGCGAACGCCCACTTACCCCTGTTTCACTCGCACTCC	1102
QY	599	CCCAACCCAGCACACGCGGCTCCATTAACTCCCTGAACCGGGGGCACTTCACGCCGAGG	658
Db	1103	CCCAGTCAGCACCAACCGCTTCCATCGGTTCCCTGAGCCGCAGCAACTACCCAGCGC	1162
QY	659	AGCAACCCAGCCCGCCCCCACGGACCACTCGCTCTCCGGAGAGCCCCCTGCCGCGCGC	718
Db	1163	AGTAACCCGAGCCCGGCACCCACCGATAGTTTCAGCTCCCAATGAGGGTCCGAC---AAGT	1219
QY	719	GCCCAGGAGCCTGCCCAACGCCCCAGGAGAACTGGCTGTCTCAACAGCAACATCCCCCTGGAG	778
Db	1220	GCCCAGGACTCCAGCAGCGGCCAGGACAACTGGCTTCTCAACAGCAACGTTCTCTCTAGAG	1279
QY	779	ACCAGGAACCTAGGCAAGCAGCCATTCTTAGGACATTGCGAGGACAACTCATTTGAGATG	838
Db	1280	ACCAGAAACATAGCAAAAGCAGACATTCTTAGAGACTTTGCGAGGACAACTTTATAGAGATG	1339
QY	839	GACATTCTCGGCGCCTCCGSCCATGATGGGGCTTACAGTGAACGGGCACTTCTCTTTCAAG	898
Db	1340	GACATACTGGCGACAGCTCGCGCGGACGGCGCTTACACTGATGGACACTTTCTTTTCAAG	1399
QY	899	CCTGAGGCACCTCCCCGCTCTTCTGCACCACATCACCAAGGTTACCCACTGACGTCACGC	958
Db	1400	CCTGGCGGACCTCGCCCTTTGTACTGCACCACCTTCAACCTGGTTACCCCTTTCAGCTCAGC	1459
QY	959	ACAGTGTACTCTCCTCCGCCCCGACCCCTGCCCGCGAGCACCTTCCGCCCGCCGCTTT	1018
Db	1460	ACGGTGTACTCTCCTCCGCCCGCGCCCTGCCAAAGAAACACTTCTCACGGCCTGCCTTT	1519
QY	1019	AACCTCAAGAAAGCCCTCCAAGTACTGTAACCTGGAAGTGGCAGGCCCTTGAGCGCCATCGTC	1078

Db	1520	AGCCTAAAGAAACCTTATAAGCACTGCAACTGGAAATGTGCTGCCCTCAGTGCCATCCTC	1579
QY	1079	ATCTAGCCACTCTGGTCATCCTGTGGCATACTTTGTGGCCATGCACCTGTTTGGCCTA	1138
Db	1580	ATCTCCGTCACCCCTGGTGTTCCGTGGCATACTTTATTGCCATGCACCTCTTTGGACTC	1639
QY	1139	AACTGGCACCTGCAGCCGATGGAGGGGAGATGTATGAGATCACGGAGGACACAGCCAGC	1198
Db	1640	AACTGSCATTTCAGCCGGTGCAGAGGCAGATATATCAGCTGACGGAGGACAACACCACT	1699
QY	1199	AGTTGGCCTGTGCCAACCGACGTCTCCCTATACCCCTCAGGGGACATGGCTTAGAGACC	1258
Db	1700	GGCCTACATCTGCCACAGATCTGGGGTGCCACCTCTGGGTAAACACAGSTCTAGAGTTT	1759
QY	1259	CCTGACAGGAAAGGCAAGGAACCAAGAGGAAAGCCAGTAGTTTCTTTCCAGAGGAC	1318
Db	1760	CCAGATCGAGGAAGCAGAGAT-----GATGGTAAACTAGATGGCTTCTTCCCGGAGGAC	1813
QY	1319	AGTTTCATAGATTCTGGAGAAATTGATGTGGGAAGCGGAGCCTCCAGAAAGATTCTCTCT	1378
Db	1814	AGCTTCATAGACATGGGCGAGATAGACGTGGGGCCGCAAAAGTGCTCAGCTGATCCCCT	1873
QY	1379	GGCACCTTTCGGAGATCTCAAGTGTTCATAGACCATCCTGTGCATCTGAAATTCATGTG	1438
Db	1874	GGAACTTTTGGAGGTCGCAGGTCTTTATTGATCACCCCATGTACCTCAAAATCAATGTG	1933
QY	1439	TCTCTGGAAAGGCAGCCCTGGTTGGCATTTATGGCAGAAAAGGCCCTCCCTCTTACAT	1498
Db	1934	TCCCTTAGTAAGATGCCTTGGTGGGATCTACGGGAGGAGGACTGCCACCGTCACAC	1993
QY	1499	ACACAGTTTGACTTTGTGGAGCTGTGGATGGCAGGAGGCTCCTAACCCAGGAGCGCGG	1558
Db	1994	ACACAGTTTGACTTTGTGGAGCTGTGGATGGTCTGTCGGCTTCTGTCGCAAGGCTTGCCA	2053
QY	1559	AGCCTAGAGGGGAC-----CCCGCGCCAGTCTCGGGGAACCTGTGCCCCCTCCAGCCAT	1612
Db	2054	GGTCTTGATGGTCCGCCCTTTTCCAGCCCGCAGCAGCGGAGCCTGGTGCCCTATAACCAATCAT	2113
QY	1613	GAGACAGGCTTCATCCAGTATTTTGGATTTCAGGAATCTGGCACCTTGGCTTTTACAATGAC	1672
Db	2114	GATACAGGATGTATACAGTACATGGACTCAGGAATCTGGCACTTGGCTGTATACAATGAT	2173
QY	1673	GGAAAGGAGTGCAGAAAGTGTTTCTTCTCACCACTGCCATTGAGTCGGTGGATACTGC	1732
Db	2174	GGGAAGGAGACTGAGCAGGTGTCTTCTTAACAACATGCAATCGACTCTATTGATGACTGT	2233
QY	1733	CCCAGCACTGCTATGGCAATGGTGACTGCATCTCTGGGACCTGCCACTGCTTCTCTGGGT	1792
Db	2234	CCTAGTAAGTGTTTGGAAATGGAGACTGTGTCTGGAACCTGCCAATGTTTCCAGGC	2293
QY	1793	TTCTTGGGCCCCGACTGTGGCAGAGCCCTCTGCCCCGTGCTCTGTAGCGGAAATGGCCAA	1852
Db	2294	TTCAGAGGACCCGACTGCAGCAGGGCATCATGTCTGTGCTGTGCAGTGGGAACGGTCAG	2353
QY	1853	TACATGAAAGGCAGATGCTTGTGCCACAGTGGCTGGAAAGGCGCTGAGTGCAGATGTGCCC	1912
Db	2354	TACCTGAAAGGACGCTGCATGTGTACAGCGGCTGGAAAGGGTCTGAATGTGATGTTCTCT	2413
QY	1913	ACCAACCACTGCTATCGATGTGGCCTGCAGCAACCATGGCACCTGCATCACGGGACCTGC	1972
Db	2414	ACAAACCACTGCATCGACATCACCTGCAGTGGACATGGAACATGCATTTGTGGAACTTGC	2473
QY	1973	ATCTGCAACCTTGGCTACAAGGGCGAGAGCTGTGAGGAAGTGGACTGCATGGACCCCA	2032
Db	2474	ATCTGCAATCTAGCTACAAAGGAGAAACTGCGAAGAAAGTGGACTGTCTGGACCCCAACC	2533
QY	2033	TGTTCAGGCCGGGTGTCTGCGTGAGAGCGCAATGCCAATGCTTTGTGGATGGGGAGGC	2092
Db	2534	TGTTCAGGGAGAGGTGTGTCGTTCCGGGAGAGTGCCACTGTTTGTGGATGGGAGGT	2593
QY	2093	ACCAACTGCGAGACCCCCAGGGCCACATGCTTAGACCAGTGTTCAGGCCACGGAACCTTC	2152



Db 2594 CCTGGATGTGAGAGTCTCGTGGTCTCTGTATGGAGCAGTGTCTTGGACACGGGAGTTTC 2653  
Qy 2153 CTCCCGGACACCGGGCTTTGCAGCTGTGACCCAAAGCTGGACTGGACACGACTGTTCTATC 2212  
Db 2654 TTGGCTGATACAAACACCTGCAACTGTGACCACAACTGGACCGGTCTAGACTGCTCCACA 2713  
Qy 2213 GAGATCTGTGCTGCCGACTGTGGTGGCCATGSCGTGTGCGTAGGGGGCACCTGCCGTGC 2272  
Db 2714 GAGCTGTGCGCAGCGGACTGTGGTGACATGGCATCTGTGTGGCGGCGAGCTGCCGTGC 2773  
Qy 2273 GAGGATGGCTGGATGGGGCAGCCTGCGACCAAGCGGGCCTGCCACCCCGCTGTGCCGAG 2332  
Db 2774 GACGAGGGCTGGATGGGCACCGGGTGCAGCAACGGGCTTGTCAACCCTCGTGCAGCGAA 2833  
Qy 2333 CATGGGACCTGCCGCGACGGCAAGTGCAGTGCAGCCCTGGCTGGAATGGCGAACACTGC 2392  
Db 2834 CACGGGACCTGCAAGGACGGAAAGTGCGAATGCAGCCGGGATGGAATGGAGAACACTGC 2893  
Qy 2393 ACCATCGCTCACTATCTGGATAGGGTAGTTAAAGAGGGTTGCCCTGGGTTGTGCAATGGC 2452  
Db 2894 ACTATC-----GAGGGCTGCCCTGGTCTGTGCAATGGC 2926  
Qy 2453 AACGCGAGATGTACCTTAGACCTGAATGGTTGGCACTGGCTCTGCCAGCTGGGCTGGAGA 2512  
Db 2927 AATGGCAGATGCACGCTGGGTAAATAATGGCTGGTACTGGCTTGTCAACTGGGCTGGCGG 2986  
Qy 2513 GGAGCTGGCTGTGACACTTCCATGGAGACTGCCCTGCGGTGACAGCAAGACAAATGATGGA 2572  
Db 2987 GGAGCAGGCTGCGACACATCAATGGAGACGGCCTGCACTGACGGCAAGGACAAATGATGGA 3046  
Qy 2573 GATGGCCTGGTGGACTGCATGGACCCCTGACTGCTGCCCTCCAGCCCCCTGTGCCAATATCAAC 2632  
Db 3047 GATGGGTTGACGGGACTGCATGGACCCGGATTGCTGCTTGCAAGCATCATGTCAACAAACA 3106  
Qy 2633 CCGCTGTGCTGGCTCCCTAACCCCTCTGGACATCATCCAGGAGACACAGGTCCCTGTG 2692  
Db 3107 TCTCTGTGTGGGCTCTCCCGATCCCTCTGGATATCATTCAGGAAACCCAAATCTCTTCC 3166  
Qy 2693 TCACAGCAGAACTACACTCCTTCTATGACCGCATCAAGTTCTCTGTTGGCAGGGACAGC 2752  
Db 3167 AGTCTGAGCACCCCTGCAGTCCCTCTATCAGCGCATCCATTTCTTGGTGGCCGGACAGC 3226  
Qy 2753 ACGCACATAATCCCGGGGAGAACCCCTTTGATGGAGGGCATGCTTGTGTTATTCGTGSC 2812  
Db 3227 ACCCATGTATACATGATGTCAATCCCTTTGATGGCATTCATGCTGCGTTATCCGGGA 3286  
Qy 2813 CAAGTGATGACATCAGATGGAACCCCTCGTGGTGTGAAACATCAGTTTTGTCAATAAC 2872  
Db 3287 CAAGTGGTGACTTCTGATGGAACCTCCTTGGTGGCGTAAATATCAGCTTCATTAACAAA 3346  
Qy 2873 CCTCTCTTTGGATATACAAATCAGCAGGCAAGATGGCAGCTTTGACTTGGTGACAAATGGC 2932  
Db 3347 CCGGCCTATGGGTATACAAATCACCAGACAGGACGGCAGCTTTGACCTGGTAAGCAACGGT 3406  
Qy 2933 GGCATCTCCATCATCCTGCGGTTTCGAGCGGGCACCTTTTCATCACACAGGAGCACACCCTG 2992  
Db 3407 GCGGTGGCCATTGGCCTGCGGTTTGACGCTGCTCCCTTTATCACTCAGGAGCACACCTTG 3466  
Qy 2993 TGGCTGCCATGGGATCGCTTCTTTGTCTATGGAACCATCATCATGAGACATGAGGAGAAT 3052  
Db 3467 TGGCTGCCGTGGGGCGTTCTTCGTCTATGGATACAAATGTTGATGCGACACGAGGTCAAC 3526  
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COMMENT Neuherberg, GERMANY  
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de; sequenced by DKFZ (German Cancer Research Center, Heidelberg/Germany) within the cDNA sequencing consortium of the German Genome Project.  
This clone (DKFZp686K11107) is available at the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further information about the clone and the sequencing project is available at http://mips.gsf.de/proj/cDNA/.

FEATURES  
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ORIGIN

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Db	4021		CGGGAAGGGGAGGAAGGCTGCGGGCCTGGACAGAGGGGGAGAAAGCAGAGTGTGAGC	4080
Qy	8225		ACAGGGCGGGTGCAAGGCTACGACGGCTTTTTCGTGATCTCTGTGAGCAGTACCCAGAA	8284
Db	4081		ACAGGGCGGGTGCAAGGCTACGACGGCTTTTTCGTGATCTCTGTGAGCAGTACCCAGAA	4140
Qy	8285		CTGTCAGACAGCGCCCAACAACATCCACTTCATGAGACAGAGCGAGATGGGCCGAGGTGA	8344
Db	4141		CTGTCAGACAGCGCCCAACAACATCCACTTCATGAGACAGAGCGAGATGGGCCGAGGTGA	4200
Qy	8345		CAGAGAGGAC	8354
Db	4201		CAGAGAGGAC	4210

RESULT 10  
AX952856 LOCUS AX952856 8964 bp DNA linear PAT 08-JAN-2004  
DEFINITION Sequence 132 from Patent WO03093305.  
ACCESSION AX952856  
VERSION AX952856.1 GI:40783120  
KEYWORDS Mus musculus (house mouse)  
SOURCE Mus musculus  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muroidea; Muridae; Murinae; Mus.  
REFERENCE 1

AUTHORS	Lovejoy,D., Chewpoy,R.B., Barsyte,D. and Rotzinger,S.
TITLE	Teneurin c-terminal associated peptides (tcap) and methods and uses thereof
JOURNAL	Patent: WO 03093305-A 132 13-NOV-2003; Lovejoy, David (CA) ; Chewpoy, R. Bradley (CA) ; Barsyte, Dalia (CA) ; Rotzinger, Susan (CA)
FEATURES	Location/Qualifiers
source	1..8964 /organism="Mus musculus" /mol_type="unassigned DNA" /db_xref="taxon:10090"
exon	50..8197
ORIGIN	
Query Match	42.4%; Score 3544.6; DB 6; Length 8964;
Best Local Similarity	65.6%; Pred. No. 0;
Matches	5458; Conservative 0; Mismatches 2679; Indels 186; Gaps 12;
Qy	35 ATGGACGTGAAGGAGAGGAAGCCTTACCCTCGCTGACCCGGCGC---CGGACGCCGAG 91 
Db	50 ATGGATGTGAAGAAACGCAGGCCTTACTGCTCTTGACCAAGAGCAGACGGGAAAGGAA 109 
Qy	92 CGCCGCTACACAGACTCGTCCGGGACAGCGAGGAGGGCAAGCCC---CGCAGAAATCG 148 
Db	110 AGCGCTATACAAATTCGTCGCGGACAATGAGGAGTGTAGGGTCCCCACGAGAGTCC 169 
Qy	149 TACAGTCCAGCGAGACCTGAAGSCCTACGACCAGG---ACGCCGCTAGCCTATGGC 205 
Db	170 TATAGTTCAGTGAAACCTTGAAAGCTTTCGATCATGATTATTCACGCTGCTTATGGA 229 
Qy	206 AGCCGCTCAAGGACATTGTGCCGCGAGGAGGCCGAGGAATTCTGCCGCACAGGTGCCAAC 265 
Db	230 AACAGAGTAAGGATTGGTCCACAGAGAAAGCCGACGAGTATACTAGACAAGGACAGAAT 289 
Qy	266 TTCACCCCTGCGGAGCTGGGGCTGGAAGAAATAACGCCCCCTCACGGGACCCTGTACCGG 325 
Db	290 TTTACCCCTAAGCAGTTAGGAGTGTGTAATCCGCAACTCGAAGAGGAGTGGCATTTGT 349 
Qy	326 ACAGACATTGGCCTGCCCCAATGCGGCTACTCCATGCGGGCTGGCTCTGATGCCGACATG 385 
Db	350 GCGGAAATGGGCTCCCTCACAGAGGTTACTCCATCAGTGCAGGGTCAGATGCGGATACG 409 
Qy	386 GAGGCTGACACGGTGTGTCCCCTGAGCACCCCGTGCCTGTGTGGGCCGAGCACACGG 445 
Db	410 GAAACGAAGCAGTGTCCCCTGAGCATGCGATGAGACTTTGGGGCAGGGGGTCAAA 469 
Qy	446 TCAGGGCGCAGCTCCTGCCTGTCCAGCCGGGCAATTCCAAATCTCACACTCACCGACACC 505 
Db	470 TCGGGCGCAGTTCCTGCCTGTCAAGCCGGTCCAACTCCGCCCTCACCTGACAGACAG 529 
Qy	506 GAGCATGAAACACTGAGACTGATCATCCGGCGGCTGCAGAACCCACGGCGGCTCCGG 565 
Db	530 GAGCAGAGAACAGGTGCGACAGTGAGAGCGAGCAACCTTCAAACAACCCAGGGCAACCC 589 
Qy	566 ACGCCGCGCGCGCTCTCGACGCCCCACACCCCAACCCAGCCCGGCCCTCCATT 625 
Db	590 ACCCTGCAGCCTTTGCCGCCATCCCAAGAGCAGCACCCGGCGCAGCATCACCCGTCCATC 649 
Qy	626 AACTCCCTGAACCGGGCAACTTCACGCGGAGGAGCAACCCAGCCCGGCCCGCCAGGAG 685 
Db	710 GCTTTGCCCGCGCAGCTGCAAC-----CACACCCGAGTCCGTCCAGCTGCAGGAC 760 
Qy	746 AACTGGCTGCTCAACAGCAACATCCCCCTGGAGACCAGGAACCTAGGCAAGCAGCCATTC 805 
Db	761 AGTGGGTCCTTGGCAGTAATGTACCACCTGGAAAGCAGGCATT----- 804 
Qy	806 CTAGGGACATTGCAGGACAAACCTCATTTGAGATGGACATTTCTCGGGCGCTCCCGCCATGAT 865 
Db	805 ----- 804



QY	866	GGGGCTTACAGTACGGGCACTTCCTCTTCAAGCCTGGAGGCACCTCCCGCTCTTCTGC	925	1946	CATGGCACCTGCATCACGGGCACCTGTCATCTGCAACCCCTGGCTACAAGGGCGAGAGCTGT	2005
Db	805	-----CCTATTCAAAACAGGCACAGGACGACGCGACGCACTGTTCAGT	844	1817	CGTGGGATTGTCATCATGGGCTCTTGGCTTGTAACCTCGGGATACAAAGGAGAAACTGT	1876
QY	926	ACCACATCACAGGTACCCACTGACGTCACGACACAGTGTACTCTCTCTCCCGCCCGACCC	985	2006	GAGGAAGTGGACTGCATGGACCCACACATGTTTCAAGCCGGGTGTCTGCGTGAGAGGCGAA	2065
Db	845	ACGGCAACCCCGGATACACAATGGCATCTGGCTCTGTTATTCTCGGCTTACCCGGCCA	904	1877	GAGGAAGCGGACTGTCTAGACCCCTGGATGTTCTAATCACGGGTGTGTATCCATGGGGAA	1936
QY	986	CTGCCCGCAGCACCTTCGCCCGCGCGCTTAAACCTCAAGAAGCCCTCCAAGTACTGT	1045	2066	TGCCATTGCTTTGTGGGATGGGAGGACCAAACTGCGAGACCCCGGGCTTTGCAGCTGTGACCCA	2125
Db	905	CTTCTTAGAAACACCCTATCAAGAAGTGCTTTTAAATTCAGAAGTCTTCAAAGTACTGC	964	1937	TGTCACGTGCAATCCAGGCTGGGTGGCAGCAAACTGTGAATACTGAAGACTATGTGTGCA	1996
QY	1046	AACTGGAAGTGCAGCCCTGAGCGCCATCGTCATCTCAGCCACTCTGGTCATCCTGCTG	1105	2126	GACCAAGTTCAGGCCACGGAACCTTCCTCCCGACACCCGGCTTTGCAGCTGTGACCCA	2185
Db	965	AGCTGGAGGTGCACCGCACTGTGTGTAGGGTCTCAGTGCTCCTGGCCATTCTCCTC	1024	1997	GACCAGTGTCTAGGCCACGGGACTTACCTTCAAGAAAAGCGGCTCCTGCACTTGCAGCCCA	2056
QY	1106	GCATACTTTGTGGCCATGCACCTGTTTGGCCTAAACTGGCACCTGCAGCCGATGGAGGG	1165	2186	AGCTGGACTGGACACGACTGTTCTATCGAGATCTGTGCTGCCGACTGTGTGGCCCATGGC	2245
Db	1025	TCCTATTTATAGCAATGCATCTATTGGCCTCAACTGGCACTTACAGCAGACGGAAAT	1084	2057	AATTGGACTGGCCCCGACTGCTCAAAATGAAATATGTTTCAGTGGACTGCGGCTCACACGGC	2116
QY	1166	CAGATGATGAGATCACGGAGGACACAGCCAGAGTGGCCTGTGCCAACCGACGCTCTCC	1225	2246	GTGTCGTAGGGGACCTGCGGCTGCCAGGATGCTGGATGGGGCAGCCTGCGACCCAG	2305
Db	1085	GACACATTCGAGA-----ATGGAAGAGTGAATTCGACACCGTGCCAAACAACACTGTA	1138	2117	GTCTGCATGGGGGCTCCTGTGCTGTGAAGAAGSCTGGACCGGCCCGCGTGTAAATCAG	2176
QY	1226	CTATACCCCTCAGGGGGCACTGGCTTAGAGACCCCTGACAGGAAAGGCAAGGAACCACA	1285	2306	CGGGCTGCCACCCGCTGTGCCGAGCATGGGACCTTCCCGCAGCGCAAGTGCGAGTGC	2365
Db	1139	TCGTTACCTTCTGGCGACA-----	1157	2177	AGAGCTTGCCACCCCTCGCTGTGCTGAGCACGGGACGTCAAGGACGGCAAGTGCGAGTGC	2236
QY	1286	GAAGGAAAGCCAGTAGTTTCTTTTCACAGAGGACAGTTCATAGATTCTGGAGAAATTGAT	1345	2366	AGCCCTGGCTGGAATGGCGAAACACTGCACCATCGCTCACTATCTGGATAGGGTAGTTAAA	2425
Db	1158	-ATGGAATAATTAGGTGGATTACACATGAAAAATAACACCATAGATTCCGGAGAACTTGAT	1216	2237	AGCCAAGGATGGAACGGAGAGCACTGCACAAATTGCTCACTATTTGGATAAGATAGTTAAA	2296
QY	1346	GTGGAAGGGCAGCCTCCAGAAAGATTCTCTCTGGCACTTTCTGGAGATCTCAAGTGTTC	1405	2426	GAGSETTGCCCTGGGTTGTGCAATGGCAACGGCAGATGTACCTTAGACCTGAATGTTGG	2485
Db	1217	ATTGGCCGGAGAGCAATTCAGAGGTTCCCGCCGGGATCTTCTGGAGATCGCAGCTCTTT	1276	2297	GAGGTTTGCCCGGCTTGTGCAACAGCAATGGAGATGCACACTGGACCAAAACGGCTGG	2356
QY	1406	ATAGACCATCCTGTGCATCTGAAATTCAAATGTGTCTCTGGGAAAGGCAGCCCTGGTTGGC	1465	2486	CACCTGCTCTGCCAGCTGGGCTGGAGAGGAGCTGGCTGTGACACTTCCATGGAGACTGCC	2545
Db	1277	ATTGATCAGCCACAGTTTCTTAAGTTCAACATCTCTTTCAGAAGGATGCATTGATCGGA	1336	2357	CACCTGCTTTGCCAGCCAGGTTGGAGAGGAGCAGGCTGTGACGTAGCCATGGAGACCCCTC	2416
QY	1466	ATTATGGCAGAAAAGCCTCCCTCTTCACATACACAGTTTGACTTTGTGAGCTGCTG	1525	2546	TGCGGTGACAGCAAAAGACAATGATGGAGATGGCCTGGTGGACTGCATGGACCCCTGACTGC	2605
Db	1337	GTGTACGGCCGGAAGGCTTACCGCCTTCCCATACTCAGTACGACTTGTGGAACACTG	1396	2417	TGTACAGACAGCAAAAGACAAACGAAGGAGACGGACTCATTGACTGCATGGATCCTGATTGC	2476
QY	1526	GATGGCAGGAGGCTCCTAAACCCAGGAGCGCGAGCCTTAGAGGGGACCCCGCCAGTCT	1585	2606	TGCCTCCAGCCCTGTGCCATATCAACCCGCTGTGCCCTTGGCTCCCTAACCCCTCTGGAC	2665
Db	1397	GATGGTAGCAGGTTAATTGCGAGAGAGCAGCGGAACCTTGGTGAGTCCGAAAGAGCCGGG	1456	2477	TGCCTCCAGAGCTCCTTGCCAAAACCCAGCCCTACTGTCTGGCTTGCCTGATCCTCAGGAT	2536
QY	1586	CGGGAACTGTGCCCCCTCCAGCCATGAGACAGGCTTCATCCAGTATTTGGATTCAGGA	1645	2666	ATCATCCAGGAGACACAGGTCCCTGTGTACAGCAGAACTTACACTCCTTCTATGACCCGC	2725
Db	1457	CGGAGGCGAGATCTGTACGCTGCACGAAGCTGSGCTTCATCCAGTACTTGGATTCTGGA	1516	2537	ATCATTAGCCAAAGCCTTCAGACACCACTCTCAGCAAGCTGCCAAGTCCCTTCTATGACCGA	2596
QY	1646	ATCTGGCACTTGGCTTTTAAATGACGGAAAGGAGTCAGAAGTGGTTTCTCTTCACC	1705	2726	ATCAAGTTCCCTCGTGGCAGGACAGCACGCAACATAAATCCCGGGAGAACCCCTTTGAT	2785
Db	1517	ATCTGGCATCTGGCTTTTATAACGACGGGAAAAACCCAGAGCAGGTCTCCTTTAAACACG	1576	2597	ATCAGTTTCTGTGATTGGATCGGATAGCACCCACCGTCTCCTGGAGAAAGTCCGTTCAAT	2656
QY	1706	ACTGCCATTGAGTCGGTGGATAACTGCCCCAGCAACTGCTATGGCAATGGTGACTGCATC	1765	2786	GGAGGCATGCTTGTGTTATTCTGTGGCCAAGTGTAGACATCAGATGGAACCCCTTGTT	2845
Db	1577	ATCGTTATAGAGTCTGTGTGGAAATGCCCCCGAAATTGCCATGGAAATGGAGAGTGTGT	1636	2657	AAGAGTCTTGCGTCCGTCAATCAGAGGCCAAGTACTAACAGCTGATGGAACCCCACTATT	2716
QY	1766	TCTGGGACCTGCCACTGCTTCTGGGTTTCTGGGCCCGACTGTGGCAGAGCCTCTGC	1825	2846	GGTGGAACATCAGTTTTTGTCAATAACCCCTCTCTTTTGGATATACAATCAGCAGGCAAGAT	2905
Db	1637	TCTGGAACCTTGCCATTGTTTCCCGGGTTTCTAGGTCGGATTGTTCAAGAGCAGCCTGT	1696	2717	GGCGTCAACGTGTGTTTTTACACTACTCGGAATATGGATATACCATTACCCGCCAGGAT	2776
QY	1826	CCCGTGCTCTGAGCGGAAATGGCCATAACATGAAAGGCAGATGCTTGTGCCACAGTGGC	1885	2906	GGCAGCTTTGACTTGGTGACAAATGGCGGCATCTCCATCATCTCGGTTTCGAGCGGCA	2965
Db	1697	CCGGTGCTCTGAGTGGCAACGGGCAATACTCCAAGGCCGCTGCCTGTGCTTCAGTGGC	1756	2777	GGAATGTTTGACTTGGTGGCAATGGTGGCGCTTCTCTGACTTTGGTATTTGAGCGTTCC	2836
QY	1886	TGGAAGGGCTGAGTGCATGTGCCCAACCAACCAAGTGTATCGATGTGGCCTGCAGCAAC	1945	2966	CCTTTTCATCACACAGGAGCACACCCCTGTGGCTGCCATGGGATCGCTTCTTTGTCAATGGAA	3025
Db	1757	TGGAAGGGCACCGAGTGTGACGTGCCGACGACCCAGTGCATTGACCCGCACTGCGGGGT	1816	2837	CCATTCTCACTCAGTACCACACTGTGTGGATTCCCTTGGAAATGCTTTTATGTGATGGAT	2896
QY				3026	ACCATCATCATGAGACATGAGGAGAAATGAGATTCCCAGCTGTGACCTGAGCAATTTTGCC	3085
Db						

Db 2897 ACCCTTGTCAGAAAGAGGAGAACGACATTCCCAGCTGTGACCTCAGTGGCTTTGTG 2956  
QY 3086 CGCCCCAACCCAGTCGTCTCTCCATCCCCACTGACGTCCCTTCGCCAGCTCCTGTGCAGAG 3145  
Db 2957 AGGCCAAGTCCCATCATTTGTGTCTTCAACCGTTATCCACCTTCTTCAAGTCTTCCCTGAG 3016  
QY 3146 AAAGGCCCAATTGTGCCGGAATAATTCAGGCTTTGCAGGAGGAAATCTCTATCTCTGGCTGC 3205  
Db 3017 GACAGCCCCATCATCCCCGAGACACAGGTCTGCATGAAGAAACCAAAATCCAGGAACA 3076  
QY 3206 AAGATGAGGCTGAGCTACCTGAGCAGCCGACCCCTGGCTACAAATCTGTCTCTGAGGATC 3265  
Db 3077 GATTTGAAACTTTCTACTACCTGAGTTCCAGAGCGGCAGGGTACAAGTCAGTTCTTAAGATT 3136  
QY 3266 AGCCTCACCCACCGACCATCCCCCTTCAACCTCATGAAGGTGCACCTCATGGTAGCGGTG 3325  
Db 3137 ACCATGACCCAGCGCTCATACCGTTTAACTCATGAAGTCCATCTGATGGTGGCCGTG 3196  
QY 3326 GAGGGCCGCTCTTCAGGAAGTGGTTCCGCTCAGGCCCCAGACCTGTCTCTATTATTTCATT 3385  
Db 3197 GTTGGGAGACTCTTCAGAAAGTGGTTTCCCTGCCTCGCCAAACTTTGGCCTACACGTTTCATC 3256  
QY 3386 TGGGACAAAGACAGACGTCTACAAACAGAAAGTGGTTTGGGCTTTCAGAAAGCTTTGTTTCC 3445  
Db 3257 TGGGATAAGACGGACGCATATAAATCAGAAAGTCTACGGCTTGTTCAGAGCGAGTTGTGTCC 3316  
QY 3446 GTGGGTTATGAATATGAATCCTGCCAGATCTPAATCTGTGGGAAAAAAGAACAAACAGTG 3505  
Db 3317 GTCGGATACGAGTACGAGTCGTCTTGGACCTGACTCTCTGGGAAAAGAGGACTGCCGTT 3376  
QY 3506 CTGCAGGGCTATGAATAATTGACGCGTCCAAAGCTTGGAGGATGGAGCCTAGACAAACATCAT 3565  
Db 3377 TTGCAAGGCTATGAGTTGGATGCTTCGAACATGSGCGCTGGACGTTGGACAAGCACCAT 3436  
QY 3566 GCCCTCAACATTCAAAGTGGTATCCTGCACAAAGGGAATGGGAGAACCAAGTTTGTGTCT 3625  
Db 3437 GTACTGGACGTTTCAGAACGGTATACTATACAAAGGAAATGGAGAAATCAGTTTCATCTCT 3496  
QY 3626 CAGCAGCCTCCTGTCAATTGGGAGCATCATGGGCAATGGGCGCCGGAGAGCATCTCTCTGC 3685  
Db 3497 CAGCAGCCTCCGGTGGTCAGCAGCATCATTGGGTAATGGTCGGAGCGGTAGCATCTCATGC 3556  
QY 3686 CCCAGCTGCAACGGCCTTGCTGACGGCAACAAGCTCCTGGCCCCAGTGGCCCTCACCTGT 3745  
Db 3557 CCAAGTTGCAATGGTCAAGCTGACGGGAACAAACTCTGGCACCCCGTGGCGCTGGCCTGT 3616  
QY 3746 GGCTCTGACGGGAGCCTCTATGTGGTGATTTCAACTACATTAGAAAGGATCTTCCCTCT 3805  
Db 3617 GGGATCGACGGCAGTCTATACGTAGGGGATTTCAATTACGTCCGGCGGATATTCCTCGTCT 3676  
QY 3806 GGAAATGTCACCAACATCCTAGAGCTGAGGAATAAAGATTTTCAGACATAGTCACAGTCCA 3865  
Db 3677 GGGAAATGTGACAAAGTGTTTAGAACTAAGAAATAAAGATTTTAGACATAGTAGCAACCCA 3736  
QY 3866 GCACACAAATACTACTGGCCACAGACCCCATGAGTGGGGCCGTCTTCTCTTCTGACAGC 3925  
Db 3737 GCTCACAGATACTACCTGGCTACGGACCCAGTCACCGAGATTTGTACGTCCTGTGATACT 3796  
QY 3926 AACAGCCGGCGGTCTTTAAAAATCAAGTCCACTGTGGTGGTGAAGGACCTTGTCAAGAAC 3985  
Db 3797 AACACCCGCAGAAATCTATCGGCCGAAATCACTACGGGAGCCAAAGACCTTGACTAAAAAAC 3856  
QY 3986 TCTGAGGTGGTTGCGGGACAGGTGACCAGTGCCTCCCTTTGATGACACTCGCTGCGGG 4045  
Db 3857 GCTGAAGTGGTGGCAGGGACCGGGAAACAGTGCCTTCCCTTTGACGAGGCCAGGTGTGGG 3916  
QY 4046 GATGGTGGGAAGGCCACAGAAGCCACACTCACCAATCCAGGGGTATTACAGTGGACAAG 4105  
Db 3917 GATGGAGGCAAGGCTGTGGAAGCAACGCTCATGAGTCCCAAAGGAATGGCAATCGATAAG 3976  
QY 4106 TTTGGGCTGATCTACTTCTGGATGGCACCATTGATCAGACGCATCGATCAGAATGGGATC 4165

Db 3977 AACGACTGATCTACTTTTGTGATGGAACCATGATCAGAAAAGTTGATCAAAAATGGAATC 4036  
QY 4166 ATCTCCACCCCTGCTCGGCTCTAATGATCTCACATCAGCCCCGGCCACTCAGCTGTGATTCT 4225  
Db 4037 ATATCAACTCTCTCGGCTCCAACGACCTCAGTCAGCTCGACCTTTAACTGTGATACT 4096  
QY 4226 GTCATGGATATTTCCAGGTAAGACTGGAGTGGCCCCACAGACTTAGCCATCAACCCCAATG 4285  
Db 4097 AGCATGCATATCAGCCAGGTGCGTCTGGAATGGCCCACTGACCTCGCGATCAACCCCATG 4156  
QY 4286 GACAACTCATTATGTCTCTCGACAACAATGTGGTCTCTGCAAAATCTCTGAAAAACCCACAG 4345  
Db 4157 GATAACTCCATCTACGTCTCTGGATAATAACGTAGTTTACAGATCACTGAAAAACCGTCAG 4216  
QY 4346 GTCGCATTTGTCCCGGAGGCCCATGCACCTGCCAGTCCCTGGCAATTGACCACCTTCCCTG 4405  
Db 4217 GTCCGCATCGTCCCGGGCGGCCCATGCACTGTCAAGTCCCTGGAGTGG--AATACCCG 4273  
QY 4406 CTAAGCAAGGTGGCCATCCACGCAACCTTGGAGTCAGCCACCGCTTTGGCTGTTTCACAC 4465  
Db 4274 GTGGGGAAGCACGCGGTTTCAGACCACCTTGGAGTCAGCCACGGCCATTGCTGTCTTAC 4333  
QY 4466 AATGGGTCTCTGTATATTGCTGAGACTGATGAGAAAAAGATCAACCCGATCAGGCAGGTC 4525  
Db 4334 AGCGGGTCTTTACATCACGGAACCTGATGAGAAAGATCAACCGAATAAGGCAGGTC 4393  
QY 4526 ACCACTAGTGGAGAGATCTCACTCTGTTGCTGGGGCCCCCAGTGGTGTGACTGTAAAAAT 4585  
Db 4394 ACGACAGACGGGAGATCTCCTTAGTGGCTGGGATACCTTCGGAATGTGACTGCAAGAAC 4453  
QY 4586 GATGCCAACTGTGATTGTTTTTCTGGAGACGATGGTTATGCCAAGGATGCAAAAGTTAAAT 4645  
Db 4454 GACGCCAACTGTGACTGTACTACCAAAAGCGGAGACGGCTACGCCAAAGATGCCAAACTCAAT 4513  
QY 4646 ACCCATCTTCTTGGCTGTGTGCTGATGGGAGCTCTACGTGGCCGACCTTGGGAAC 4705  
Db 4514 GCGCGTCTCTCTGGCCGCTCGCCAGATGGCACTCTGTACATTTGCAGATCTGGGAAT 4573  
QY 4706 ATCCGAATTCGGTTTATCCGGAAGAACAAAGCCTTTCTCAACACCCAGAACATGTATGAG 4765  
Db 4574 ATCAGGATCCGGGCCGTTTCGAAGAAATAAACCTTTACTGAACTCAATGAATTTTACGAA 4633  
QY 4766 CTGTCTTCAACCAATTGACCAGGAGCTCTATCTGTTTGTATACCACCGGCAAGCACCTGTAC 4825  
Db 4634 GTTGCTCTCCAACATGATCAAGAGCTCTACATCTTTGACATCAACGGTACTCACCAGTAC 4693  
QY 4826 ACCCAAAGCCTGCCACAGGAGACTACCTGTACAACTTCACCTACACTGGGACGGCGAC 4885  
Db 4694 ACCGTAGCCTGTGTACGGGTGACTACCTATATAAATTTTAGTTACAGCAATGACAAATGAC 4753  
QY 4886 ATCACACTCATCAGACAAACAATGGCAACATGGTAAATGTCCCGCAGACTCTACTGGG 4945  
Db 4754 GTCACCGCTGTAACTGACAGCAATGGCAACACCCCTCCGAATCCGAAGGGATCCGAATCGG 4813  
QY 4946 ATGCCCCCTGTGGTGGTCCAGATGGCCAGGTGTACTGGGTGACCATGGGCACCAAC 5005  
Db 4814 ATGCCGTTGCGGTTGGTGTCTCTGTATAACAGGTGATATGGTTGACCATAGGCACCAAC 4873  
QY 5006 AGTGCACTCAAGAGTGTGACCACACAAAGGACACGAGTTGGCCATGTATGATACCATGGC 5065  
Db 4874 GGGTGTCTGAAAAAGCATGACCGCTCAGGGCTCGAACTGGTTTTGTACTTACCATGGC 4933  
QY 5066 AATTCCGGCCTTCTGGCAACCAAAAGCAATGAAAAACGGATGGACAACATTTTATGAGTAC 5125  
Db 4934 AACAGTGGGCTTTTAGCCACCAAAAGTACGAAACTGGATGGACAACATTTTGTGACTAT 4993  
QY 5126 GACAGCTTTGGCCGCTGACAAATGTGACCTTCCCTACTGGCCAGGTGAGCAGTTTCCGA 5185  
Db 4994 GACAGTGAAGGTCGCTGACGAATGTTACCTTCCCACTGGGGTGGTTACAACCTGCAC 5053  
QY 5186 AGTGATACAGACAGTTCAGTGCATGTCCAGGTAGAGACCTCCAGCA---AGGATGATGTC 5242  
Db 5054 GGGACATGGACAAGGCTATCACGGTGGACATCGAGTCAATCCAGCAGAGAGAAAGATGTC 5113



QY	5243	ACCATAAACCACCAACTGTCTGCCCTCAGGCGCCTTCTACACACTGCTGCAAGACCAAGTC	5302	QY	6323	GTGATCAACGAGACCCCACTGCCATTGATCTCTATCGCTATGATGTGTGTCAGGCAAG	6382
Db	5114	AGCATCACTTCGAACCTGTCTCCATCCATCGATTCCCTTCTACACCAATGGTCCAAGACCAGTTA	5173	Db	6194	GTTCATCAATGAAACACCACTGCCATTGATCTATACCACTTTGATGACATCTCTGGCAAA	6253
QY	5303	CGGAACAGCTACTACATCGGGCCGATGGCTCCTTGGCTGCTGCGCTGCTGCGCCAACCGCATG	5362	QY	6383	ACAGAGCAGTTTGGGAGTTTGGTGTCACTTTACTATGACATTAACCAAGATCATCACCACA	6442
Db	5174	AGAAACAGTTACCAGATTGGGTATGATGGTCCCTTAGAATCTTCTATGCCAGTGGTCTG	5233	Db	6254	GTCGAGCAGTTTGGAAATTCGGAGTGATATACTACGACATCAACCAAAATCATTTCCACG	6313
QY	5363	GAGGTGGCGCTGCAGACTGAGCCCCACCTTGTGGCTGGCACCGCTCAACCCACCGTGGGC	5422	QY	6443	GCTGTATGACCCACACCAAGCATTTTGTATGCATATGGCAGGATGAAGGAAGTGAGTAT	6502
Db	5234	GACTCTCACTACCAGACAGAGCCCCACGTTCTGGCTGGCACGGCGAATCCACAGTAGCC	5293	Db	6314	GCGTGTAGACTTATACAAAGCACTTTGATGCTCATGGCGCATCAAGGAGATCCAATAT	6373
QY	5423	AAGAGGAATGTACAGCTGCCCATCGACAACGGCCTCAACCTGGTGGAGTGGCGCCAGCGC	5482	QY	6503	GAGATCTTCGCTCGCTCATGTACTGGATGACCGCTCCAGTCCAGTATGATAACATGGGCGAGTA	6562
Db	5294	AAAGAAACATGACTCTTCCCGGTGAGAACGGGCAAGTCAACGTATTTCGGCCGGAAGCTCAGGGTCAATGGGCGC	5413	Db	6374	GAGATATTTAGGTCACTCATGTACTGGATTACAATTCAAATTCAAATATGATAATATGGGCCGGSTA	6433
QY	5483	AAAGAGCAGGCTCGGGGCCAGGTCACTGTCTTTGGGCGCGGCTCGGGGTGCACAAACCGA	5542	QY	6563	GTGAAGAAGGAGCTGAAGGTAGGACCCCTACGCCAAATACCACTCGCTACTCCTATGAGTAT	6622
Db	5354	AAAGAAACAGCCAGGGCAAAAGTCAACGTATTTCGGCCGGAAGCTCAGGGTCAATGGGCGC	5413	Db	6434	ACCAAGAGAGAGATTAAATTTGGGCTTTTGGCCAACTACCAAAATACGCGTACGAGTAC	6493
QY	5543	AATCTCTATCTCTGGACTTTGATCGCGTAAACACGCAAGAGAGATCTATGATGACCCAC	5602	QY	6623	GATGTGACGGCCAGCTGCAGACAGTCTCCATCAATGACAAAGCCACTCTGGCGCTACAGC	6682
Db	5414	AACCTACTCTCAGTGGACTTTGATCGGACCACCAAGACGGAAAGATCTATGATGACCCAC	5473	Db	6494	GACGTCGATGGACAGCTCCAAACAGTTTACCTAAACGAAAAGATCATGTGGCGGTACAAAC	6553
QY	5603	CGAAGTTCAACCTTCGGATTCTGTACGACCAAGCGGGGCGGCCAGCCCTCTGCTCACCC	5662	QY	6683	TACGACCTCAATGGGAACCTGCACTTACTGAGCCCTGGGAACAGTGCACGGCTCACACCA	6742
Db	5474	CGGAAATTTCTCTGAGGATCGCTTACGACACGTTCGGGGCACCCGACTCTCTGGCTGCCG	5533	Db	6554	TACGACCTAAATGGAAACCTCCACTTGCTCAACCCCAAGCAGCAGCGCCCGCTGACCCCT	6613
QY	5663	AGCAGAGSCTGAATGGTGTCAAAGTACATATCTCCCTTGGGGGTTACATTTGCTGGCATC	5722	QY	6743	CTACGGTATGACATCCGCGACCGCATCACTCGGCTGGGTGACGTGCAATACAAGATGGAT	6802
Db	5534	AGTAGCAAGCTAATGGCAGTGAACGTCACTACTCATCCACCGGTCAAAATTGCCAGCATC	5593	Db	6614	CTGCGCTATGACCTGCGCGACAGAAATCAACCCGCTGGGCGATGTTAGTACCGGCTGGAT	6673
QY	5723	CAGAGGGGCATCATGTCTGAAAGAAATGGAATACGACGAGCGGGCCGCATCACATCCAGG	5782	QY	6803	GAGGATGGCTTCTGAGGCAGCGGGCGGTGATATCTTTGAGTACAACTCAGTGGCCTG	6862
Db	5594	CAGAGAGGGACCAACGAGCGGAAAGGTGGACTATGACAGCCAGGGGAGGATCGTATCTCGG	5653	Db	6734	CTGACTCGAGTCTACAGTAAAGGCAGTGGCTGGACAGTGTCTATCGGTACGACGGCCTG	6793
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Db	5954	CAGACCAGGCTATCAGAAATTTTATACGACAGCACAAGAGTCAGTTTACCTACGACGAA	6013	Db	7034	CTGAAACAGACCCAGTACACTGCCTATGGTGAGATCTACTTTGACTCCAACGTCGACTTT	7093
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ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (sites)  
Oohashi,T., Zhou,X., Feng,K., Richter,B., Moergelin,M., Perez,M.T., Su,W., Chiquet-Ehrismann,R., Rauch,U. and Faessler,R.  
Mouse Ten-m/Odz is a new family of dimeric type II transmembrane proteins expressed in many tissues  
J. Cell Biol. (1999) In press  
2 (bases 1 to 8964)  
Oohashi,T.  
Direct Submission  
Submitted (29-MAR-1999) Toshitaka Oohashi, Okayama University  
Medical School, Dept. Mol. Biol. & Biochem.; 2-5-1 Shikata-cho, Okayama, Okayama 700-8252, Japan  
(E-mail:oohashi@cc.okayama-u.ac.jp, Tel:+81-86-235-7128, Fax:+81-86-222-7768)  
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ORIGIN

Query Match 42.4%; Score 3544.6; DB 9; Length 8964;  
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QY 2726 ATCAAGTTCCCTGTGGGAGGGACAGCACGCAATAATCCCCGGGAGAACCCCTTTGAT 2785  
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Db 2597 ATCAGTTTCCTGATTGGATCGGATAGCACCCACGTCCTCCTGGAGAAAGTCCGTTCAAT 2656  
QY 2786 GGAGGGCATGCTTGTTGTTATTCGTGGCCAAGTGATGACATCAGATGGAACCCCTGGTT 2845  
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QY 2846 GGTGTGAACATCAGTTTGTCAATAACCCCTCTCTTTGGATATACAATCAGCAGGCAAGAT 2905  
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Db 2717 GCGTCAACGTCGTTTTTACACTACTCGGAATATGGATATACCAATTACCGCCAGGAT 2776  
QY 2906 GGCAGCTTTGACTTGGTGACAAATGGCGGCATCTCCATCATCCTGCGGTTTCGAGCGGGCA 2965  
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QY 2966 CCTTTTCATCACAGGAGCACACCTGTGGCTGCCATGGGATCGCTTCTTTGTTCATGGAA 3025  
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QY 3026 ACCATCATCATGAGACATGAGGAGAATGAGATTCACGACTGTGACCTGAGCAATTTTGCC 3085  
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Db 2957 AGCCCAAGTCCCATCATTTGTGTCTTTCACCGTTATCCACCTTCTTCAGGCTCTCCCTGAG 3016  
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Db 3017 GACAGCCCCATCATCCCCGAGACACAGTCTCTGCATGAAGAAACCAATTCAGGAACA 3076  
QY 3206 AAGATGAGGCTGAGCTACCTGAGCAGCCGACCCCTGGCTACAAATCTGTCTGAGGATC 3265  
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Db 3137 ACCATGACCCAGGCCGTATACCCGTTTAACTCATGAAGGTCCATCTGATGGTGGCCGTG 3196  
QY 3326 GAGGGCCGCTCTTTCAGGAAGTGGTTCGTGACGCCCCAGACCTGTCTTATTTTCATT 3385  
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QY 3986 TCTGAGGTGGTGGGGGACAGGTGACAGTGGCTCCCCCTTTGATGACACTCGTGCGGG 4045  
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Db 3977 AACGGACTGATCTACTTTGTTGATGGAACCATGATCAGAAAGTTGATCAAAATGGAATC 4036  
QY 4166 ATCTCCACCCCTGCTCGGCTCTAATGATCTCACATCAGCCCCGCCACTCAGCTGTGATTCT 4225  
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QY	4286	GACAACTCACTTTATGTCTCGACAAACAATGTGGTCTTGAAATCTCTGAAACCAACCG	4345	Db	5234	GACTCTCACTACCAGACAGAGCCCAACGTTCTGGCTGGCACGGCGAATCCCACAGTAGCC	5293
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Db	4274	GTGGGAAGCACGCGGTTACAGACCACCCCTGGAGTCAGCCACGGCCATTGCTGTCTTAC	4333	QY	5543	AAATCTCTATCTCTGGACTTTGATCGCGTAACACGCAACGCAAGAGATCTATGATGACCAC	5602
QY	4466	AATGGGGTCTGTATATTGCTGAGACTGATGAGAAAAAGATCAACCGCATCAGGCAGGTC	4525	Db	5414	AACCTACTCTCAGTGGACTTTGATCGGACCAACCAAGACGGAAGAGATCTATGATGACCAC	5473
Db	4334	AGCGGGTCTTTACATACGGAAACTGATGAGAAAGAGATCAACCGAATAAGGCAGGTC	4393	QY	5603	CGAAGTTCACCCCTTCGGATTCTGTACGACCAAGCGGGGGCGGCCAGCCTCTGTTCAACC	5662
QY	4526	ACCACTAGTGAGAGATCTCACTCGTTGCTGGSGCCCCAGTGGCTGGCTGTGACTGTAAAAAT	4585	Db	5474	CGGAAATTTCTCTGAGGATCGCTTACGACACGTCGGGGCACCCGACTCTCTGGTGCCG	5533
Db	4394	ACGACAGACGGGAGATCTCCTTAGTGGTGATACCTTCGGAATGTGACTGCAAGAAC	4453	QY	5663	AGCAGCGCTGAATGGTGTCAACGTGACATACTCCCCCTGGGGTTACATTGCTGGCATC	5722
QY	4586	GATGCCAACTGTGATTGTTTTCTGGAGACGATGGTTATGCAAGGATGCAAACTAAAT	4645	Db	5534	AGTAGCAAGCTAATGGCAGTGAACGTCACTACTCATCCACCGTCAAAATGCCAGCATC	5593
Db	4454	GACGCCAACTGTGACTGTACCAAAGCGGAGACGGCTACGCCAAAGATGCCAACTCAAT	4513	QY	5723	CAGAGGGGCATCATGTCTGAAAGAAATGGAATACGACCAGSGCGCGCATCACATCCAGG	5782
QY	4646	ACCCCATCTTCCTTGGCTGTGTGCTGATGGGGAGCTCTACGTGGCCGACCTTGGGAAC	4705	Db	5594	CAGAGAGGGACCAACGAGCGGAAAGGTGACTATGACAGCCAGGGAGGATCGTATCTCG	5653
Db	4514	GCGCCGTCTCCTTGGCCGCTCGCCAGATGGCACTCTGTACATTGCAGATCTGGGAAAT	4573	QY	5783	ATCTTCGCTGATGGGAAGACATGGAGCTACACATACTTAGAGAAAGTCCATGGTGTGCTA	5842
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Db	4874	GGGTGCTGAAAAGCATGACCGCTCAGGGCCTGGAACCTGGTTTGTTTACTTACCATGGC	4933	QY	6014	ACAGCGGAGTCTTGAAAACAGTAAACCTTCAGAGTGTGGTTTATTGCAACCATTAGA	6073
QY	5066	AATTCCGGCCTTCTGGCAACCAAAAGCAATGAAAACGGATGGACAACATTTTATGAGTAC	5125	Db	6203	TACCGTCAGATTGGGCCCCCTGATGACCGGACAGATCTTCCGCTTCACTGAGGAAGGCATG	6262
Db	4934	AACAGTGGGCTTTTAGCCCAACAAAGTGACGAAACTGGAATGGATGGACAAACATTTTGA	4993	QY	6074	TACAGGCAAAATGGTCCCTGATGACAGACAGATTTTCCGCTTCAGCGAGGATGGAATG	6133
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
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TITLE Proteins and nucleic acids encoding same  
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ORIGIN  
Query Match 41.9%; Score 3502.2; DB 6; Length 8645;  
Best Local Similarity 65.3%; Pred. No. 0;  
Matches 5449; Conservative 0; Mismatches 2688; Indels 204; Gaps 13;  
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RESULT 13  
AX662353  
LOCUS

AX662353 8675 bp DNA linear PAT 22-MAR-2003









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RESULT 14

AX662357

LOCUS AX662357 8473 bp DNA linear PAT 22-MAR-2003

DEFINITION Sequence 39 from Patent WO02062999.

ACCESSION AX662357

VERSION AX662357.1 GI:29163218

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

1

REFERENCE

AUTHORS Spytek,K.A., Li,L., Wolenc,A.R., Vernet,C.A., Eisen,A., Liu,X., Malyankar,U., Shinkets,R.A., Tchernev,V.T., Spaderna,S.K., Gorman,L., Kekuda,R., Patturajan,M., Gusev,V., Gangolli,B.A., Guo,X., Shenoy,S., Rastelli,L., Casman,S.J., Boldog,F., Burgess,C.E., Edinger,S., Ellerman,K., Gunther,E., Smithson,G., Millet,I. and Macdougall,J.R.

TITLE Proteins and nucleic acids encoding same

JOURNAL Patent: WO 02062999-A 39 15-AUG-2002;

FEATURES

source Location/Qualifiers

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ORIGIN

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Best Local Similarity 67.1%; Pred. No. 0;

Matches 5027; Conservative 0; Mismatches 2370; Indels 93; Gaps 9;

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QY	5356	CGGCATGGAGGTGGCGCTGCAGACTGAGCCCACTTGCTGGTGGCAGCGTCAACCCAC	5415	Dd	6254	TTCTACAGCTGTATGACCTATACGAAGCACTTTGATGCTCATGGCCGTATCAAGGAGAT	6313
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QY 6916 TGGCCTGGGGCGCGCTGTCCAGCAAGAGCAGCCACAGCCACCCTGCAGTCTTCTA 6975

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QY 6976 TGCAGACCTGACCAACCCCAACCAAGGTCAACCCACCTGTACAACCACTCCAGCTCTGAGAT 7035

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RESULT 15

AX662359 LOCUS AX662359 8487 bp DNA linear PAT 22-MAR-2003

DEFINITION Sequence 41 from Patent WO02062999.

ACCESSION AX662359

VERSION AX662359.1 GI:29163219

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

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TITLE Proteins and nucleic acids encoding same

JOURNAL Patent: WO 02062999-A 41 15-AUG-2002;

Curagen Corporation (US)

FEATURES Location/Qualifiers

source

1..8487

/organism="Homo sapiens"

/mol\_type="unassigned DNA"

/db\_xref="taxon:9606"

ORIGIN

Query Match 40.7%; Score 3398.8; DB 6; Length 8487;

Best Local Similarity 67.0%; Pred. No. 0;

Matches 5008; Conservative 0; Mismatches 2362; Indels 102; Gaps 9;

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QY 937 AGGTACCCACTGACGTCCAGCACAGTGTACTCTCTCCGCCCGACCCCTGCCCCGAG 996

Db 826 AGGATACACAATGSCATCTGGCTCTGTTTATTACCACTACTCGGCCCACTACTAGAAA 885

QY 997 CACCTTCGCGCGCGGCCTTTAACCTCAAGAGCCCTCCAAGTACTGTAACTGGAAGTG 1056



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Db 946 CACTGCACGTGTGCGGTAGGGGTCTCGGTGCTCGCAATACTCCTGTCTTATTTAT 1005  
Qy 1117 GGCCATGCACCTGTTGGCCTAAACTGGCACTGCGACCCGATGGAGGGGCGAGATGTATGA 1176  
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Qy 2197 ACACGACTGTTCTATCGAGATCTGTGCTGCCGACTGTGGTGGCCATGGCGTGTGCGTAGG 2256  
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QY	5734	CATGCTGTAAAGAATGGAATACGACAGCGCGGCCGCATCACATCCAGGATCTTCGCTGA	5793	Dd	6628	CCTACGTCAAAGGGCACGGAAATCTTTGAATATAGCTCCAAGGGGCTTCTAACTCGAGT	6687
Dd	5548	CACTAGCGAGAAAGTAGATTTAGACGGACAGGGGAGGATCGTGTCTCGGGTCTTTGCTGA	5607	QY	6874	CTACAAACCGGGCTGGCAGCTGGAGTGTCAAGTACCGCTACGATGGCCTGGGGCGGCGGT	6933
QY	5794	TGGGAAGACATGGAGCTACACATACTTAGAGAAGTCCATGGGTGCTGCTACTACAGCCCA	5853	Dd	6688	TTACAGTAAAGGCAGTGGCTGGACAGTGATCTACCGTTATGACGGCCTGGGAAGGCGGTG	6747
Dd	5608	TGGTAAACATGGAGTTACACATATTAGAAAAGTCCATGGTCTTCTGCTTCATAGCCA	5667	QY	6934	GTCCAGCAAGAGCAGCCACAGCCACCACTGCAGTTCTTCTATGCAGACCTGACCAACCC	6993
QY	5854	GAGGCAGTATATCTTTGAGTTCGACAAGAATGACCGCCCTCTCTTCTGTGACGATGCCCAA	5913	Dd	6748	TTCTAGCAAAAACCCAGTCTAGGACAGCACCTGCAGTTTTTTTTATGCTGACTTAACCTTATCC	6807
Dd	5668	GCGGCAGTACATCTTCGAATACGATATGTGGACCGCCTGTCTGCCATCACCATGCCCAG	5727	QY	6994	CACCAAGGTCACCCACCTGTGTACAAACCACTCCAGCTCTGAGATCACTCCCTCTACTACGA	7053
QY	5914	CGTGGCGCGGACACACTAGAGACCACTCGCTCAGTGGGCTACTACAGAAACATCTATCA	5973	Dd	6808	CACTAGGATTACTCATGTCTACAAACCACTCGAGTTCAGAAATTAACCTCCCTGTATTATGA	6867
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QY	5974	GCCCCCTGAGGGCAATGCCCTCAGTCATACAGGACTTCACTGAGGATGGGCACCTCCTTCA	6033	Dd	6868	TCTCCAAGGACATCTTTTGGCATGGAAATCAGCAGTGGGGATGAAATCTATATTGCATC	6927
Dd	5788	CCCCCGGAAAGCAACGCCCTCCATCATCACGGACTACAACGAGGAAGGCTGCTTCTTACA	5847	QY	7114	TGACAAACATCGGACCCCTCTTGTGTCTTTAGTGGAAACAGGTTTGTGATCAAGCAAT	7173
QY	6034	CACCTTCTACCTGGGCACCTGCGCGCAGGGTGATATACAAGTATGGCAAACTGTCAAAGCT	6093	Dd	6928	GGATAACACAGGGACACCACTGGCTGTGTTCAGTAGCAATGGGCTTATGCTGAAACAGAT	6987
Dd	5848	AACAGCTTTCTTGGGTACAAGTCGGAGGGTCTTATTCAAATACAGAAAGGCAGACTAGGCT	5907	QY	7174	CCTGTACACAGCCTATGGGGAGATCTACATGGATACCAACCCCAACTTTCAGATCATCAT	7233
QY	6094	GGCAGAGACGCTCTATGACACCAACCAAGTCACTGAGGATGGGCACCTCCTTCA	6153	Dd	6988	TCAGTACACTGCATATGGGAAATCTATTTTGACTCTAATATTGACTCTAATATTGACTTTCAACTGGTAAT	7047
Dd	5908	CTCAGAAATTTTATATGATAGCACAAAGAGTCAAGTTTACCTATGATGAAACAGCAGGAGT	5967	QY	7234	AGGCTACCATGGTGGCCCTCTATGATCCACTCAACCAAGCTTGTCCACATGGGCGCGGAGA	7293
QY	6154	GCTGAAGACCATCAACCTACAGAATGAGGGCTTCACTGCACCATCCGCTACCGTCAGAT	6213	Dd	7048	TGGATTTCATGGTGGCCTGTATGACCCCACTACCAAAATTAATCCAATTTGGAGAAAGAGA	7107
Dd	5968	CCTAAAGACAGTAAACCTCCAGAGTGATGGTTTTATTGTGCCATTTAGACCAATTAGATACAGGCCAAAT	6027	QY	7294	TTATGATGTGCTGGCCGACCGCTGGACTAGCCAGACCAACAGCTGAGAGTGTGGAGGACCTTAG	7353
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Dd	6028	TGGTCCCCTGATTGACAGGCAGATTTTCCGCTTTAGTGAAGATGGGATGGTAAATGCAAG	6087	QY	7354	TAGCAGCAACGTCAATGCCCTTTTAATCTCTATATGTTCAAAAAACAACACCCCATCAGCAA	7413
QY	6274	TTTTGACTACAACTATGACAACAGCTTCCGGGTGACCAAGCATGCAGGCTGTGATCAACGA	6333	Dd	7165	TGGAAAGGACCCAGCTCCTTTTAACTTGTACATGTTTAGGAATAACAACCCCTGCAAGCAA	7224
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QY	6334	GACCCCACTGCCATTGATCTCTATCGCTATGATGATGTGTGAGGCAAGACAGAGCAGTT	6393	Dd	7225	AATCCATGACGTGAAAAGATTACATCACAGATGTTTAAACAGCTGGCTGGTGACATTTGGTTT	7284
Dd	6148	AACGCCACTGCCTATTGATCTGTATCAGTTTGTATGACATTTCTGGCAAGTTTGAGCAGTT	6207	QY	7474	CCAGCTACAAACGTGATCCCTGGTTATCCCAACCCAGACATGGATGCCATGGAACCCCTC	7533
QY	6394	TGGGAAGTTTGGTGTCAATTTACTATGACATTTAACCCAGATCATCACCAAGCTGTATGAC	6453	Dd	7285	CCATCTGCACAAATGCTATTTCTCTGGATTCCCTGTTCCCAAAATTTGATTTAAACAGAACCTTC	7344
Dd	6208	TGGAAAGTTTGGAGTTATATATATATGATATTAACCCAGATCATTTCTACAGCTGTAATGAC	6267	QY	7534	CTACGAGCTCATCCACACACAGATGAAAACGCAGGAGTGGGACAAACAGCAAGTCTATCCT	7593
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Db	7453	CGAGGTGCAGGTGAGCGCGCGCCGGGCCGC--GGCGCGCAGTCCCTGGCTGTGGTTCCG	7509
QY	7714	ATCCAGCGGCTCAGTCTTTGGCAAGGGGCTCAAGTTTGCTTTGAAGGATGGCCGAGTGAC	7773
Db	7510	CACGGTCAAGTCGCTGATCGGCAAGGGCGTCACTGTGCCGTCAGCCAGGCGCCGTGCA	7569
QY	7774	CACAGACATCATCAGTGTGGCCAATGAGGATGGGCGAAGGTTGCTGCCATCTTGAACCA	7833
Db	7570	GACCAACGTGCTCAACATGCCAACGAGGACTGCATCAAGGTGGCGGCCGTGCTCAACAA	7629
QY	7834	TGCCCACTACCTAGAGAACCTGCACCTTCAACATTGATGGGTGGATACCCATTACTTTGT	7893
Db	7630	CGCCTTCTACCTGGAGAACCTGCACCTTCACCATCGAGGGCAAGGACACGCACACTTTCAT	7689
QY	7894	GAAACCAAGACCTTCAGAAAGGTGACCTTGGCCATCTGGGCCTCAGTGGGGGGCGGGAAC	7953
Db	7690	CAAGACCACACCGCCGAGAGCGACCTTGGGCAGCTGCGGTTGACCAAGCGCGCCGCAAGGC	7749
QY	7954	CCTGGAGAATGGGGTCAACGTCACTGTGTCCAGATCAACACAGTACTTAATGGCAGGAC	8013
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QY	8014	TAGACGCTACACAGACATCCAGCTCCAGTACGGGGCACTGTGCTTGAACACACACGCTACGG	8073
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QY	8194	GACAGAGGGGAGAGCAGCAGGTTGCTGAGCACAGGGCGGGTGCAAGGCTACGACGGCTT	8253
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QY	8254	TTTCGTGATCTCTGTCCAGCAGTACCCAGAACTGTGAGACAGCGCCCAACACATCCACTT	8313
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QY	8314	CATGAGACAGAGCGGATGGGCCGGAGGTGAC	8345
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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 9, 2005, 19:04:25 ; Search time 29280 Seconds  
(without alignments)  
13349.019 Million cell updates/sec

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Scoring table: IDENTITY NUC  
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Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : EST:\*  
1: gb\_est1:\*  
2: gb\_est2:\*  
3: gb\_est3:\*  
4: gb\_htc:\*  
5: gb\_est4:\*  
6: gb\_est5:\*  
7: gb\_est6:\*  
8: gb\_est7:\*  
9: gb\_gss1:\*  
10: gb\_gss2:\*  
11: gb\_gss3:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5857.4	70.1	6246	10 AY413475	AY413475 Homo sapi
2	5045.8	60.4	5970	10 AY413476	AY413476 Pan trogl
3	3289	39.4	8027	4 CR936703	CR936703 Homo sapi
4	2353	28.2	5094	10 AY405420	AY405420 Homo sapi
5	2347.8	28.1	3190	10 AY413477	AY413477 Mus muscu
6	2282.2	27.3	5069	10 AY405421	AY405421 Pan trogl
7	2232.8	26.7	5087	10 AY405422	AY405422 Mus muscu
8	1407.8	16.9	3038	4 AK037897	AK037897 Mus muscu
9	1217.4	14.6	2926	4 HSM802230	AL137500 Homo sapi
10	743.8	8.9	1284	4 AK039472	AK039472 Mus muscu
11	713.8	8.5	718	1 AL045768	AL045768 DKFZp434F
12	695.2	8.3	856	6 CF534506	CF534506 UI-M-G10-
13	646.8	7.7	762	7 CV559879	CV559879 UI-M-H20-
14	630.8	7.6	827	3 BM947883	BM947883 UI-M-EG0p
15	629	7.5	870	2 BG036207	BG036207 602326960
16	613.6	7.3	728	6 CF536185	CF536185 UI-M-G10-
17	609.2	7.3	770	6 CB524534	CB524534 UI-M-FY0-
18	602.6	7.2	2627	4 AK050784	AK050784 Mus muscu
19	585.2	7.0	797	7 CO043142	CO043142 UI-M-G10-
20	581	7.0	1031	10 CNS02PHB	AL207992 Tetraodon
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22	571.8	6.8	840	8 CX889461	CX889461 JGI_CAAM2

23	567.2	6.8	572	5	BX504178	BX504178	BX504178	DKFZp686D
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25	561.4	6.7	668	5	BQ563239	BQ563239	BQ563239	gi01b09.Y
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c	558.2	6.7	1125	10	CL649832	CL649832	CH213-255	CL649832
28	544.8	6.5	694	6	CF723353	CF723353	UI-M-GV0-	CF723353
29	539.4	6.5	545	7	CN358072	CN358072	170005999	CN358072
30	536.8	6.4	1214	8	DN736264	DN736264	CNB85-H08	DN736264
31	534.6	6.4	637	6	CF171639	CF171639	B0845C10-	CF171639
32	533.8	6.4	786	8	CX801335	CX801335	JGI_CAAJ1	CX801335
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35	531.2	6.4	798	2	BF144774	BF144774	601791454	BF144774
36	528.6	6.3	632	2	BB655038	BB655038	BB655038	BB655038
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38	518.6	6.2	525	1	AL046228	AL046228	DKFZp434E	AL046228
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ALIGNMENTS

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DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
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COMMENT  
FEATURES  
source  
gene  
ORIGIN

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GSS.  
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1 (bases 1 to 6246)  
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.  
Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios  
Science 302 (5652), 1960-1963 (2003)  
14671302  
2 (bases 1 to 6246)  
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.  
Direct Submission  
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA  
This sequence was made by sequencing genomic exons and ordering them based on alignment.  
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Query Match 70.1%; Score 5857.4; DB 10; Length 6246;  
Best Local Similarity 95.4%; Pred. No. 0;  
Matches 6006; Conservative 0; Mismatches 233; Indels 57; Gaps 4;





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Db 3851 TGGGCTACTACAGAAACATCTATCAGCCCCCTGAGGGCAATGCCCTCAGTCATACAGGACT 3910

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Db 3911 TCACTGAGGATGGGCACCTCCTTCA C A C C T T A C C T G G C A C T G G C C G C A G G T G A T A T 3970

Qy 6069 ACAAGTATGGCAAACTGTCAAAGCTGGCAGAGACGCTCTATGACACCACCAAGGTCAGTT 6128

Db 3971 ACAAGTATGGCAAACTGTCAAAGCTGGCAGAGACGCTCTATGACACCACCAAGGTCAGTT 4030

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Qy 6189 CCTGCACCATCCGCTACCGTCAGATTGGGGCCCTGATTGACCCGACAGATCTTCCGCTTCA 6248

Db 4091 CCTGCACCATCCGCTACCGTCAGATTGGGGCCCTGATTGACCCGACAGATCTTCCGCTTCA 4150

Qy 6249 CTGAGGAAGGCATGGTCAACGCCCGTTTGTGACTACAACTATGACAACAGCTTCCGGGTGA 6308

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DB	4691	AATACAAGATGGATGAGTGGCTTCCAGAGCAGCGGGCGGTGATATCTTTGAGTACA	4750
QY	6849	ACTCAGCTGGCCTGCTCATCAAGGCCTACAACCGGCTGGCAGCTGGAGTGTCAAGTACC	6908
DB	4751	ACTCAGCTGGCCTGCTCATCAAGGCCTACAACCGGCTGGCAGCTGGAGTGTCAAGTACC	4810
QY	6909	GCTACGATGGCCTGGGCGGCGGTGTCCAGAAAGAGCAGCCACAGCCACCACTGCAGT	6968
DB	4811	GCTACGATGGCCTGGGCGGCGGTGTCCAGAAAGAGCAGCCACAGCCACCACTGCAGT	4870
QY	6969	TCTTCTATGCAGACTGTACGACTTGCAGAAAGTCAACCACTGTACCAACCACTCCAGCT	7028
DB	4871	TCTTCTATGCAGACTGTACGACTTGCAGAAAGTCAACCACTGTACCAACCACTCCAGCT	4930
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DB	5231	ACCAACAGCTGTGGAAGCACTTATGAGCAGCAACGTCATGCTTTTAAATCTCTATATGT	5290
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DB	5291	TCAAAAAACAACACCCCATCAGCAACTCCAGGACATCAAGTGTCTCATGACAGATGTTA	5350
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Qy	7749	TTGCCTTGAAAGGATGGCCGAGTGACCAACAGACATCATCAGTGTGGCCAATGAGGATGGGC	7808
Db	5651	TTGCCTTGAAAGGATGGCCGAGTGACCAACAGACATCATCAGTGTGGCCAATGAGGATGGGC	5710
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Qy	8289	CAGACAGCGCCAAACAACATCCACTTCATGAGACAGAGCGAGATGGGCCGAGGTGA	8344
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RESULT 2  
AY413476

**LOCUS**  
**DEFINITION**

**ACCESSION**

**VERSION**  
**KEYWORDS**

**SOURCE ORGANISM**

REFERENCE  
AUTHORS

**FOUO**



Adams,M.D. and Cargill,M.  
Inferring nonneutral evolution from human-chimp-mouse orthologous  
gene trios  
JOURNAL Science 302 (5652), 1960-1963 (2003)  
PUBMED 14671302  
REFERENCE 2 (bases 1 to 5970)  
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,  
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,  
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,  
Adams,M.D. and Cargill,M.  
Direct Submission  
TITLE Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,  
JOURNAL Rockville, MD 20850, USA  
COMMENT This sequence was made by sequencing genomic exons and ordering  
them based on alignment.  
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gene <1..>5970  
/locus\_tag="HCM4903"  
ORIGIN  
Query Match 60.4%; Score 5045.8; DB 10; Length 5970;  
Best Local Similarity 85.6%; Pred. No. 0;  
Matches 5149; Conservative 0; Mismatches 815; Indels 54; Gaps 3;  
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QY 2393 ACCATCGCTCACTATCTGGATAGGGTAGTTAAAGAGGGTTGCCCTGGGTTGTGCAATGGC 2452  
Db 61 ACCATCGNN 112  
QY 2453 AACGGCAGATGTACCTTAGACCTGAATGGTTGGCACTGCGTCTGCCAGCTGGGCTGGAGA 2512  
Db 113 -----NN 153  
QY 2513 GGAGCTGGCTGTGACACTTCCATGGAGACTGCGCTGCGGTGACAGCAAGACAATGATGGA 2572  
Db 154 NNN 213  
QY 2573 GATGGCCTGGTGGACTGCATGGACCCCTGACTGCTGCCCTCCAGCCCTGTGCCATATCAAC 2632  
Db 214 NATGGCCTGTTGGACTGCAATGGACCCCTGACTGCTGCCCTCCAGCCCATGTGCCATATCAAC 273  
QY 2633 CCGTGTGCTTGGCTCCCCTAACCTCTTGACATCATCCAGGAGACACAGGTCCTGTG 2692  
Db 274 CCGTGTGCTTGGCTCCCTTAACCTCTGGACATCATCCAGGAGACACAGGTCCTGTG 333  
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QY 2753 ACGCACAATAATCCCGGGGAGAACCCCTTTGATGGAGGSCATGCTTGTGTTATTCTGTGGC 2812  
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Qy	4193	CTCACATCAGCCCGGCCACTC	AGCTGTGATTCTGTCAATGGATATTTCCAGGTAAGACTG	4252
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RESULT 3	
CR936703	
LOCUS	CR936703
DEFINITION	Homo sapiens mRNA; cDNA DKFZp686A1568 (from clone DKFZp686A1568).
ACCESSION	CR936703



VERSION CR936703.1 GI:60219614  
KEYWORDS HTC.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
REFERENCE 1 (bases 1 to 8027)  
AUTHORS Ottenwaelder,B., Obermaier,B., Deutschenbaur,S., Schaipp,A.,  
Mewes,H.W., Weil,B., Amid,C., Osanger,A., Fobo,G., Han,M. and  
Wiemann,S.  
CONSRM The German cDNA Consortium  
TITLE Direct Submission  
JOURNAL Submitted (22-FEB-2005) MIPS, Ingolstaedter Landstr.1, D-85764  
Neuherberg, GERMANY  
COMMENT Clone from S. Wiemann, Molecular Genome Analysis, German Cancer  
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;  
sequenced by Medigenomix (Martinsried/Germany) within the cDNA  
sequencing consortium of the German Genome Project.  
This clone (DKFZp686A1568) is available at the RZPD Deutsches  
Ressourcenzentrum fuer Genomforschung GmbH in Berlin, Germany.  
Please contact RZPD for ordering:  
http://www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=DKFZp686A1568  
Further information about the clone and the sequencing project is  
available at http://mips.gsf.de/projects/cdna/.  
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DB 683 ACAGCAGCATAGACAGTGGTGAAGCAGAAAGTTGGTCGGCGGGTAACACAAGAAGTCCCCAC 742  
QY 1377 CTGGCACTTTCTGGAGATCTCAAGTGTTCATAGACCATCCTGTGCATCTGAAATTCAAATG 1436  
DB 743 CAGGGGTGTTTGGAGGTCACAAATTCGCATCAGTCAGCCCCAGTTCTTAAAGTTCAACA 802  
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QY 4917 TGGTAAATGTCGCGCCGAGACTCTACTGGGATGCCCTCTGCTGGTGGTCCAGATGGCC 4976  
Db 4238 CCCTGAAGATCCGTCGGGACAGCAGTGGCATGCCCGTCACCTGTCTCATGCTGACAACC 4297  
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QY 5037 ACGAGTTGGCCATGATGACATACCATGGCAATTCGGCCTTCTGGCAACCAAAAGCAATG 5096  
Db 4358 TGGAGCTTGGTCTCATGACCCTATGATGGCAACACTGGGCTCCTGGCCACCAAGAGCGATG 4417

QY	5097	AAAACGGATGGACAACATTTTATGAGTACGACAGCTTTGGCCGCTGACAAATGTGACCT	5156
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Db 7337 TTGAGTTCAGTACTCCACGCTGCTGCTCAGCATCCGCTATGGCCTCACCCCCGACACCC 7396

QY 8082 TGGATGAGGAGAAGCACGGGTCTTGAGCTGGCCCGGCAGAGAGCCGTGCGCCCAAGCGT 8141

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RESULT 4

AY405420

LOCUS

DEFINITION

AY405420 Homo sapiens HCM2218 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.

ACCESSION

AY405420

VERSION

AY405420.1 GI:39761394

KEYWORDS

GSS.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

1 (bases 1 to 5094)

AUTHORS

Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.

TITLE

Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios

JOURNAL

Science 302 (5652), 1960-1963 (2003)

PUBMED

14671302

REFERENCE

2 (bases 1 to 5094)

AUTHORS

Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.

TITLE

Direct Submission

JOURNAL

Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA

COMMENT

This sequence was made by sequencing genomic exons and ordering them based on alignment.

FEATURES

Location/Qualifiers

source

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/mol\_type="genomic DNA"

/db\_xref="taxon:9606"

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/locus\_tag="HCM2218"

ORIGIN

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Best Local Similarity 67.0%; Pred. No. 0;

Matches 3442; Conservative 0; Mismatches 1647; Indels 45; Gaps 6;

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QY 2972 ATCACACGAGGACACACCCTGTGTGGTCGCATGGGATCGCTTCTTTGTCATGGAACCATC 3031

Db 62 CTCACCTCAGTATCATACTGTGTGGATTCCATGGAAATGTCTTTATGTGATGGATACCCTA 121

QY 3032 ATCATGAGACATGAGGAGAAATGAGATTCCCAGCTGTGACCTGAGCAATTTTGCCTCC 3091

Db 122 GTCATGAAGAAAGAGAGAAATGACATTCCCAGCTGTGATCTGATGTGATTCGTGAGGCCA 181

QY 3092 AACCCAGTCGTCTCTCCATCCCCACTGACGCTCCTTCGCCAGCTCCTGTGCAGAGAAAGGC 3151

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Db 302 AAACCTCTCTACTTGAAGTTCAGAGCTCCAGAGCTGAGGGGTATAAGTCAGTTCTCAAGATCACCATG 361

QY 3272 ACCCACCCGACCATCCCCTTCAACCTCATGAAGGTGCACCTCATGTGTCGGTGGAGGC 3331





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Qy	5609	TTCAACCCCTTCGGAATCTGTACGACAGGCGGGCGGCCAGCCTCTGGTCACCCAGCAGC	5668	Qy	6689	CTCAATGGGAAACCTGCACATTACTAGCCCTGGGAGAACAGTGACCGGTACACACCCTACGG	6748
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Db	2858	GCTGATGGTAAACAATGGAGTTACACATATTTAGAAAAGTCCATGGTCTTCTGCTTCAT	2917	Db	3938	CGAGTTTACAGTAAAGGCAGTGGCTGGACAGTGATCTACCGTTATGACGGCCTGGGAAGG	3997
Qy	5849	AGCCAGAGGCAGTATATCTTTGAGTTCGACAAGAATGACCGCTCTCTTCTGTGTGACGATG	5908	Qy	6929	CGCGTGTCCAGCAAAGAGCAGCCACAGCCACCTGTACAACCACTCCAGCTCTGAGATCACCTCCTCTAC	6988
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Qy	5969	TATCAGCCCCCTGAGGCAATGCCTCAGTTCATACAGGACTTCACGTAGGATGGGCACCTC	6028	Qy	7049	TACGACTTGCAAAGGACACCTCTTTTGCCATGGAGCTGAGCAGTGGTGATGAGTTTACATA	7108
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Qy	6029	CTTCACACCTTTCTACCTGGGCACCTGGCCGCAGGCTGATATACAAGTATGSCAAACTGTCA	6088	Qy	7109	GCTTGTGACAAACATCGGGACCCCTCTTGCTGTCTTTAGTGGAAACAGGTTTGATGATCAAG	7168
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Qy	6209	CAGATTGGGCCCCCTGATTGACCGGACAGATCTTCGCTTCACTGAGGAAGGCATGGTCAAC	6268	Qy	7289	CGAGATTATGATGTCTGGCCGGACGCTGGACTAGCCACAGACCAGCTGTGGAAAGCAC	7348
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Qy	6269	GCCCGTTTGTGACTACAACTATGACAACAGCTTCCGGGTGACCAGCATGCAGGCTGTGATC	6328	Qy	7349	CTTAGTAGCAAGCAACGTTCATGCTCTTTTAAATCTCTATATGTTTCAAAAACAACACCCCATC	7408
Db	3338	GCAAGATTTGACTATAGCTATGACAACAGCTTTCGAGTGACCGATGCAGGGTGTGATC	3397	Db	4415	AGAAATGGGAAGGACCCAGCTCCTTTTAACTTGTAATGTTAGGAATAACAACCCCTGCA	4474
Qy	6329	AACGAGACCCCACTGCCCATTTGATCTCTATCGCTATGATGTGTCAAGGCAAGACAGAG	6388	Qy	7409	AGCAACTCCAGGACATCAAGTGTCTTATGACAGATGTTAACAGCTGGTGTGCTCACCTTT	7468
Db	3398	AATGAAACGCCACTGCCTATTGATCTGTATCAGTTTGATGACATTTCTGGCAAAAGTTGAG	3457	Db	4475	AGCAAAATCCATGACGTGAAAGATTACATCACAGATGTTAACAGCTGGTGGTGACATTT	4534
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Db 2217 CCTGCAAAATCTCCGAAAAACCACCAGGTAACCATTTGTGGTGGGAGGCCCATGCACTGCCA 2276  
QY 4381 GGTCCCTGGCAATTGACCACACTTCTCTGCTAAGCAAGGTGGCCATCCACGCAACCCCTGGAGTC 4440  
Db 2277 GGTCCCTGGCATCGACCACTTCTCTGCTGAGCAAGGTAGCCATCCATGCGACCTGGAGTC 2336  
QY 4441 AGCCACCGCTTTGGCTGTTTTCACACAATGGGGTCTGTATATTGCTGAGACTGATGAGAA 4500  
Db 2337 AGCCACTGCTCTGGCCGTTTTCACACAATGGAGTCTTGTACATCGCTGAGACGACGAGAA 2396  
QY 4501 AAAGATCAACCGCATCAGGCAGGTCAACCACCTAGTGGAGAGATCTCACTCGTTGCTGGGC 4560  
Db 2397 AAAGATCAATCGCATCAGGCAGGTCACTACAAGTGGTGAGATCTCACTGTTGCTGGTGC 2456  
QY 4561 CCCAGTGGCTGTGACTGTAAAAAATGATGCCAACTGTGATTGTTTCTGGAGACGATGG 4620  
Db 2457 CCCAGTGGCTGTGACTGTAAAAAATGATGCCAACTGTGACTGCTTCTCTGGAGATGATGG 2516  
QY 4621 TTATGCCAAGGATGCAAAAGTTAAATACCCCATCTTCTCTGGCTGTGTGCTGATGGGA 4680  
Db 2517 TTACGCCAAGGATGCAAAAGCTGAATACCCCATCGTCTTGGCTGTGTGCTGACGGGA 2576  
QY 4681 GCTCTACGTGGCCGACCTTTGGGAACATCCGAATTCGGTTTATCCGGAAGAAACAAGCCTTT 4740  
Db 2577 GCTCTATGTGGCCGACCTTGGGAACATCCGAATTCGATTATCCGGAAGAAACAAGCCTTT 2636  
QY 4741 CCTCAACACCCAGAACATGTATGAGTGTCTTCAACCAATTGACCAGGAGTCTATCTGTT 4800  
Db 2637 CCTGAACACTCAGAACATGTACGAGCTATCTCTCCCATCGACCAGGAGCTGTACCTCTT 2696  
QY 4801 TGATACCACCGGAAGCACCTGTACACCCCAAGCCCTGCCACAGGAGACTACCTGTACAA 4860  
Db 2697 TGATACCAGTGGCAAGCATCTGTACACTCAGAGCCTACCCACAGGGGACTACTGTACAA 2756  
QY 4861 CTTCACTTACACAGGGGACGGGACATCACACATATCACCGACAACAATGGCAACATGGT 2816  
Db 2757 CTTCACTTACACAGGGGACGGGACATCACACATATCACCGACAACAATGGCAACATGGT 2876  
QY 4921 AAATGTCCGCGAGACTCTACTGGGATGCCCTCTGGCTGGTGGTCCCAGATGGCCAGGT 4980  
Db 2817 GAACGTCCGCGAGACTCTACCGGGATGCCCTCTCTGGCTGGTAGTCCCAGATGGCCAGGT 2876  
QY 4981 GTACTGGGTGACCATGGGCACCAACAGTGCATCAAGAGTGTGACCAACAGGACACGA 5040  
Db 2877 ATACTGGGTAAACCATGGGCACCAACAGCGCACTCAGAAAGTGTGACCAACAGGACACGA 2936  
QY 5041 GTTGGCCATGATGACATACCATGGCAATTCGGGCTTCTGGCAACCAAAAGCAATGAAAA 5100  
Db 2937 GCTAGCCATGATGACCTACCATGGCAACTCTGGCCTCTTGGCAACCAAAAGCAATGAAAA 2996  
QY 5101 CGGATGGACAACAATTTATGAGTACGACAGCTTTGGCCGCTTGACAAATGTGACCTTCCC 5160  
Db 2997 CGGGTGGACAACGTTTATGAGTATGACAGTTTGGTTCGCTGACAAACGTCGACCTTCC 3056  
QY 5161 TACTGGCCAGGTGAGCAGTTTCCGAAAGTGTATACAGACAGTTTCAAGTGCATGTCAGGTAGA 5220  
Db 3057 AACTGGCCAGGTGAGCAGTTTCCGAAGCGATACAGACAGCTCAGTGCACGTGCGAGGTAGA 3116  
QY 5221 GACCTCCAGCAAGGATGATGTCAACCAATACCAACCAACCTGTCTGCTCAGGCGCTTCTA 5280  
Db 3117 GACCTCAAGCAAAAGATGACGTCAACCATAACCAACCAACCTGTCTGCTTCGGGTGCTTCTA 3176  
QY 5281 CACACTGCTGCAAG 5294  
Db 3177 CACCCTGTTACAAG 3190

RESULT 6  
AY405421  
LOCUS  
DEFINITION Pan troglodytes HCM2218 gene, VIRUAL TRANSCRIPT, partial sequence,  
AY405421  
genomic survey sequence.  
AY405421  
ACCESSION









Db	3758	CTGAATGGAACCTTCATTTACTGAACCCAAAGTAACAGTGC	CGCGTCTGACACCCCTTCGC	3817
QY	6749	TATGACATCCGGACCGCATCACTCGGCTGGTGACGTGCAATACAAGATGGATGAGGAT		6808
Db	3818	TATGACCTCGGAGACAGAATCACTCGACTGGTGATGTTCAATATCGGTTGGATGAAGAT		3877
QY	6809	GGCTTCTGAGGACGCGGGCGGTGATATCTTTGAGTACAACCTCAGCTGGCCTGCTCATC		6868
Db	3878	GGTTTCTCACTACGTCAAAGGGCACGGAATCTTTGAATATAGCTCCAAGGGCTTCTAACT		3937
QY	6869	AAGGCCTACAACCGGGCTGGCAGCTGGAGTGTCAAGTACCGCTACGATGGCCTGGGCGG		6928
Db	3938	CGAGTTTACAGTAAAGGCAGTGGCTGGACAGTGANNNACCGTTATGACGGCTGGGAAGG		3997
QY	6929	CGCTGTCCAGCAAGAGAGCCACAGCCACCACTGCAGTTCTTCTATGCAGACCTGACC		6988
Db	3998	CGTGTNNNAGCAAAACCAAGTCTAGGACAGCACCTGCAGCTTTTATGCTGACTTAACT		4057
QY	6989	AACCCACCAAGGTCACCCACCTGTACAACCACTCCAGCTCTGAGATCACTCCCTCTAC		7048
Db	4058	TATCCCACTAGGATTACTCATGTCTACAACCACTTCGAGTTCAGAAATTACCTCCCTGTAN		4117
QY	7049	TACGACTTGCAAAGGACACCTCTTTGCCATGGAGCTGAGAGTGGTGATGAGTTTACATA		7108
Db	4118	NNTGATCTCCAAGGACATCTTTTGCCATGGAAATCAGCAGTGGGATGAATTTCTATATT		4177
QY	7109	GCTTGTGACAACATCGGGACCCCTCTTGCTGTCTTTAGTGGAAACAGGTTTGATGATCAAG		7168
Db	4178	GCATCAGATAACACAGGACACCACTGGCTGTGTTTCAGTAGCAATGGGCTTATGCTGAAA		4237
QY	7169	CAAATCCTGTACACAGCCTATGGGGAGATCTACATGGATACCAACCCCAACTTTTCAGATC		7228
Db	4238	CAGATTCACTGACTGCATATGGTGAATCTATTTTGACTCTAATATTGACTTTCAACTG		4297
QY	7229	ATCATAGGCTACCATGGTGGCCTCTATGATCCACTCACCAAGCTTGTCCACATGGGCCGG		7288
Db	4298	GTAATTGGATTTCATGGTGGCCTGTATGACCCACTCACCAAAATTAATCCACTNNNNNNN		4357
QY	7289	CGAGATTATGATGTCTGGCCGGACGCTGGAAGTGTGGAAGCAC		7348
Db	4358	NN		4414
QY	7349	CTTAGTAGCAGCAACGTCATCGCCTTTTAATCTCTATATGTTTCAAAAACAACCCCATC		7408
Db	4415	AGAATCGGAAGGACCCAGCTCCTTTTAACTTGTACATGTTTAGGAATAACAACCTGCA		4474
QY	7409	AGCAACTCCAGGACATCAAGTGCTTTCATGACAGATGTTTAAACAGCTGCTGCACCTTT		7468
Db	4475	AGCAAAATCCATGACGTGAAAGATTACATCAAGATGTTAACAGCTGGCTGGTGACATTT		4534
QY	7469	GGATTCCAGCTACACAACTGATCCCTGGTTATCCCAAACCCAGACATGGATGCCATGGAA		7528
Db	4535	GGTTTCCATCTGCACAATGTATTCCTGGATTCCCTGTTCCCAAATTTGATTTAACAGAA		4594
QY	7529	CCCTCCTACGAGCTCATCCACACACAGATGAAAACGAGGAGTGGGACAAAGCAAGTCT		7588
Db	4595	CCTTCTTACGA-----ACTGTGAAGAGTCAGCAGTGGGATGATGTACCGCCC		4642
QY	7589	ATCCTCGGGGTACAGTGTGAGTACAGAAAGCAGCTCAAGGCCCTTTGTACCTTAGAACGG		7648
Db	4643	ATCTTCGAGTCCAGCAGCAAGTGGCGGCGGAGCCCAAGGCCCTTCCTGCTGGGGGAAAG		4702
QY	7649	TTTGACCAGCTCTATGGCTCCACAATCACCAAGCTGCCAGCAGGCTCCAAAAGACCAAGAAG		7708
Db	4703	ATGGCCGAGGTGCAGGTGAGCCGCGCGGGCCGGC---GGCGGCAGTCTCTGGGTGTGG		4759
QY	7709	TTTGATCCAGCGGCTCAGTCTTTGGCAAGGGGTCAAGTTTGCTTTGAAGGATGGCCGA		7768
Db	4760	TTCGCCAAGGTCAAGTCGCTGATCGCAAGGGCGTCAATGCTGCGCCGTCAGCCAGGCGCG		4819
QY	7769	GTGACCAAGACATCATCAGTGTGCCCAATGAGGATGGCGCAAGGTTGTGCTGCCATCTTG		7828
Db	4820	GTGCAGACCAACGTGCTCAACATCGCCAACGAGGACTGCATCAAGGTGGCGCGGTGCTC		4879
QY	7829	AACCATGCCACTACCTAGAGAACCTTGACACTTCACCATTTGATGGGTGGATACCCATTAC		7888
Db	4880	AACAAAGCCTTCTACCTGGAGAACCTTGACACTTCACCATCGAGGGCAAGGACACGCACTAC		4939
QY	7889	TTTGTGAAACGAGGACCTTCAGAAAGGTGACCTGGCCATCTCTGGCCCTCAGTGGGGGGCGG		7948
Db	4940	TTTATCAAGACCAACGCGCGAGAGCGACCTGGGCACGCTGCGGCTGACGAGCGCGCGC		4999
QY	7949	CGAACCTTGAGAAATGGGTCAACGTCACTGTGTCCCAGATCAACACAGTACTTAATGGC		8008
Db	5000	AAGGCGCTGGAGAACGGCATCAACGTGACGGTGTGCGAGTCCACCCAGTGGTGTGAACGGC		5059
QY	8009	AGGAC 8013		
Db	5060	AGGAC 5064		
RESULT 7				
AY405422	AY405422	5087 bp	DNA	linear
LOCUS	Mus musculus	HCM2218	gene,	VIRTUAL TRANSCRIPT, partial sequence,
DEFINITION	genomic survey sequence.			
ACCESSION	AY405422	GI:39761396		
VERSION	AY405422.1			
KEYWORDS	GSS.			
SOURCE	Mus musculus (house mouse)			
ORGANISM	Mus musculus			
REFERENCE	1 (bases 1 to 5087)			
AUTHORS	Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.			
TITLE	Inferred nonneutral evolution from human-chimp-mouse orthologous gene trios			
JOURNAL	Science	302 (5652),	1960-1963 (2003)	
PUBMED	14671302			
REFERENCE	2 (bases 1 to 5087)			
AUTHORS	Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.			
TITLE	Direct Submission			
JOURNAL	Submitted (16-NOV-2003)	Celera Genomics,	45 West Gude Drive,	
COMMENT	This sequence was made by sequencing genomic exons and ordering them based on alignment.			
FEATURES	Location/Qualifiers			
source	1. 5087			
gene	/organism="Mus musculus"			
	/mol_type="genomic DNA"			
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	<1..>5087			
	/locus_tag="HCM2218"			
ORIGIN				
Query Match	26.7%;	Score	2232.8;	DB 10; Length 5087;
Best Local Similarity	68.4%;	Pred. No.	0;	
Matches	3178;	Conservative	0;	Mismatches 1432; Indels 36; Gaps 5;
QY	2912	TTTGACTTGGTGACAAATGGCGGCATCTCCATCATCTCGGTTGAGCGGCACCTTTC	2971	
Db	1	TTTGACTTGGTGACAAATGGTGGCGCTTCTCTGACTTTTGGTATTGAGCGTTTCCCCATTC	60	
QY	2972	ATCACAGGAGCACACCTGTGGCTGCCATGGGATCGTCTTCTTGTTCATGGAAACCATC	3031	
Db	61	CTCACTCAGTACCACACTGTGTGGATTCCCTGGAATGCTCTTTATGTGATGATACCCCTT	120	
QY	3032	ATCATGAGACATGAGGAGAAATGAGATTCCCAGCTGTGACCTGAGCAATTTTGCCGCCCC	3091	

Db 121 GTCATGAAGAAAGAGGAGAACGACATTCCCGAGCTGTGACCTCAGTGGCTTTGTGAGGCCA 180  
QY 3092 AACCAGTCGTCTCTCCATCCCCACTGACGTCTCTCGCCAGCTCCTGTGCGAGAGAAAGGC 3151  
Db 181 AGTCCCATCATTTGTGTCTTCAACCGTTATCCACCTCTTTCAGGTCTTCCCCCTGAGGACAGC 240  
QY 3152 CCCATTGTGCCGGAAATTCAAGGCTTTGCAGGAGGAAATCTCTATCTCTCGGCTGCAAGATG 3211  
Db 241 CCCATCATCCCCGAGACACAGGTCCTGCATGAAGAAACCACAATTCACGGAACAGATTG 300  
QY 3212 AGGCTGAGCTACCTGAGCAGCCGGACCCCTGGCTACAAATCTGTCTGAGGATCAGCCCTC 3271  
Db 301 AAACTTTCCTACCTGAGTTCAGAGCGGCAGGGTACAAGTCAGTTCAGTTCCTTAAGATTACCATG 360  
QY 3272 ACCCACCCGACCATCCCTTCAACCTCATGAAGGTGCACCTCATGGTAGCGGTGAGGGC 3331  
Db 361 ACCAGGCCGTCTATACCGTTTAAACCTCATGAAGGTCATCTGATGGTGGCCGTGGTGGG 420  
QY 3332 CGCCTCTTCAGGAAGTGGTTCGCTGCAGCCCCCAGACCTGTCTCTATTATTTCATTTGGGAC 3391  
Db 421 AGACTCTTCAGAAAGTGGTTCCTGCCTCGCCAACTTGGCCTACACGTTTCATCTGGGAT 480  
QY 3392 AAGACAGACGTCTACAACAGAAAGGTGTTTGGGCTTTCAGAAAGCCTTTGTTCCTGGTGGT 3451  
Db 481 AAGACGGACGCATATAATCAGAAAGTCTACGGCTTGTGAGAGGCAGTTGTGTCGTCGGA 540  
QY 3452 TATGAATATGAATCCTGCCAGATCTAATCTGTGGGAAAAAGAACAAACAGTGTGCAG 3511  
Db 541 TACGAGTACGAGTCGTGCTTGGACCTGACTCTCTGGAAAAAGAGGACTGCCGTTTTCGAA 600  
QY 3512 GGCTATGAAATTGACGCGTCAAGCTTGGAGGATGGAGCCTTAGACAAACATCATGCCCTC 3571  
Db 601 GGCTATGAGTTGGATGCTTCGAACATGGCGGCTGACGTTGGACAAGCACCATGTACTG 660  
QY 3572 AACATTCAAAGTGGTATCTGCACAAAGGGAATGGSGAGAACAGTTTGTGTCTCAGCAG 3631  
Db 661 GAGGTTCAGAACGGTATACTATACAAGGAAATGGAGAAATCAGTTTCATCTCTCAGCAG 720  
QY 3632 CTTCTGTCAATTGGGAGCATCATGGGCAATGGGCGCCGGAGAGCATCTCCTGCCCCAGC 3691  
Db 721 CTTCCGGTGGTCAGCAGCATCATGGGTAATGGTCGGAGCGGTAGCATCTCATGCCCAAGT 780  
QY 3692 TGCAAACGGCCTTGCTGACGGCAACAAAGCTCTTGCCGCCAGTGGCCCTCACCTGTGGCTCT 3751  
Db 781 TGCAATGGTCAAGCTGACGGGAACAAACTCTTGGCACCGGTGGCGCTTGCCCTGTGGGATC 840  
QY 3752 GACGGGAGCCTCTATGTGGGTGATTTCAACTACATTAGAAGGATCTTCCCTCTGGAAAT 3811  
Db 841 GACGGCAGTCTATACGTAGGGGATTTCAATTACGTCCGGCGGATATTCCCGTCTGGGAAT 900  
QY 3812 GTCACCAACATCCTTAGAGCTGAGGAATAAAGATTTTCAGACATAGTCACAGTCCAGCACAC 3871  
Db 901 GTGACAAGTGTTTTAGA-----ACTAAGTAGCAACCCAGCTCAC 939  
QY 3872 AAATACTACCTGGCCACAGACCCCATGAGTGGGGCCGTCTTCTCTGACAGCAACAGC 3931  
Db 940 AGATACTACCTGGCTACGGACCCAGTCACCGAGATTGTACGTCTCTGTATACTAACACC 999  
QY 3932 CGCGGGTCTTTAAAAATCAAGTCCACTGTGGTGTGAAGACCTTGTCAAGAACTCTGAG 3991  
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QY 3992 GTGGTTGCGGGGACAGGTGACAGTGCCTTCCCTTTGATGACACTCGCTGCGGGGATGGT 4051  
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Db 1120 GGCAGGCTGTGGAAGCAACGCTCATGAGTCCCAAAGGAATGGCAATCGATAAGACGGA 1179  
QY 4112 CTGATCTACTTCGTGGATGGACCATGATCAGACCGCATCGATCAGAATGGGATCATCTCC 4171

Db 1180 CTGATCTACTTTGTTGATGGAACCATGATCAGAAAAGTTTGATCAAAAATGGAATCATATCA 1239  
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Db 1240 ACTCTCCTGGGCTCCAACGACCTCAGCTCAGCTCGACCTTTAAACCTGTGATAGTACTAGCATG 1299  
QY 4232 GATATTTCCAGGTAAGACTGGAGTGGCCACAGACTTAGCCATCAACCCCAATGGACAAC 4291  
Db 1300 CATATCAGCCAG-----CTGGAATGGCCCACTGACCTCGCGATCAACCCCATGGATAAC 1353  
QY 4292 TCACCTTATGTCTCGACAAACAATGTGTCTCTGCAAAATCTCTGAAACACACAGGTGCCG 4351  
Db 1354 TCCATCTACGTCTCTGGATAATAACGTAGTTTACAGATCACTGAAACCCGTCAGGTCCGC 1413  
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Db 1414 ATCGCTGCCGSGGCCCATGCACTGTCACTGTCACTCCCTGGAGTGG---AATACCCGTTGGG 1470  
QY 4412 AAGTGGCCATCCACGCAACCCCTGGAGTCAAGCCAGCTTTTGGCTGTTTCAACAATGGG 4471  
Db 1471 AAGCACGGGTTCAGACCAACCTGGAGTCAGCCACGGCCATTGCTGTCTCTACAGCGGG 1530  
QY 4472 GTCCTGTATATTGCTGAGACTGATGAGAAAAAGATCAACCGCATCAGGCAAGTCAACCACT 4531  
Db 1531 GTCCTTTTACATCACGGAAACTGATGAGAAAGATCAACCGAATAAGGCAGGTCAAGACA 1590  
QY 4532 AGTGAGAGATCTCACTCGTTGCTGGGCCCCCAGTGGCTGTGACTGTAAAAATGATGCC 4591  
Db 1591 GACGGGGAGATCTCCTTAGTGGCTGGGATACCTTCGGAATGTACTGCAAGAACGACGCC 1650  
QY 4592 AACTGTGATTTTCTTGAGACGATGGTTATGCCAAGGATGCAAAAGTTAAATACCCCA 4651  
Db 1651 AACTGTGACTGTACCAAGCGGAGACGGCTACGCCAAAGATGCCAAACTCAATGCGCG 1710  
QY 4652 TCTTCTTGGCTGTGTGCTGATGGGGAGCTTACGTGGCCGACCTTGGGAAACATCCGA 4711  
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QY 4712 ATTGGTTTTATCCGGAAGAACAAAGCCTTTCTCAACACCCAGAACATGTATGAGCTGTCT 4771  
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QY 4772 TCACCAATTGACCAAGAGCTCTATCTGTTTGTATPACCACCGGAAGCACCTGTACACCCAA 4831  
Db 1831 TCTCCAACGTATCAAGAGCTCTACATCTTTTGACATCAACGGTACTCACCAAGTACACCGTG 1890  
QY 4832 AGCTGCCCCACAGGAGACTACCTGTACAACCTTCACTTACCTTACCTGGGACGGCGACATCACA 4891  
Db 1891 AGCTGGTCACGGTGACTACCTATATAATTTTAGTTACAGCAATGACAAATGACGTCAACC 1950  
QY 4892 CTCATCACAGACAACAATGGCAACATGGTAAATGTCCGCCGAGACTCTACTGSGATGCCC 4951  
Db 1951 GCTGTAACTGACAGCAATGGCAACACCCCTCCGAATCCGAAGGATCCGAATCGATGCCG 2010  
QY 4952 CTCTGGTGGTGGTCCAGATGGCCAGGTGACTGGGTGACCATGGGCACCAACAGTGCA 5011  
Db 2011 GTGCGGGTGGTGTCTCTGTATAACAGGTGATATGGTTGACCATAGGCACCAACGGGTGT 2070  
QY 5012 CTCAAGAGTGTGACCACACAAGGACACGAGTTGGCCATGATGACATACCATGGCAATTC 5071  
Db 2071 CTGAAAAGCATGACCGCTCAGGGCCTGGAACCTGGAACCTGTTTACTTACCATGGCAACAGT 2130  
QY 5072 GGCTTCTGGCAACCAAAAGCAATGAAAACGGATGGACAAACATTTTATGAGTAGACAGC 5131  
Db 2131 GGGCTTTTAGCCACCAAAAGTGACGAAACTGGATGGACAAACATTTTGTACTATGACAGT 2190  
QY 5132 TTTGGCCGCTGACAAATGTGACCTTCCCTACTTGGCCAGGTGAGCAGTTTCCGAAAGTAT 5191  
Db 2191 GAAGTGCCTGACGAATGTTACCTTCCCCACTGGGGTGGTTACAAACCTGACCGGGAC 2250  
QY 5192 ACAGACAGTTTCAGTGCATGTCCAGGTAGAGACTTCCAGCA---AGGATGATGTACACCATA 5248  
Db 2251 ATGGACAAGGCTATCAGCGTGGACATCGAGTCACTCCAGCAGAGAGGAAGATGTACAGCATC 2310



QY	5249	ACCACCAACCTGTCTGCCTCAGGCGCTTCTACACACTGCTGTGCAAGACCAAGTCCGGAAC	5308	6329	AACGAGACCCCACTGCCCCATTGATCTCTATCGCTATGATGTGTCAAGCAAGACAGAG	6388
Db	2311	ACTTCGAACCTTGCTCTCCATCGATTCTCTTACACCAATGGTCCAAGACCAGTTAAGAAAC	2370	3391	AATGAAACACCACCTGCCCCATTGATCTATACCAAGTTTGATGACATCTCTGGCAAAAGTCGAG	3450
QY	5309	AGCTACTACATCGGGCCGATGGCTCCTTGGGCTGCTGTGGCCAAACGGCATGGAGGTG	5368	6389	CAGTTTGGGAAGTTTGGTGTCAATTTACTATGACATTAACAGATCAACCAACAGCTGTC	6448
Db	2371	AGTTACCAGATTGGGTATGATGGTCCCTTCCCTTAGAATCTTCTATGCCAGTGGTCTGGACTCT	2430	3451	CAGTTTGGAAAAATTCGGAGTGATACTACTACGACATCAACCAAAATCAATTTCCACGGCCGTG	3510
QY	5369	CGCGTCGAGACTGAGCCCCACTTGTGGCTGGCACCGTCAACCCCAACCGTGGGCAAGAGG	5428	6449	ATGACCCACACCAAGCAATTTTGATGCATATGGCAGGATGAAGGAAGTGAGTATGAGATC	6508
Db	2431	CACCTACGACAGAGCCCCACGTTCTGGCTGGCAGCGGCGAATCCACAGTAGCCAAAAGA	2490	3511	ATGACTTATACAAAGCACTTTGATGCTCATGGCGGCATCAAGGAGATCCAATATGAGATA	3570
QY	5429	AATGTCACGCTGCCCATCGACAACGGCCCTCAACCTGGTGGAGTGGCGCCAGCGCAAAAGAG	5488	6509	TTCCGCTCGCTCATGTACTGTGATGACCGTCCAGTATGATAACATGGGCGAGTAGTGAAG	6568
Db	2491	AACATGACTCTTCCCGGTGAGAACGGGCAGAAATCTGGTGGAGTGGAGATTCCGAAAAAGAA	2550	3571	TTTAGGTCACATCATGTACTGGATTACAAATTCAAATATGATAATATGGGCCGGTAACCAAG	3630
QY	5489	CAGGCTCGGGCCAGGTCACTGTCTTTGGGCGCCGCTGCGGGTGCAACACGAAAAATCTC	5548	6569	AAGGAGCTGAAGTAGGACCCCTACGCCAATACCACCTCGCTACTCCTATGATATGATGCT	6628
Db	2551	CAAGCCAGGGCAAAAGTCAACGTATTTCGGCCGGAAGCTCAGGGTCAATGGGCGCAACCTA	2610	3631	AGAGAGATTAAAAATTTGGGCTTTTGGCCAACACTACCAAAATACGGTACGAGTACGACGTC	3690
QY	5549	CTATCTCTGGACTTTTGATCGCGTAACACGCACAGAGAAGATCTATGATGACCACCGCAAG	5608	6629	GACGCCAGCTGCAGACAGTCTCCATCAATGACAAGCCACTCTGGCGCTACAGCTTACGAC	6688
Db	2611	CTCTCAGTGGACTTTGATCGGACCACCAAGACGGAAGATCTATGATGACCACCGGAAA	2670	3691	GATGACAGCTCCAAACAGTTTACCTAAACGAAAAAGATCATGTGGCGGTACAACCTACGAC	3750
QY	5609	TTTACCCCTTCGGATTCTGTACGACCAAGGGGGGGCCAGCCCTCTGGTCAACCAGCAGC	5668	6689	CTCAATGGGAAACCTGCATTTACTGAGCCCTGGGAAACAGTGCACCGCTCACACCCTACCGG	6748
Db	2671	TTTCTCCTGAGGATCGTTTACGACAGCTCGGGGCACCCGACTCTCTGGCTGCCGAGTAGC	2730	3751	CTAAATGGAAACCTCCACTTGCTCAACCCCAAGCAGCAGCGCCCGCTGACCCCTCTGCGC	3810
QY	5669	AGGCTGAATGGTGTCAACGTGACATACTCCCTCCCTGGGGTTACATTTGCTGGCATCCAGAGG	5728	6749	TATGACATCCGCGACCGCATCACTCGGCTGGGTGACGTGCAATACAAGATGGATGAGGAT	6808
Db	2731	AAGCTAATGGCAGTGAACGTCACTACTCATCCACCGTCAAAATTTGCCAGCATCCAGAGA	2790	3811	TATGACCTGCGGACAGAAATACCCGCTGGCGCATGTTCAGTACCGGCTGGATGAAGAT	3870
QY	5729	GGCATCATGTCTGAAAGAANTGGAATAGACACAGCGGGCCCGCATCATCCAGGATCTTC	5788	6809	GGCTTCTTGAGGCAGCGGGCGGTGATATCTTTGAGTACAACCTCAGCTGGCCTGCTCATC	6868
Db	2791	GGGACCACGAGCGAAAAAGTGGACTATGACAGCCAGGGGAGGATCGTATCTCGGGTCTTT	2850	3871	GGTTTCTCTCGCTCAGAGGGGCACTGAAAATTTTGAATACAGTCCAAAGGGCTTCTGACT	3930
QY	5789	GCTGATGGGAAGACATGGAGCTACACATACTTAGAGAAAGTCCAATGGTGTCTGTACTACAC	5848	6869	AAGGCCTACAAACCGGCTGGCAGCTGGAGTGTCAAGGTACCGTACGATGGCCTGGGGCGG	6928
Db	2851	GCCGATGGGAAACATGGAGTTACACGTACTTGGAAAGTCCATGGTCTTCTGTCTCCAT	2910	3931	CGAGTCTACAGTAAAGGCAGTGGCTGGACAGTGTCTATCGGTACGACGGCTGGGAAGA	3990
QY	5849	AGCCAGAGGCAGTATATCTTTGAGTTCGACAAAGAATGACCGCCTCTCTCTGTGACGATG	5908	6929	CGCGTGTCCAGCAAGAGCAGCCACAGCCACCAACCTGCAGTTCCTCTATGCAGACCTGACC	6988
Db	2911	AGCCAGCGGCAGTACATCTTCGAATACGACATGTGGGACCGCTGTCCGCCATCACCATG	2970	3991	CGTGTTTCTAGCAAAACCGAGCCTGGGACAGCACCTTCAGTTTTTCTACGCCGACCTGACA	4050
QY	5909	CCCAACGTGGCGCGCAGACACTAGAGACCACTCCGCTCAGTGGGTACTACAGAAACATC	5968	6989	AACCCCAACCAAGGTCAACCCACCTGTACAAACCACTCCAGCTCTGAGATCACTCCCTCTAC	7048
Db	2971	CCCAGTGTGGCTCGCCACACCATGCAGACCCATCCGCTCCATTTGGCTACTACCGCAACATC	3030	4051	TACCCCAACGAGAAATTACTACGCTCTACAAACCATTCAGTTTCAGAAATCACCTCCCTGTAC	4110
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Db	3031	TACAAATCCCCAGAAAGCAATGCCTCTATCATCACCGACTACAACGAGGAAGGGTGTCTT	3090	4111	TATGACCTCCAAAGGACATCTCTTCGCCATGGAGATCAGCAGTGGGGATGAGTTCTACATC	4170
QY	6029	CTTCACACCTTCTACCTGGGCACTGGCCGCAAGGTGATATACAAGTATGGCAAACTGTCA	6088	7109	GCTTGTGACAAACATCGGACCCCTCTTTGCTGTCTTTAGTGGAAACAGGTTTGATGATCAAG	7168
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QY	6089	AAGCTGGCAGAGACGCTCTATGACACCAACCAAGGTCAAGTTTCACCTATGACGACGGCA	6148	7169	CAAAATCCTGTACACAGCCTATGGGGAGATCTACATGGATACCAACCCCAACTTTTCAGATC	7228
Db	3151	AGGCTATCAGAAAATTTTATACGACAGCACAAGAGTCAGTTTACCTACGACGAAACAGCG	3210	4231	CAGATCCAGTACACTGCCCTATGGTGAGATCTACTTTGACTCCAACGTCGACTTTTCAGCTG	4290
QY	6149	GGCATGCTGAAGACCATCAACTACAGAAATGAGGGCTTCACTGCCACCATCCGCTACCGT	6208	7229	ATCATAGGCTACCATGGTGGCCTCTATGATCCAATCACCAGCTTGTCCACATGSGCCGG	7288
Db	3211	GGAGTCTGAAAAACAGTAAACCTTCAGAGTATGGTATTATTGCAACCATTAGATACAGG	3270	4291	GTAATGGATTCCACGGGGCTGTATGACCCGCTCACCAAACTAATCCACTTTGGAGAA	4350
QY	6209	CAGATTGGCCCTTGATTGACCGACAGATCTTCCGCTTCACTGAGGAAGGCATGGTCAAC	6268	7289	CGAGATTATGATGTGCTGGCGGACGCTGGACTAGCCAGACCAACGAGCTGTGGAAAGCAC	7348
Db	3271	CAAAATGGTCCCTTGATTGACACAGAGATTTTCCGCTTCAGCGAGGATGGAATGGTAAAT	3330	4351	AGAGATTATGACATTTTGGCGGGAAGATGGACCACACCGGACATTTGAAATCTGGA---AA	4407
QY	6269	GCCCCGTTTGTACTACAACCTATGACAAACAGCTTCCGGGTGACCAAGCATGCAGGCTGTGATC	6328	7349	CTTAGTAGCAGCAACGTCATGCTTTTAAATCTCTATATGTTCAAAAAACAACCCCATC	7408
Db	3331	CGGAGATTTGACTATAGCTACGACAAACAGCTTTTCGAGTGACCAAGCATGCAGGGTGTCAATC	3390	4408	AGGATCGGAAAGGACCCCTGCTCTTTTAAACCTGTATATGTTTCGGAATAACAACCCCGCG	4467
				7409	AGCAACTCCAGGACATCAAGTGTTCATGACAGATGTTAAACAGCTGGCTGCTCACCTTT	7468



Db 4468 AGCAAATCCATGATGTGAAGATTACATCAGGATGTTAACAGCTGGCTGGTACGTTT 4527  
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Db 4528 GGCTTCCATCTGCACAATGCTATTCTCTGGATCCCTGTTCCCAAATTGATTAACTGAG 4587  
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Db 4588 CTTTCCTATGAGCTTGTGAAGAGTCA 4613

RESULT 8  
AK037897  
LOCUS AK037897 3038 bp mRNA linear HTC 03-APR-2004  
DEFINITION Mus musculus 16 days neonate thymus cDNA, RIKEN full-length enriched library, clone:Al30060L24 product:odd Oz/ten-m homolog 1 (Drosophila), full insert sequence.

ACCESSION AK037897  
VERSION AK037897.1 GI:26332325  
KEYWORDS HTC; CAP trapper.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1  
AUTHORS Carninci,P. and Hayashizaki,Y.  
TITLE High-efficiency full-length cDNA cloning  
JOURNAL Meth. Enzymol. 303, 19-44 (1999)  
PUBMED 10349636  
REFERENCE 2  
AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.  
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes  
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)  
PUBMED 11042159  
REFERENCE 3  
AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.  
TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer  
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)  
PUBMED 11076861  
REFERENCE 4  
AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.

TITLE Functional annotation of a full-length mouse cDNA collection  
JOURNAL Nature 409, 685-690 (2001)  
PUBMED 11076861  
REFERENCE 5  
AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.  
TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs  
JOURNAL Nature 420, 563-573 (2002)  
PUBMED 11076861  
REFERENCE 6  
AUTHORS Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T., Kato,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Nunazaki,R., Ohno,M., Ohsato,N., Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,

Muramatsu,M. and Hayashizaki,Y.  
Direct Submission  
Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)  
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.  
Please visit our web site for further details.  
URL:http://genome.gsc.riken.jp/  
URL:http://fantom.gsc.riken.jp/.  
FEATURES  
Location/Qualifiers  
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ORIGIN  
Query Match 16.9%; Score 1407.8; DB 4; Length 3038;  
Best Local Similarity 67.4%; Pred. No. 0;  
Matches 2014; Conservative 0; Mismatches 967; Indels 6; Gaps 2;  
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Qy 5662 CAGCAGCAGGCTGAATGGTGTCAACGTGACAFACCTCCCTGGGGGTTACATTGCTGGCAT 5721

Db 302 TGTGAGCAGATATAATGAAGTGAACATCACGTATTCACCTTCAGGAATTAGTCACATTTAT 361

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Db	1847	GAA-----GGACAGGTCAATTACTAAAAAAGCTCCACGCCAGCATCCGAGAGAAACAGGAT	1900
QY	7703	AAGAAGTTTGCATCCAGCGGCTCAGTCTTTGGCAAGGGGTCAAGTTTGCCTTGAAGGAT	7762
Db	1901	CACCTGGTTGCCACCACCAACGCCCATCATTTGGCAAAGGCATCATGTTGCCATCAAAGAA	1960
QY	7763	GGCCGAGTGACCACAGACATCATAGTGTGGCCAAATGAGGATGGCGAAGGGTTGCTGCC	7822
Db	1961	GGCGGGTGACCACCGGGGTGTCCAGCATCGCCAGCGAAGATAGCCGCAAGGTGGCATCT	2020
QY	7823	ATCTTGAAACATGCCCACTACCTAGAGAAACCTGCACCTTCAACATGATGGGTGGATACC	7882
Db	2021	GTGCTGAACAACGCCTACTACCTGGACAAGATGCACCTACAGCATCGAGGGCAAGGACACC	2080
QY	7883	CATTACTTTTGAAACCCAGGACCTTCAGAAGGTGACCTGGCCATCCTGGGCCCTCAGTGGG	7942
Db	2081	CACTACTTTGTGAAGATTGGCTCAGCCGATGGCGACCTGTGCCAGCATAGGCCACCATC	2140
QY	7943	GGCGGGCGAACCCCTGGAGAAATGGGGTCAACGTCACTGTGTCCAGATCAACACAGTACTT	8002
Db	2141	GGCCGCAAGGTGTAGAGAGCGGGGTGAACGTGACCGTGTGCCAGCCACGCTGCTGGTC	2200
QY	8003	AATGGCAGGACTAGACGCTACACAGACATCCAGCTCCAGTCCAGTACGGGCACTGTGCTTGAAC	8062
Db	2201	AACGGCAGGACTCGAAGGTTACGAAACATTGAGTTCAGTACTCCAGCTCTGCTGCACG	2260
QY	8063	ACACGCTACGG-----GACAACTTGATGAGGAGAAAGCAAGGCTCCTGGAGCTG	8113
Db	2261	ATCCGCTATGGCCTACCCCCGACACCCCTGGACGAAGAAAGGCCCGCTCCTGGACCA	2320
QY	8114	GCCTGGCAGAGAGCCGTGCGCCAAAGCGTGGGCCCGCAGCAGCAGAGACTCGGGAAGGG	8173
Db	2321	GCGAGACAGAGGGCCCTGGGCACGGCCTGGGCCAAGGACGACGAGAAAGCCAGGACGGG	2380
QY	8174	GAGGAAGCCCTGCGGGCCTGGACAGAGGGGGAAGCAGCAGGTGCTGACACAGGGCGG	8233
Db	2381	AGAGAGGGGAGCCGCTGTGGACTGAGGGCGAGAAGCAGCAGCTTCTGAGCACCGGGCGC	2440
QY	8234	GTGCAAGGCTACGACGGCTTTTTCGTGATCTCTGTGAGCAGTACCCAGAACTGTGACAC	8293
Db	2441	GTGCAAGGGTACGAGGGGATATTACGTGCTTCCCGTGGAGCAATACCCAGAGCTTCAGAC	2500
QY	8294	AGGCCCAACATCCACTTCATGACAGAGCGGAGATGGGCCGAGGTGACAGA	8348
Db	2501	AGTAGAGCAACATCCAGTTTAAAGACAGAAATGAGATGGGAAAGAGGTAACAAA	2555

RESULT 10  
AK039472  
LOCUS  
DEFINITION

AK039472	1284 bp	mRNA	linear	HTC 03-APR-2004
Mus musculus adult male spinal cord cDNA, RIKEN full-length				
enriched library, clone:A330048C04 product:neuregulin 1, full				

ACCESSION AK039472  
VERSION AK039472.1 GI:26087188  
KEYWORDS HTC; CAP trapper.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muridae; Murinae; Mus.  
1  
REFERENCE Carninci,P. and Hayashizaki,Y.  
AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,  
TITLE Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.  
JOURNAL Normalization and subtraction of cap-trapper-selected cDNAs to  
PUBMED prepare full-length cDNA libraries for rapid discovery of new genes  
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)  
REFERENCE 11042159  
2  
AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,  
TITLE Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.  
JOURNAL Normalization and subtraction of cap-trapper-selected cDNAs to  
PUBMED prepare full-length cDNA libraries for rapid discovery of new genes  
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)  
REFERENCE 11042159  
3  
AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,  
TITLE Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,  
JOURNAL Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,  
PUBMED Yamamoto,H., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,  
AUTHORS Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,  
TITLE Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,  
JOURNAL Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.  
PUBMED RIKEN integrated sequence analysis (RISA) system--384-format  
REFERENCE sequencing pipeline with 384 multicapillary sequencer  
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)  
PUBMED 11076861  
4  
AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the  
TITLE FANTOM Consortium.  
JOURNAL Functional annotation of a full-length mouse cDNA collection  
REFERENCE Nature 409, 685-690 (2001)  
5  
AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research  
TITLE Group Phase I & II Team.  
JOURNAL Analysis of the mouse transcriptome based on functional annotation  
REFERENCE of 60,770 full-length cDNAs  
AUTHORS Nature 420, 563-573 (2002)  
6  
TITLE (bases 1 to 1284)  
JOURNAL Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P.,  
REFERENCE Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W.,  
AUTHORS Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T.,  
TITLE Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T.,  
JOURNAL Kato,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M.,  
REFERENCE Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M.,  
AUTHORS Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N.,  
TITLE Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N.,  
JOURNAL Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,  
REFERENCE Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S.,  
AUTHORS Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,  
TITLE Muramatsu,M. and Hayashizaki,Y.  
JOURNAL Direct Submission  
REFERENCE Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of  
AUTHORS Physical and Chemical Research (RIKEN), Laboratory for Genome  
TITLE Exploration Research Group, RIKEN Genomic Sciences Center (GSC),  
JOURNAL RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,  
REFERENCE Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp,  
AUTHORS URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,  
TITLE Fax:81-45-503-9216)  
JOURNAL cDNA library was prepared and sequenced in Mouse Genome  
REFERENCE Encyclopedia Project of Genome Exploration Research Group in Riken  
AUTHORS Genomic Sciences Center and Genome Science Laboratory in RIKEN.  
TITLE Division of Experimental Animal Research in Riken contributed to  
JOURNAL prepare mouse tissues.  
REFERENCE Please visit our web site for further details.  
AUTHORS URL:http://genome.gsc.riken.jp/  
TITLE URL:http://fantom.gsc.riken.jp/.

FEATURES		Location/Qualifiers	
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		/dev_stage="adult"	
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Query Match	8.9%;	Score 743.8;	DB 4; Length 1284;
Best Local Similarity	86.3%;	Pred. No. 5.5e-177;	
Matches	845;	Conservative 0;	Mismatches 107; Indels 27; Gaps 1;
QY	2195	GGACACGACTGTTCTATCGAGATCTGTGCTGCCGACTGTGGTGGCCATGGCGTGTGCGTA	2254
Db	80	GGACAACACCGAAACCCAGATCTGTGCCGCTGACTGTGGTGGCCATGGCGTGTGCGTA	139
QY	2255	GGGGGCACCTGCCGCTGCGAGGATGGCTGGATGGGGGCGAGCCTGCGACCGAGCGGCGCTGC	2314
Db	140	GGAGGCACCTGCCGCTGTGAGGATGGTTGGATGGGGCCGCATGCGACCAACGGGCCTGC	199
QY	2315	CACCCGCGCTGTGCCGAGCATGGGACCTGCCGCGACGGCAAGTGCAGTGCAGCCCTGGC	2374
Db	200	CACCCACGCTGTGCAGAACACCGGACCTGCCGGGACGGCAAGTGCAGATGCAGCCCCGGC	259
QY	2375	TGGAATGGCGAAACACTGCACCATCGCTCACTATCTGGATAGGGTAGTTAAAGAGGGTTGC	2434
Db	260	TGGAATGGAGAGCACTGCACCATC-----GAGGGCTGT	292
QY	2435	CCTGGGTTGTGCAATGGCAACGGCAGATGTACCTTAGACCTGAATGGTTGGCACTGCGTC	2494
Db	293	CCTGGCTTGTGCAATGGAAATGGCAGATGTACCTTGACCTGAATGGGTGGCACTGTGTC	352
QY	2495	TGCCAGCTGGGCTGGAGAGGAGCTGGCTGTGACACATTCATGGAGACTGCTTGGGTGAC	2554
Db	353	TGCCAGCTGGGCTGGCAGGGGACTGGCTGCGACACATCCATGGAAACGGGCTGTGGAGAC	412
QY	2555	AGCAAAGACAATGATGGAGATGGCCTGGTGGACTGCATGGACCCCTGACTGCTGCCCTCCAG	2614
Db	413	GGCAAGGACAACGACGGAGATGGCTTGGTGGACTGCATGGACCCCTGACTGCTGCCCTCCAG	472
QY	2615	CCCCTGTGCCATATCAACCCGCTGTGCCTTGGCTCCCCTAACCCCTCTGGACATCATCCAG	2674
Db	473	CTCTCTGTGTCATGTCAACCCGCTGTGCCTAGGCTCCCCTGACCCCTTGGACATCATCCAA	532
QY	2675	GAGACACAGGTCCCTGTGTACAGCAGAACCTACACTCCTTCTATGACCCGCATCAAGTTC	2734
Db	533	GAGACACAGGCCCTGTATCCCAGCAGAACCTGAACTCCTTCTACGATCGAATCAAGTTC	592
QY	2735	CTCGTGGGCAGGGACAGCACGACATAATCCCCGGGGAGAACCCCTTTGATGGAGGGCAT	2794
Db	593	CTCGTGGGCAGGGACAGCACACAGCATCCCCGGGGAGAACCCCTTTGACGGAGGGCAT	652
QY	2795	GCTTGTGTTATTCGTGGCCAAAGTATGATGACATCAGATGGAACCCCCCTTGGTGTGTAAC	2854
Db	653	GCTTGTGTGTCATCCGTGGACAAGTATGACGTGAGATGGGACCCCATTTGGTGTGCGTGAAC	712
QY	2855	ATCAGTTTGTCAATAACCCCTCTCTTTGGATATACAATCAGCAGGCAAGATGGCAGCTTT	2914
Db	713	ATCAGTTTCATCAATAACCCCTCTCTTTGGATACACAATCAGCAGGCAAGATGGCAGCTTT	772
QY	2915	GACTTGGTGACAAATGGCGGCATCTCCATCATCTTCCGTTTCGAGCGGGCACCTTTTCATC	2974
Db	773	GACCTGGTCACAAATGGCGGCATCTCCATCATCTTGAGATTCGAAAGGGCACCTTTCATC	832

QY	2975	ACACAGGAGCACACCCCTGTGGCTGCCATGGGATCGCTTCTTTGTCTATGGAACCAACCATCATC	3034
Db	833	ACACAGGAGCATACCCCTCTGGCTACCCCTGGGATCGCTTCTTTGTCTATGGAACCAACCATCGTC	892
QY	3035	ATGAGACATGAGGAGAATGAGATTCCACGCTGTGACCTGAGCAATTTTGCCCGCCCCAAC	3094
Db	893	ATGAGACACGAGGAGAATGAGATCCCCAGCTGTGACCTGAGCAACTTTGCCCGTCCCAAC	952
QY	3095	CCAGTCGTCTCTCCATCCCCACTGACGTCTTGGCCAGCTCCTGTGCAGAGAAAGGCCCC	3154
Db	953	CCTGTGGTCTCTCCATCCCCACTGACATCCTTCGCCAGTCTCCTGTGTGAGAAAGGCCCC	1012
QY	3155	ATTGTGCCGGAATTTCAGG	3173
Db	1013	ATTGTCCCAGAAATCCAGG	1031
RESULT 11			
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LOCUS	AL045768	718 bp	mRNA
DEFINITION	DKFZp434F206_r1 434 (synonym: htes3) Homo sapiens cDNA clone		
ACCESSION	AL045768		
VERSION	AL045768.1	GI:5433880	
KEYWORDS	EST.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.			
REFERENCE	1	(bases 1 to 718)	
AUTHORS	Koehler,K., Beyer,A., Mewes,H.W., Gassenhuber,J. and Wiemann,S.		
TITLE	EST (Koehler, et al.)		
JOURNAL	Unpublished (1999)		
COMMENT	Contact: MIPS		
MIPS			
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany			
This is the 5' sequence of the clone insert			
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz- heidelberg.de;			
sequenced by BMFZ (Biomedical Research Center at the Charite, Berlin/Germany) within the cDNA sequencing consortium of the German Genome Project.			
s1 sequence also available.			
This clone (DKFZp434F206) is available at the RZPD in Berlin.			
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.			
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Matches 715; Conservative 0; Mismatches 2; Indels 0; Gaps 0;			
QY	7431	GCTTCATGACAGATGTTAAACAGCTGGCTGCTCACCTTTGGATTCCAGCTACACAACGTGA	7490
Db	1	GCTTCATGACAGATGTTAAACAGCTGGCTGCTCACCTTTGGATTCCAGCTACACAACGTGA	60
QY	7491	TCCCTGGTTATCCCAACCCAGACATGGATGCCATGGAAACCTCTACGAGCTCATCCACA	7550
Db	61	TCCCTGGTTATCCCAACCCAGACATGGATGCCATGGAAACCTCTACGAGCTTATCCACA	120
QY	7551	CACAGATGAAAAACGCAGGAGTGGGACACAGCAAGTCTATCCTCGGGGTACAGTGTGAAG	7610

Db	121	CACAGATGAAAAACGCAGGAGTGGGACACAGCAAGTCTATCCTCGGGGTACAGTGTGAAG	180
QY	7611	TACAGAAGCAGCTCAAGGCCCTTTGTCACTTAGAACGGTTTGACCAGCTCTATGGTCCA	7670
Db	181	TACAGAAGCAGCTCAAGGCCCTTTGTCACTTAGAACGGTTTGACCAGCTCTATGGTCCA	240
QY	7671	CAATCACCAAGTGCACGAGGCTCCAAAGACCAAGAAAGTTTGCATCCAGCGGCTCAGTCT	7730
Db	241	CAATCACCAAGTGCACGAGGCTCCAAAGACCAAGAAAGTTTGCATCCAGCGGCTCAGTCT	300
QY	7731	TTGGCAAGGGGTCAAGTTTGCCTTGAAGGATGGCCGAGTGACCAACAGACATCATCAGTG	7790
Db	301	TTGGCAAGGGGTCAAGTTTGCCTTGAAGGATGGCCGAGTGACCAACAGACATCATCAGTG	360
QY	7791	TGGCCAATGAGGATGGCGAAGGGTTGCTGCCATCTTGAACCATGCCCACTACCTAGAGA	7850
Db	361	TGGCCAATGAGGATGGCGAAGGGTTGCTGCCATCTTGAACCATGCCCACTACCTAGAGA	420
QY	7851	ACCTGCACCTTCACCATTTGATGGGGTGGATACCCATTTTGTGTAACCCAGGACCTTCAG	7910
Db	421	ACCTGCACCTTCACCATTTGATGGGGTGGATACCCATTTTGTGTAACCCAGGACCTTCAG	480
QY	7911	AAGGTGACCTGGCCATCCTGGCCCTCAGTGGGGGGCGGCGAACCCCTGGAGAATGGGTCA	7970
Db	481	AAGGTGACCTGGCCATCCTGGCCCTCAGTGGGGGGCGGCGAACCCCTGGAGAATGGGTCA	540
QY	7971	ACGTCACTGTGTCCCAGATCAACACAGTACTTAAATGGCAGGACTAGACGCTACACAGACA	8030
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QY	8031	TCCAGCTCCAGTACGGGGCACTGTCTTGAACACACACGCTACGGGCAACCGTTGGATGAGG	8090
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QY	8091	AGAAGGCACCGGTCTCTGGAGCTGCCCCGGCAGAGAGCCGTGCGCAAGCGTGGGCC	8147
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RESULT 12			
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LOCUS	UI-M-G10-chg-a-23-0-UI.r1 NIH_BMAP_G10		linear
DEFINITION	IMAGE:30536758 5', mRNA sequence.		
ACCESSION	CF534506		
VERSION	CF534506.1	GI:34586474	
KEYWORDS	EST.		
SOURCE	Mus musculus (house mouse)		
ORGANISM	Mus musculus		
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.			
REFERENCE	1	(bases 1 to 856)	
AUTHORS	NIH-MGC	http://mgc.nci.nih.gov/.	
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)		
JOURNAL	Unpublished (1999)		
COMMENT	Contact: Robert Strausberg, Ph.D.		
	Email: cgapbs-r@mail.nih.gov		
	Tissue Procurement: Dr. Jim Lin, University of Iowa		
	cDNA Library preparation: Dr. M. Bento Soares, University of Iowa		
	DNA Sequencing Arrayed by: Dr. M. Bento Soares, University of Iowa		
	Clone Distribution: Distribution information can be found at		
	http://genome.uiowa.edu/distribution/mousefl.html		
	This clone was contributed by the Brain Molecular Anatomy Project (BMAP)		
FEATURES	Seq primer: pYX-5.		
source	Location/Qualifiers		
	1..856		
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	/mol_type="mRNA"		
	/strain="C57BL/6"		





Tissue Procurement: Dr. James Lin, Univeristy of Iowa  
cDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa  
cDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa  
DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa  
Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
This clone was contributed by the Brain Molecular Anatomy Project (BMAP)

FEATURES  
source

Seq primer: pYX-5.  
Location/Qualifiers  
1. .827  
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/clone="IMAGE:5690214"  
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/dev\_stage="embryo 18.5 dpc"  
/lab\_host="DH10B (T1 phage resistant)"  
/clone\_lib="NIH BMAP\_EG0p"  
/note="Organ: brain; Vector: pYX-Asc; Site 1: EcoR I; Site 2: Not I; The library was constructed according to Bonaïdo, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured mRNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with Not I, and then cloned directionally into pYX-Asc vector. The library tag sequence located between the Not I site and the polyA tail, is CAGCCACGAC. This library was created for the University of Iowa Mouse Brain Molecular Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH), Hemin Chin, Ph.D., program coordinator."

ORIGIN

	Query Match	7.6%;	Score	630.8;	DB	3;	Length	827;
	Best Local Similarity	89.3%;	Pred. No.	2.6e-148;				
	Matches	734;	Conservative	0;	Mismatches	81;	Indels	7;
	Gaps	5;						
QY	6504	AGATCTTCGGCTCATGTACTGGATGACCGTCCAGTATGATAACATGGGCGGAGTAG	6563					
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QY	6564	TGAAGAAGGAGCTGAAGTAGGACCCCTACGCCAATACCACCTCGCTACTCCTATGAGTATG	6623					
Db	61	TGAAGAAGGAGCTGAAGTGGGACCCCTATGCCAACTACCTACCCGCTACTCCTATGAGTATG	120					
QY	6624	ATGCTGACGGCCAGCTGCAGACAGTCTCCATCAATGACAAGCCACTCTGGCGCTACAGCT	6683					
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QY	6684	ACGACCTCAATGGGAACCTGCACCTTACTGAGCCCTGGGAACAGTGCACGGCTCACACCAC	6743					
Db	181	ATGACCTCAATGGGAACCTACACTTGCTGAGCCCTGGGAACAGCGCACGGCTCACACCAC	240					
QY	6744	TACGGTATGACATCCGCGACCGCATCACTCGGCTGGTGACGTGCAATACAAGATGGATG	6803					
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QY	6804	AGGATGGCTTCCTGAGGCAGCGGGCGGTGATATCTTTGAGTACAACCTCAGCTGGCCTGC	6863					
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QY	6924	GGCGGCGCTGTCCAGCAAGAGCAGCCACAGCCACCACCTGCAGTTCTTCTATGCAGACC	6983					
Db	421	GACGCCGAGTATCCAGCAAGAGCAGCCACAGCCACCACCTGCAGTTCTTCTACGCAGACC	480					

QY	5833	GGTGCTGCTACTACACAGCCAGAGGAGTATATCTTTTGAGTTGCGACAAGATGACCGCCT	5892					
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QY	5893	CTCTTCTGTGACGATGCCAACAGTGGCGCGGACACACTAGAGACCATCCGCTCAGTGGG	5952					
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QY	5953	CTACTACAGAAACATCTATCAGCCCCCTTGAGGGCAATGCCTCAGTCAATCAGGACTTCAC	6012					
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QY	6013	TGAGGATGGGCACCTCCTTCACACCTTCTACCTGGGCACCTGGCCGACAGTGGGTGATATACAA	6072					
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QY	6073	GTATGGCAAACTGTCAAAGCTGGCAGAGACGCTCTATGACACACCACCAAGGTCAGTTTCAC	6132					
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Db	301	CTACGACGAGACCGCAGGGATGCTGAAGACTGTCAACCTACAGAATGAGGGCTTCACCTG	360					
QY	6193	CACCATCCGTACCGTCAGATTGGGCCCTGATTGACCGCAGACATCTTCGGCTTCACTGA	6252					
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QY	6253	GGAAGGCATGTTCAACGCCCGTTTGACTACAACATATGACAACAGCTTCGGGTGACCAG	6312					
Db	421	AGAAGGCATGTTCAATGCCCGTTTGTGATTACAACACTATGACAACAGTTTCCGTGTGACTAG	480					
QY	6313	CATGCAGGCTGTGATCAACGAGACCCCACTGCCCATTTGATCTCTATCGCTATGATGATGT	6372					
Db	481	CATGCAGGCTGTGATCAATGAGACCCCACTGCCCATTTGACCTCTACCGCTATGATGATGT	540					
QY	6373	GTCAGGCAAGACAGACAGCAGTTTGGGAAGTTTGGTGTCAATTTACTATGACATTAACAGAT	6432					
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QY	6433	CATCACCACAGCTGTCAATGACCCACACCAAGCATTTTGATGCAATATGGCAGGATGAAGGA	6492					
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QY	6493	AGTGCAGTATGAGATCTTCGGCTCGTCACTGATGACTGATGACCGTCCAGTATGATAACAT	6552					
Db	661	AGTACAGTATGAGATTTTCGGGTCACTCATGTACTGGATGACTGTTTCAGTATGATAACAT	720					
QY	6553	GGGGCGAGTAGTGAAGAAGGAGCTGAAGGTAGGACCCTACGC	6594					
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RESULT 14	BM947883	827 bp	mRNA	linear	EST 14-MAR-2002
LOCUS	UI-M-EG0p-bvc-j-07-0-UI.r1	NIH BMAP_EG0p	Mus musculus	cDNA clone	
DEFINITION	IMAGE:5690214 5', mRNA sequence.				
ACCESSION	BM947883				
VERSION	BM947883.1	GI:19431473			
KEYWORDS	EST.				
SOURCE	Mus musculus (house mouse)				
ORGANISM	Mus musculus				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;				
	Sciurognathi; Muridea; Muridae; Murinae; Mus.				
REFERENCE	1 (bases 1 to 827)				
AUTHORS	NIH-MGC <a href="http://mgc.nci.nih.gov/">http://mgc.nci.nih.gov/</a> .				
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)				
JOURNAL	Unpublished (1999)				
COMMENT	Contact: Robert Strausberg, Ph.D. Email: <a href="mailto:cgaps-r@mail.nih.gov">cgaps-r@mail.nih.gov</a>				

QY 6984 TGACCAACCCACCAAGGTCACCCACCTGTACAACTCCAGCTCCAGCTCTGAGATCACCTCCC 7043  
Db 481 TGACCAACCCACCAAGGTCACCCACCTCTACAACTCCAGCTCCAGCTCTGAGATACATCCC 540  
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Db 661 TTAAGCAGATCCTATACACGGGCTATGGGAGATCTACATGGACA-CANACCCANCTTCC 719  
QY 7224 AGATCATATAGGCTACCATGGTGGCCTCTATGATCCACTCACCAAGCTTGTCACATGG 7283  
Db 720 AGATCATCATCGGCTA-CACGGCGNCTCTATGAT---CACTCACANGCTTGTACATGG 775  
QY 7284 GCCGGCGAGATTATGATGTGCTGGCCGGACGCTGGACTAGCC 7325  
Db 776 GCCGACGGGA-TATGATGTGTGGCTGG-CGCTGGACAAGCC 815

RESULT 15  
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DEFINITION 602326960F1 NIH\_MGC\_91 Homo sapiens cDNA clone IMAGE:4428351 5',  
mRNA sequence.  
ACCESSION BG036207  
VERSION BG036207.1 GI:12431132  
KEYWORDS EST.  
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ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
REFERENCE 1 (bases 1 to 870)  
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: [cgabbs-r@mail.nih.gov](mailto:cgabbs-r@mail.nih.gov)  
Tissue Procurement: DCTD/DTP  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: LLAM10178 row: h column: 16  
High quality sequence stop: 713.  
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/lab\_host="DH10B (phage-resistant)"  
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/note="Organ: prostate; Vector: pCMV-SPORT6; Site 1: NotI;  
Site 2: SalI; Cloned unidirectionally; oligo-dT primed.  
Average insert size 1.4 kb. Library enriched for  
full-length clones and constructed by Life Technologies.  
Note: this is a NIH\_MGC Library."

FEATURES  
source  
1. .870  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:4428351"  
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/note="Organ: prostate; Vector: pCMV-SPORT6; Site 1: NotI;  
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Average insert size 1.4 kb. Library enriched for  
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Note: this is a NIH\_MGC Library."

ORIGIN

Query Match 7.5%; Score 629; DB 2; Length 870;  
Best Local Similarity 98.2%; Pred. No. 7.5e-148;  
Matches 700; Conservative 0; Mismatches 5; Indels 8; Gaps 6;

QY 904 AGGCACCTCCCGCTCTTCTGCACCACATCACAGGGTACCCACTGACGTCAGCACAGT 963  
Db 1 AGGCACCTCCCGCTCTTCTGCACCACATCACCA-GGTACCCACTGACGTCAGCACAGT 59  
QY 964 GTACTCTCCTCCGCCCCGACCCCTGCCCGCAGCACCTTCGCCCGCGCCTTTAACTT 1023  
Db 60 GTACTCTCCTCCGCCCCGACCCCTGCCCGCAGCACCTTCGCCCGCGCCTTTAACTT 119  
QY 1024 CAAGAAGCCCTCCAAGTACTGTAACTGGAACTGCGCAGCCCTGAGCGCCATCGTCATCTC 1083  
Db 120 CAAGAAGCCCTCCAAGTACTGTAACTGGAACTGCGCAGCCCTGAGCGCCATCGTCATCTC 179  
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